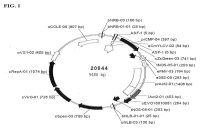
Industria y Comercio
SUPERINTENDENCIA

Radicación	14 108302 0000 0000	2014-05-20 14:08:32	
Trámite	11	PCT-PATENTE DE INVENCION CAPITULOS I Y II	
Evento	378	FASE NACIONAL INCLUIDO CAPITULO I	
Actuación	411	PRESENTACION	Folios: 94
Dependencia	2020	DIRECCION DE NUEVAS CREACIONES	
Pago #1	52976	$ 182150.0	
Pago #2	52977	$ 1102250	

DIRECCIÓN DE NUEVAS CREACIONES
SOLICITUD FASE NACIONAL - PCT



1	**Titulo de la Invención**(200 caractares o espacios máximos)			
	COMPOSICIONES Y MÉTODOS PARA INCREMENTAR LA RESISTENCIA A NEMATODOS EN PLANTAS			
2	**Datos del Solicitante / Titular**			
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	Dirección:	Schwarzwaldallee 215, Basilea (CH4058) SUIZA	**Domicilio/País de constitución:**	SUIZA - BASEL-STADT - BASILEA
	Identificación: ☐ CEDULA DE CIUDADANIA ☐ CEDULA DE EXTRANJERIA ☒ EMPRESA EXTRANJERA ☐ NIT ☐ PASAPORTE **Número:** 90004808961-			
3	**Solicitantes**			

	Apellidos - Nombres o Razón Social	Tipo	Identificación
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Identificación:

☐ CEDULA DE CIUDADANIA ☐ CEDULA DE EXTRANJERIA
☐ EMPRESA EXTRANJERA ☐ NIT
☐ PASAPORTE ☒ No Aplica

Número: -

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Identificación:

☒ CEDULA DE CIUDADANIA ☐ CEDULA DE EXTRANJERIA
☐ EMPRESA EXTRANJERA ☐ NIT
☐ PASAPORTE

Número: 39779654-

Presentación de Poder

Año de Radicación	
Número de Radicación	

8	**Datos Solicitud: PCT / WO**		
Número Solicitud:	PCT/US2012/065959	**Fecha Solicitud:**	20/11/2012
Número Publicacion:	WO 2013/078153 A1	**Fecha Publicacion:**	30/05/2013

9	**Declaraciones de prioridad**	☒ SI ☐ NO

	(33) País de origen	**Codigo del país**	**(31) No. Solicitud**	**(32) Fecha**
1.	ESTADOS UNIDOS DE AMÉRICA	US	61/562,060	21/11/2011
2.	ESTADOS UNIDOS DE AMÉRICA	US	61/684,234	17/08/2012

10	Reivindicaciones			
Número reivindicaciones:		37	**Pago Reivindicaciones:**	Si

11	Reducción de tasas.

Declaro que carezco de medios económicos para presentar la solicitud de patente.

☐ SI ☒ NO

Nota: En caso de ser persona natural y carecer de medios económicos, y por lo tanto, aplique la reducción de tasas a que se refiere la resolucón vigente en tarifas, debe firmar la presente solicitud bajo la gravedad de juramento.

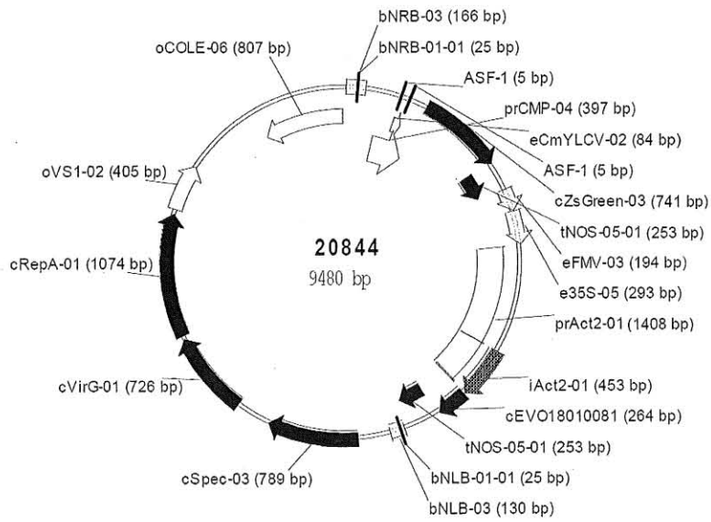
☐ Micro, pequeñas y medianas empresas
☐ Universidades públicas o privadas
☐ Entidades sin ánimo de lucro

Debe aportar los documentos que se indican en el numeral 17 de anexos

12	Documentos Anexos

☒ Reivindicaciones
☒ Descripción
☐ Dibujos y/o Figuras
☒ Resumen
☐ Certificado Depósito Material Biológico
☐ Uso de Conocimiento tradicional
☒ Listado de secuencias
☒ Artes finales 12 x 12 cm
☒ Poderes, si fuere el caso
☐ Copia de la primera solicitud si se reivindica prioridad
☐ Traducción simple de la primera solicitud, si se reivindica prioridad
☒ Otros Anexos

FIG. 1


bNRB-03 (166 bp)
bNRB-01-01 (25 bp)
ASF-1 (5 bp)
prCMP-04 (397 bp)
eCmYLCV-02 (84 bp)
ASF-1 (5 bp)
cZsGreen-03 (741 bp)
tNOS-05-01 (253 bp)
eFMV-03 (194 bp)
e35S-05 (293 bp)
prAct2-01 (1408 bp)
iAct2-01 (453 bp)
cEVO18010081 (264 bp)
tNOS-05-01 (253 bp)
bNLB-01-01 (25 bp)
bNLB-03 (130 bp)
cSpec-03 (789 bp)
cVirG-01 (726 bp)
cRepA-01 (1074 bp)
oVS1-02 (405 bp)
oCOLE-06 (807 bp)
20844
9480 bp

COMPOSICIONES Y MÉTODOS PARA INCREMENTAR LA RESISTENCIA A NEMATODOS EN PLANTAS

DECLARACIÓN SOBRE LA PRESENTACIÓN EN FORMATO ELECTRÓNICO DE UNA LISTA DE SECUENCIAS

Se proporciona una Lista de secuencias en formato de texto ASCII, presentada según 37 C.F.R. § 1.821, titulada 9207-58WO_ST25.txt, con un tamaño de 3 013 855 bytes, generada el 14 de noviembre de 2012 y presentada a través de EFS-Web, en lugar de una copia impresa. Por lo tanto, esta lista de secuencias se incorpora a la presente a modo de referencia en la memoria descriptiva para su divulgación.

DECLARACIÓN DE PRIORIDAD

Esta solicitud reivindica el beneficio de la Solicitud Provisional de EE. UU. N.º 61/562.060, presentada el 21 de noviembre de 2011, y de la Solicitud Provisional de EE. UU. N.º 61/684.234, presentada el 17 de agosto de 2012, cuyos contenidos se incorporan a la presente en su totalidad a modo de referencia.

CAMPO DE LA INVENCIÓN

La invención se refiere a composiciones y métodos para controlar plagas de nematodos en plantas.

ANTECEDENTES

Los nematodos son gusanos redondos simétricos y alargados que constituyen uno de los filos más abundantes y prósperos del reino animal. Muchas especies de nematodos viven en libertad y se alimentan de bacterias, mientras que otras han evolucionado en forma de plagas o parásitos de plantas y animales, incluidos los seres humanos.

Las plagas de nematodos en plantas son responsables de pérdidas económicas de muchos miles de millones de dólares anualmente. Las plagas de nematodos que atacan plantas se alimentan de los tallos, brotes, hojas y, en particular, raíces de más de 2000 hortalizas, frutas y plantas ornamentales, y provocan una pérdida de los cultivos a nivel mundial estimada en 100-125 mil millones de dólares. Los nematodos están presentes en diferentes partes de los Estados Unidos (EE. UU.), pero suponen un problema principalmente en áreas húmedas cálidas del sur y el oeste, así como también en terrenos arenosos. La plaga de nematodos que atacan plantas más perjudicial desde el punto de vista económico pertenece a la familia *Heterderidae* del orden *Tylenchida*, e incluye los nematodos que inducen quistes [géneros *Heterodera* y *Globodera*, p. ej., nematodos que inducen quistes en la soja (*Heterodera glycines*, SCN, por sus siglas en inglés) y nematodos que inducen quistes en la papa (*G. pallida* y G*. rostochiensis*)] y los nematodos noduladores de raíz (género *Meloidogyne*).

Los nematodos noduladores de raíz infestan miles de especies de plantas diferentes, que incluyen hortalizas, frutas y cultivos en hilera. Existe constancia de que los nematodos que inducen quistes infestan cultivos de tabaco, cereales, remolachas azucareras, papas, arroz, maíz, soja y muchos otros cultivos. *Heterodera schachtii* (BCN) ataca principalmente a las remolachas azucareras y *Heterodera avenae* es una plaga de los cereales. *Heterodera zeae* se alimenta de maíz, y *Globodera rostochiensis* y *G. pallida* se alimentan de papas. El nematodo que induce quistes en la soja (SCN, por sus siglas en inglés) está presente en todos los estados productores de soja de los EE. UU., y provoca pérdidas totales del rendimiento de la soja estimadas cerca de mil millones de dólares cada año. Una vez que el SCN está presente en un campo, no es posible erradicarlo empleando métodos conocidos. Aunque la soja es el cultivo de mayor importancia económica atacado por el SCN, dicho SCN ataca un total de cincuenta huéspedes, que incluyen cultivos de campo, hortalizas, plantas ornamentales y maleza.

El nematodo nodulador de raíz (RKN, por sus siglas en inglés) del algodón es un nematodo destructivo que forma agallas en las raíces de las plantas de algodón. El agente causante es *Meloidogyne incognita* (Kofoid y White) Chitwood, un nematodo que puede infestar varias especies de plantas. En las plantas infestadas se reduce la absorción de agua y nutrientes, y las plantas se pueden volver vulnerables a patógenos, especialmente a la fusariosis. Como consecuencia, en las plantas infestadas con RKN se reduce el rendimiento. Solo en los EE. UU., se estima que un 10.93% de la pérdida de rendimiento del algodón en 2004 se atribuyó a RKN (Blasingame y Patel, Proceedings of the Beltwide Cotton Conferences 1:259-262, 2005). El RKN se ha extendido a lo largo de toda la franja algodonera de los EE. UU. Los métodos para mitigar los daños del RKN incluyen alternar los cultivos de algodón con cultivos que no sean susceptibles y aplicar nematicidas de elevado costo. Sin embargo, el modo más eficaz para los productores de algodón de reducir la pérdida de rendimiento y los daños de los cultivos debidos a RKN consiste en desarrollar cultivares de algodón resistentes a RKN.

Los síntomas del daño provocado por los nematodos incluyen la atrofia y clorosis de las hojas, así como también el marchitamiento de las plantas durante periodos cálidos. Sin embargo, los nematodos, incluidos los SCN, pueden provocar una pérdida significativa del rendimiento sin síntomas evidentes en la superficie. Por ejemplo, una infestación de SCN en una planta puede provocar enanismo o atrofia de las raíces, una reducción del número de nódulos fijadores de nitrógeno en las raíces y/o puede hacer que las raíces sean más vulnerables al ataque por parte de otros patógenos o plagas de plantas que se transmiten por el suelo.

A diferencia del caso de muchos patógenos víricos y bacterianos, existe poca información sobre la base molecular de la interacción nematodo-planta, lo que limita las estrategias disponibles útiles para el control de nematodos. Los agentes químicos útiles para el control de plagas de nematodos que atacan plantas incluyen organofosfatos y carbamatos, la clase más antigua existente de nematicidas, los cuales actúan sobre la acetilcolinesterasa. Los derivados de tipo imidazol, tales como el bencimidazol, ejercen sus efectos nematicidas uniéndose a la tubulina. El levimasol actúa como agonista sobre el receptor nicotínico para la acetilcolina, y las avermectinas actúan como agonistas irreversibles en los canales de cloruro regulados por glutamato. Desafortunadamente, existen ciertas infestaciones de nematodos debilitantes que son difíciles de erradicar, si no imposible, con las medidas de control existentes. Además, los agentes para el control de nematodos disponibles actualmente presentan inconvenientes en cuanto a la eficacia, el costo y la seguridad medioambiental. Por ejemplo, el bromuro de metilo, que es un fumigante eficaz para el suelo antes de plantar empleado para controlar nematodos en muchos cultivos de gran valor y con gran uso de insumos en los EE. UU., se está eliminando gradualmente debido a cuestiones medioambientales y relacionadas con la salud humana. Sin embargo, debido a que el bromuro de metilo ha proporcionado una rentabilidad estable para el control de nematodos, muchos productores de cultivos de gran valor se podrían ver afectados negativamente si no se identifican alternativas eficaces y económicas. Además, ciertas cuestiones medioambientales, principalmente la contaminación de aguas subterráneas, la destrucción de la capa de ozono y los residuos pesticidas en alimentos, han suscitado la retirada de Aldicarb, DGBCP y otros nematicidas tóxicos del mercado por parte de la Agencia de Protección del Medioambiente de los EE. UU. Se han utilizado medidas de control físico (tales como solarización y tratamiento con agua caliente), medidas de control biológico (p. ej., alternación de cultivos) y estrategias integradas para mejorar los daños provocados por las plagas de nematodos que atacan plantas, pero ningún método ni combinación de medidas resulta uniformemente eficaz.

Las plantas transgénicas y el plasma germinal resistentes a nematodos también han sido considerados como alternativas o complementos para las medidas de control químico. Por ejemplo, las plantas transgénicas que expresan un inhibidor de proteasas muestran cierta resistencia a nematodos que inducen quistes y nematodos noduladores de raíz (Urwin *et al.* 1997. *Plant J.* 12:455-461). El uso de tales medidas alternativas de control requiere un mayor conocimiento de la interacción nematodo-planta para obtener resultados satisfactorios. Varios estudios han generado datos de expresión génica que sugieren que muchos genes de plantas huésped se sobreexpresan o subexpresan como respuesta a la invasión de nematodos (Szakasits *et al.* 2009. *Plant J.* 57:771-784; Puthoff

et al. 2003. *Plant J.* 33:911-921; Bethke *et al.* 2009. *Proc. Natl. Acad. Sci.* 106:8067-8072; Stepanova *et al.* 2007. *Plant Cell* 19:2169-2185 y Kilian *et al.* 2007. *Plant J.* 50:347-363). Sin embargo, ninguno de estos estudios puede ayudar a un experto a la hora de predecir cuál de estos genes, si alguno, podría utilizarse con éxito para controlar nematodos, particularmente en constructos de genes quiméricos para emplear en plantas transgénicas.

Por consiguiente, la invención resuelve las deficiencias de la técnica proporcionando composiciones y métodos que comprenden moléculas de ácido nucleico recombinante y sus polipéptidos codificados para el control de infestaciones de plagas de nematodos en plantas.

COMPENDIO DE LA INVENCIÓN

Las necesidades descritas anteriormente quedan cubiertas por la invención, la cual, en varias realizaciones, proporciona composiciones y métodos nuevos para controlar plagas de nematodos importantes desde el punto de vista económico. En particular, se ha descubierto que las plantas y/o partes de plantas transgénicas que expresan al menos una molécula de ácido nucleico recombinante de la invención, la cual modula la expresión de las proteínas de la invención, reducen la capacidad de las plagas de nematodos para sobrevivir, desarrollarse y reproducirse, o limitan las pérdidas o los daños relacionados con los nematodos de las plantas transgénicas. La invención también se refiere a plantas transgénicas resistentes a nematodos que sobreexpresan o que presentan una expresión reducida de una proteína de la invención en la planta trasngénica y a métodos para emplear las plantas transgénicas solos o combinados con otras medidas de control de nematodos para conferir la máxima eficacia en el control de nematodos con un impacto medioambiental reducido. Las plantas y partes de plantas transgénicas que tienen una proteína de la invención sobreexpresada o inhibida (p. ej., una cantidad reducida y/o una actividad reducida y similares, en comparación con un control) son más tolerantes o resistentes a la infestación de plagas de nematodos. Por ejemplo, una plaga de nematodos importante desde el punto de vista económico, el nematodo que induce quistes en la soja (*Heterodera glycines*), se puede controlar mediante plantas de soja transgénicas que sobreexpresan una proteína de la invención o que comprenden una molécula de ácido nucleico de la invención que reduce la expresión de una proteína de la invención.

En un aspecto de la invención, se proporciona un método para controlar una plaga de nematodos que atacan plantas, comprendiendo el método poner en contacto la plaga de nematodos con una planta transgénica, o una de sus partes, que ha incorporado a su genoma una molécula de ácido nucleico recombinante que modula la expresión de uno o

más polipéptidos que tienen la secuencia de aminoácidos de **SEQ ID NOs:29-42**, **SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046** o cualquier combinación de estas, con lo que se controla la plaga de nematodos que atacan plantas. En otro aspecto de la invención, la molécula de ácido nucleico recombinante es capaz de producir un ARN bicatenario que comprende una hebra antisentido y una hebra sentido, donde la hebra antisentido es complementaria respecto a una porción de una secuencia de nucleótidos que codifica dichos polipéptidos, donde la porción comprende, está constituida esencialmente por o está constituida por de aproximadamente 18 a aproximadamente 25 nucleótidos consecutivos con identidad sustancial respecto a cualquiera de las secuencias de nucleótidos de **SEQ ID NOs:1-28**, **SEQ ID NOs:43-134**, **SEQ ID NOs:210-242, SEQ ID NOs:261-664** o cualquier combinación de estas.

En otro aspecto más de la invención, se proporciona una molécula de ácido nucleico recombinante, comprendiendo la molécula de ácido nucleico una secuencia de nucleótidos unida operativamente a un promotor que funciona en una planta o célula vegetal, donde la secuencia de nucleótidos es: (a) una secuencia de nucleótidos de cualquiera de **SEQ ID NOs:1-28**, **SEQ ID NOs:43-134**, **SEQ ID NOs:210-242, SEQ ID NOs:261-664**; (b) una secuencia de nucleótidos que codifica un polipéptido que comprende la secuencia de aminoácidos de cualquiera de **SEQ ID NOs:29-42**, **SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046**; (c) una secuencia de nucleótidos que presenta al menos un 70% de identidad secuencial respecto a la secuencia de nucleótidos de (a) y (b) anteriores; (d) una secuencia de nucleótidos que se aparea en condiciones rigurosas de hibridación con la secuencia de nucleótidos de (a), (b) o (c); (e) una secuencia de nucleótidos que difiere de las secuencias de nucleótidos de (a), (b), (c) o (d) anteriores debido a la degeneración del código genético; o (f) cualquier combinación de las secuencias de nucleótidos de (a)-(e).

En otro aspecto de la invención, se proporciona un polipéptido, donde el polipéptido comprende, está constituido esencialmente por o está constituido por una secuencia de aminoácidos de cualquiera de **SEQ ID NOs:29-42**, **SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046** o cualquier combinación de estas.

En un aspecto adicional de la invención, se proporciona un método para producir una célula vegetal transgénica, que comprende introducir en una célula vegetal una molécula de ácido nucleico recombinante, comprendiendo la molécula de ácido nucleico recombinante una secuencia de nucleótidos unida operativamente a un promotor que funciona en una planta o célula vegetal, donde la secuencia de nucleótidos es: (a) una secuencia de nucleótidos de cualquiera de **SEQ ID NOs:1-28**, **SEQ ID NOs:43-134**, **SEQ ID NOs:210-242, SEQ ID NOs:261-644**; (b) una secuencia de nucleótidos que codifica un

polipéptido que comprende la secuencia de aminoácidos de cualquiera de las secuencias de aminoácidos de **SEQ ID NOs:29-42**, **SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046**; (c) una secuencia de nucleótidos que presenta al menos un 70% de identidad secuencial respecto a la secuencia de nucleótidos de (a) y (b) anteriores; (d) una secuencia de nucleótidos que se aparea en condiciones rigurosas de hibridación con la secuencia de nucleótidos de (a), (b) o (c); (e) una secuencia de nucleótidos que difiere de las secuencias de nucleótidos de (a), (b), (c) o (d) anteriores debido a la degeneración del código genético; o (f) cualquier combinación de las secuencias de nucleótidos de (a)-(e), con lo que se produce una célula vegetal transgénica que puede regenerar una planta con una mayor resistencia a una plaga de nematodos que atacan plantas.

Un aspecto adicional más de esta invención proporciona un método para producir una planta de soja con mayor resistencia a la infestación por parte de una plaga de nematodos que atacan plantas, comprendiendo el método los pasos de (a) cruzar la planta transgénica de la invención consigo misma o con otra planta para producir una semilla que comprenda la molécula de ácido nucleico de esta invención o el vector de la invención; (b) cultivar una planta de la progenie a partir de dicha semilla para producir una planta con mayor resistencia a la infestación por parte de plagas de nematodos que atacan plantas.

En aspectos adicionales de la invención, se proporcionan células vegetales transgénicas, plantas transgénicas y partes de estas que comprenden una molécula de ácido nucleico que comprende una o más secuencias de nucleótidos de la invención, y métodos para emplearlas con el fin de controlar, suprimir y/o reducir la capacidad infecciosa de una plaga de nematodos que atacan plantas. Además, se proporcionan polipéptidos de la invención y métodos para emplearlos con el fin de controlar, suprimir y/o reducir la capacidad infecciosa, la infestación y/o el desarrollo de quistes de una plaga de nematodos que atacan plantas, que comprenden poner en contacto una plaga de nematodos que atacan plantas con una cantidad eficaz del o los polipéptidos. En algunas realizaciones, la puesta en contacto de la plaga de nematodos que atacan plantas con una cantidad eficaz de un polipéptido comprende poner en contacto la plaga de nematodos que atacan plantas con una planta transgénica que comprende una molécula de ácido nucleico de la invención.

La invención proporciona adicionalmente un cultivo que comprende una pluralidad de plantas transgénicas de la invención plantadas conjuntamente en un campo agrícola. En algunos aspectos, la invención proporciona un método para mejorar el rendimiento de un cultivo vegetal que está en contacto con una plaga de nematodos que atacan plantas, comprendiendo el método cultivar una pluralidad de plantas que comprenden una

molécula de ácido nucleico de la invención como cultivo vegetal, donde la pluralidad de plantas de dicho cultivo vegetal tiene una mayor resistencia a la infección de nematodos, con lo que se mejora el rendimiento de dicho cultivo vegetal.

La invención proporciona además un método para mejorar el rendimiento de un cultivo que está en contacto con una plaga de nematodos que atacan plantas, comprendiendo el método poner en contacto la plaga de nematodos que atacan plantas con una cantidad eficaz del polipéptido de la invención o la composición nematicida de la invención, donde se mejora el rendimiento del cultivo.

Estos y otros aspectos de la invención se exponen con más detalle en la descripción de la invención a continuación.

BREVE DESCRIPCIÓN DE LAS FIGURAS

La **Figura 1** es un vector binario útil para transformar plantas y/o células vegetales con una molécula de ácido nucleico recombinante de la invención.

La **Figura 2** es un vector vacío útil como control negativo en experimentos de transformación de plantas y/o células vegetales.

La **Figura 3** es un vector binario útil para transformar plantas y/o células vegetales con una molécula de ácido nucleico recombinante de la invención.

La **Figura 4** es un vector vacío útil como control negativo en experimentos de transformación de plantas y/o células vegetales.

La **Figura 5** es una ilustración esquemática del plásmido binario pGI modificado que contiene el promotor At6669 y el intrón GUS (pQYN 6669), el cual se puede utilizar para expresar las secuencias de polinucleótidos aisladas de la invención. RB – borde derecho del ADN-T; LB – borde izquierdo del ADN-T; MCS – sitio de clonación múltiple; RE – cualquier enzima de restricción; NOS pro = promotor de nopalina-sintasa; NPT-II = gen de la neomicina-fosfotransferasa; NOS ter = terminador de nopalina-sintasa; señal de Poli-A (señal de poliadenilación); intrón GUS – gen marcador GUS (secuencia codificante e intrón). En algunas realizaciones, las secuencias de polinucleótidos aisladas de la invención se clonaron en el vector a la vez que se reemplazó el gen marcador del intrón GUS.

La **Figura 6** es una ilustración esquemática del plásmido binario pGI modificado que contiene el promotor At6669 (pQFN o pQFNc) utilizado para expresar las secuencias de polinucleótidos aisladas de la invención. RB – borde derecho del ADN-T; LB – borde izquierdo del ADN-T; MCS – sitio de clonación múltiple; RE – cualquier enzima de restricción; NOS pro = promotor de nopalina-sintasa; NPT-II = gen de la neomicina-fosfotransferasa; NOS ter = terminador de nopalina-sintasa; señal de Poli-A (señal de poliadenilación); intrón GUS – gen marcador GUS (secuencia codificante e intrón). En

algunas realizaciones, las secuencias de polinucleótidos aisladas de la invención se clonaron en el MCS del vector.

La **Figura 7** es una ilustración esquemática del plásmido pQXNc, el cual es un plásmido binario pGI modificado utilizado para expresar las secuencias de polinucleótidos aisladas de algunas realizaciones de la invención. RB – borde derecho del ADN-T; LB – borde izquierdo del ADN-T; NOS pro = promotor de nopalina-sintasa; NPT-II = gen de la neomicina-fosfotransferasa; NOS ter = terminador de nopalina-sintasa; RE = cualquier enzima de restricción; señal de Poli-A (señal de poliadenilación); 35S – el promotor 35S. En algunas realizaciones, las secuencias de polinucleótidos aisladas se clonaron en el MCS (sitio de clonación múltiple) del vector.

BREVE DESCRIPCIÓN DE LAS SECUENCIAS DE LA LISTA DE SECUENCIAS

Las **SEQ ID NOs:1-14** son secuencias de nucleótidos de la invención que comprenden regiones no traducidas y regiones codificantes.

Las **SEQ ID NOs:15-28** son secuencias codificantes de la invención que codifican las secuencias de aminoácidos de **SEQ ID NOs:29-42**.

Las **SEQ ID NOs:29-42** son secuencias de aminoácidos de proteínas de la invención que, cuando se sobreexpresan o inhiben en plantas transgénicas, confieren tolerancia o resistencia a nematodos.

Las **SEQ ID NOs:43-134** son secuencias de nucleótidos que codifican las secuencias de aminoácidos de **SEQ ID NOs: 29-42, 135-209**.

Las **SEQ ID NOs:135-209** son secuencias de aminoácidos de homólogos de **SEQ ID NOs:29-42**.

Las **SEQ ID NOs: 210-223** son secuencias de nucleótidos de la invención que comprenden regiones no traducidas y regiones codificantes.

Las **SEQ ID NOs:224-242** son secuencias codificantes de la invención que codifican las secuencias de aminoácidos de **SEQ ID NOs:243-260**.

Las **SEQ ID NOs: 243-260** son secuencias de aminoácidos de proteínas de la invención que, cuando se sobreexpresan o se reduce su cantidad o actividad en plantas transgénicas, confieren tolerancia o resistencia a nematodos.

Las **SEQ ID NOs:261-664** son secuencias de nucleótidos de la invención que codifican homólogos de las **SEQ ID NOs:210-242**.

Las **SEQ ID NOs:665-1046** son secuencias de aminoácidos de proteínas de la invención que, cuando se sobreexpresan o se reduce su cantidad o actividad en plantas transgénicas, confieren tolerancia o resistencia a nematodos.

DESCRIPCIÓN DETALLADA DE LA INVENCIÓN

Esta descripción no pretende ser un catálogo detallado de todas las diferentes formas en que se puede implementar la invención ni de todas las características que se pueden añadir a la presente invención. Por ejemplo, las características ilustradas con relación a una realización se pueden incorporar a otras realizaciones y las características ilustradas con relación a una realización particular se pueden eliminar de dicha realización. De este modo, la invención contempla el hecho de que, en algunas realizaciones de la invención, se puede excluir u omitir cualquier característica o combinación de características expuestas en la presente. Además, para los expertos en la técnica resultarán evidentes numerosas variaciones y adiciones para las diversas realizaciones sugeridas en la presente que no se alejen de la presente invención, teniendo en cuenta la presente divulgación. Por lo tanto, las siguientes descripciones pretenden ilustrar algunas realizaciones particulares de la invención y no pretenden especificar exhaustivamente todas sus permutaciones, combinaciones y variaciones.

A menos que se defina de otro modo, todos los términos técnicos y científicos empleados en la presente tienen el mismo significado que el que sobreentienden habitualmente los expertos en la técnica a la que pertenece esta invención. La terminología utilizada en la descripción de la invención en la presente tiene como propósito describir realizaciones particulares únicamente y no pretende limitar la invención.

Todas las publicaciones y solicitudes de patente mencionadas en esta memoria descriptiva son indicativas del nivel de experiencia de los expertos en la técnica a la que se refiere esta invención. Además, las publicaciones, solicitudes de patente, patentes y otras referencias mencionadas en la presente se incorporan a modo de referencia en su totalidad.

Se pretende que las formas en singular "un/a", "el/la", tal como se utilizan en la descripción de las realizaciones de la invención y las reivindicaciones adjuntas, también incluyan las formas en plural, a menos que el contexto indique claramente lo contrario.

La expresión "y/o", tal como se utiliza en la presente, engloba y se refiere a todas y cada una de las combinaciones posibles de uno o más de los elementos enumerados asociados.

Se pretende que el término "aproximadamente", tal como se utiliza en la presente, cuando se refiera a un valor medible tal como una cantidad de un compuesto, dosis, tiempo, temperatura y similares, englobe variaciones de un 20%, 10%, 5%, 1%, 0.5% o incluso un 0.1% de la cantidad especificada.

Los términos "comprenden", "comprende" y/o "que comprende/n", cuando se utilizan en esta memoria descriptiva, especifican la presencia de características, números

enteros, pasos, operaciones, elementos y/o componentes mencionados, pero no excluyen la presencia o adición de una o más características, números enteros, pasos, operaciones, elementos, componentes y/o grupos de estos.

La frase de transición "constituido/a esencialmente por" (y variantes gramaticales), tal como se utiliza en la presente, se refiere a que se debe considerar que el alcance de una reivindicación contempla los materiales o pasos especificados que se mencionan en la reivindicación y aquellos que no afectan materialmente a la o las características básicas y novedosas de la invención reivindicada. Por lo tanto, cuando se utilice la expresión "constituido/a esencialmente por" en una reivindicación de esta invención no se pretende que se considere como equivalente a "que comprende".

La invención se refiere en parte al descubrimiento de que el hecho de modular la expresión mediante la sobreexpresión o la reducción de la expresión en una planta de al menos un polipéptido descrito en la presente puede dar como resultado que la planta presente una mayor resistencia a plagas de nematodos. El término "modular" o "que modula", en el contexto de la invención, se refiere a una alteración de la expresión de una proteína de la invención mediante la sobreexpresión de la proteína o la reducción de la expresión de la proteína.

Por consiguiente, en una realización, la invención proporciona un método para controlar una plaga de nematodos que atacan plantas que comprende poner en contacto la plaga de nematodos con una planta transgénica, o una de sus partes, que ha incorporado a su genoma una molécula de ácido nucleico recombinante que modula la expresión de uno o más polipéptidos que tienen cualquiera de las secuencias de aminoácidos de **SEQ ID NOs:29-42**, **SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046** o cualquier combinación de estas, con lo que se controla la plaga de nematodos que atacan plantas. En otra realización, la molécula de ácido nucleico recombinante comprende una secuencia de nucleótidos unida operativamente a un promotor heterólogo que funciona en una planta o célula vegetal, donde la secuencia de nucleótidos comprende, está constituida esencialmente por o está constituida por: (a) una secuencia de nucleótidos de cualquiera de **SEQ ID NOs:1-28**, **SEQ ID NOs:43-134**, **SEQ ID NOs:210-242, SEQ ID NOs:261-644**; (b) una secuencia de nucleótidos que codifica un polipéptido que comprende una secuencia de aminoácidos de cualquiera de **SEQ ID NOs:29-42**, **SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046**; (c) una secuencia de nucleótidos que presenta al menos un 70% de identidad secuencial respecto a la secuencia de nucleótidos de (a) o (b); (d) una secuencia de nucleótidos que se aparea en condiciones rigurosas de hibridación con la secuencia de nucleótidos de (a), (b) o (c), o un complemento de estas; (e) una secuencia de nucleótidos que difiere de las

secuencias de nucleótidos de (a), (b), (c) o (d) anteriores debido a la degeneración del código genético; y (f) cualquier combinación de las secuencias de nucleótidos de (a)-(e). En realizaciones más particulares, la secuencia de nucleótidos puede comprender, estar constituida esencialmente por o estar constituida por: (a) una secuencia de nucleótidos de cualquiera de **SEQ ID NOs:15, 17, 20, 22, 23, 24, 26, 226, 227, 228, 230, 232**, **233**; (b) una secuencia de nucleótidos que codifica un polipéptido que comprende una secuencia de aminoácidos de cualquiera de **SEQ ID NOs:29-38**, **40-42, 52, 243, 244, 245, 246, 248-252, 254, 256-259**; (c) una secuencia de nucleótidos que presenta al menos un 70% de identidad secuencial respecto a la secuencia de nucleótidos de (a) o (b); (d) una secuencia de nucleótidos que se aparea en condiciones rigurosas de hibridación con la secuencia de nucleótidos de (a), (b) o (c), o un complemento de estas; (e) una secuencia de nucleótidos que difiere de las secuencias de nucleótidos de (a), (b), (c) o (d) anteriores debido a la degeneración del código genético; y (f) cualquier combinación de las secuencias de nucleótidos de (a)-(e). En realizaciones adicionales, la secuencia de nucleótidos puede comprender, estar constituida esencialmente por o estar constituida por: (a) una secuencia de nucleótidos de cualquiera de **SEQ ID NOs: 56-63, 66-127, 389-401, 408-633, 637-642**; (b) una secuencia de nucleótidos que codifica un polipéptido que comprende una secuencia de aminoácidos de cualquiera de **SEQ ID NOs: 56-63, 66-127, 389-401, 408-633, 637-642**; (c) una secuencia de nucleótidos que presenta al menos un 70% de identidad secuencial respecto a la secuencia de nucleótidos de (a) o (b); (d) una secuencia de nucleótidos que se aparea en condiciones rigurosas de hibridación con la secuencia de nucleótidos de (a), (b) o (c), o un complemento de estas; (e) una secuencia de nucleótidos que difiere de las secuencias de nucleótidos de (a), (b), (c) o (d) anteriores debido a la degeneración del código genético; y (f) cualquier combinación de las secuencias de nucleótidos de (a)-(e).

En otra realización más, la molécula de ácido nucleico recombinante es capaz de producir un ARN bicatenario que comprende una hebra antisentido y una hebra sentido, donde la hebra antisentido es complementaria respecto a una porción de una secuencia de nucleótidos que codifica dichos polipéptidos, donde la porción comprende, está constituida esencialmente por o está constituida por de aproximadamente 18 a aproximadamente 25 nucleótidos consecutivos (p. ej., aproximadamente 18, 19, 20, 21, 22, 23, 24 o 25 nucleótidos consecutivos) con identidad sustancial respecto a cualquiera de las secuencias de nucleótidos de **SEQ ID NOs:1-28**, **SEQ ID NOs:43-134**, **SEQ ID NOs:210-242, SEQ ID NOs:261-644** o cualquier combinación de estas. En otra realización más, la molécula de ácido nucleico recombinante modula la expresión de dichos polipéptidos de la invención (p. ej., **SEQ ID NOs:29-42**, **SEQ ID NOs:135-209,**

SEQ ID NOs:243-260, SEQ ID NOs:665-1046) provocando la sobreexpresión de dichos polipéptidos en la planta transgénica. En otra realización, la molécula de ácido nucleico recombinante modula la expresión de dichos polipéptidos de la invención (p. ej., **SEQ ID NOs:29-42**, **SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046**) provocando la reducción de o reduciendo la expresión de dichos polipéptidos en la planta transgénica.

En otra realización, la planta o parte de planta transgénica de la invención es una planta de soja transgénica, una planta de remolacha azucarera transgénica, una planta de maíz transgénica, una planta de algodón transgénica, una planta de canola transgénica, una planta de trigo transgénica, una planta de caña de azúcar transgénica o una planta de arroz transgénica, o una de sus partes.

En otra realización más, la plaga de nematodos se selecciona del grupo constituido por: un nematodo que induce quistes (*Heterodera* spp.), un nematodo nodulador de raíz (*Meloidogyne* spp.), un nematodo lanza (*Hoplolaimus* spp.), un nematodo estilete (*Tylenchorhynchus* spp.), un nematodo en espiral (*Helicotylenchus* spp.), un nematodo lesionador (*Pratylenchus* spp.), un nematodo de aguijón (*Belonoluimus* spp.), un nematodo reniforme (*Rotylenchulus reniformis*), un nematodo barrenador (*Radopholus similis*), un nematodo anillado (*Criconema* spp.) y cualquier combinación de estos. En otra realización, el nematodo es un nematodo que induce quistes en la soja o un nematodo que induce quistes en la remolacha azucarera.

La sobreexpresión o la expresión reducida de un polipéptido descrito en la presente puede dar como resultado que la planta presente una mayor resistencia a las plagas de nematodos que atacan plantas. De este modo, en un aspecto, la invención proporciona una molécula de ácido nucleico recombinante que comprende una o más (p. ej., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15 y similares) secuencias de nucleótidos, cada una de las cuales, cuando se expresa en una planta, le confiere una mayor resistencia a una plaga de nematodos que atacan plantas, donde dichas secuencias de nucleótidos comprenden, están constituidas esencialmente por o están constituidas por: (a) una secuencia de nucleótidos de cualquiera de **SEQ ID NOs:1-28**, **SEQ ID NOs:43-134**, **SEQ ID NOs:210-242, SEQ ID NOs:261-644**; (b) una secuencia de nucleótidos que codifica un polipéptido que comprende, está constituido esencialmente por o está constituido por la secuencia de aminoácidos de cualquiera de **SEQ ID NOs:29-42**, **SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046**; (c) una secuencia de nucleótidos que presenta al menos un 70% de identidad secuencial respecto a la secuencia de nucleótidos de (a) y (b) anteriores; (d) una secuencia de nucleótidos que se aparea en condiciones rigurosas de hibridación con la secuencia de nucleótidos de (a), (b)

o (c); (e) una secuencia de nucleótidos que difiere de las secuencias de nucleótidos de (a), (b), (c) o (d) anteriores debido a la degeneración del código genético; o (f) cualquier combinación de las secuencias de nucleótidos de (a)-(e). En realizaciones más particulares, las secuencias de nucleótidos pueden comprender, estar constituidas esencialmente por o estar constituidas por: (a) una secuencia de nucleótidos de cualquiera de **SEQ ID NOs:15, 17, 20, 22, 23, 24, 26, 226, 227, 228, 230, 232**, **233**; (b) una secuencia de nucleótidos que codifica un polipéptido que comprende, está constituido esencialmente por o está constituido por la secuencia de aminoácidos de cualquiera de **SEQ ID NOs: 29, 31, 34, 36-38, 40, 244-246, 250, 251**; (c) una secuencia de nucleótidos que presenta al menos un 70% de identidad secuencial respecto a la secuencia de nucleótidos de (a) y (b) anteriores; (d) una secuencia de nucleótidos que se aparea en condiciones rigurosas de hibridación con la secuencia de nucleótidos de (a), (b) o (c); (e) una secuencia de nucleótidos que difiere de las secuencias de nucleótidos de (a), (b), (c) o (d) anteriores debido a la degeneración del código genético; o (f) cualquier combinación de las secuencias de nucleótidos de (a)-(e). En realizaciones adicionales, las secuencias de nucleótidos pueden comprender, estar constituidas esencialmente por o estar constituidas por: (a) una secuencia de nucleótidos de cualquiera de **SEQ ID NOs: 56-63, 66-127, 389-401, 408-633, 637-642**; (b) una secuencia de nucleótidos que codifica un polipéptido que comprende, está constituido esencialmente por o está constituido por la secuencia de aminoácidos de cualquiera de **SEQ ID NOs: 56-63, 66-127, 389-401, 408-633, 637-642**; (c) una secuencia de nucleótidos que presenta al menos un 70% de identidad secuencial respecto a la secuencia de nucleótidos de (a) y (b) anteriores; (d) una secuencia de nucleótidos que se aparea en condiciones rigurosas de hibridación con la secuencia de nucleótidos de (a), (b) o (c); (e) una secuencia de nucleótidos que difiere de las secuencias de nucleótidos de (a), (b), (c) o (d) anteriores debido a la degeneración del código genético; o (f) cualquier combinación de las secuencias de nucleótidos de (a)-(e).

En algunas realizaciones, además de las secuencias de nucleótidos descritas previamente, una molécula de ácido nucleico de la invención puede comprender una o más secuencias de nucleótidos que confieran una mayor resistencia a la planta frente a una plaga de nematodos que atacan plantas cuando se expresan en la planta, donde dichas secuencias de nucleótidos comprenden, están constituidas esencialmente por o están constituidas por: una secuencia de nucleótidos de cualquiera de **SEQ ID NOs:1-28**, **SEQ ID NOs:43-134**, **SEQ ID NOs:210-242, SEQ ID NOs:261-644** o cualquier combinación de estas. En algunas realizaciones particulares, una molécula de ácido nucleico de la invención puede comprender una o más secuencias de nucleótidos que

confieran una mayor resistencia a la planta frente a una plaga de nematodos que atacan plantas cuando se expresan en la planta, donde dichas secuencias de nucleótidos comprenden, están constituidas esencialmente por o están constituidas por: una secuencia de nucleótidos de cualquiera de **SEQ ID NOs: 15, 17, 20, 22, 23, 24, 26, 226, 227, 228, 230, 232**, **233** o cualquier combinación de estas.

De este modo, en algunas realizaciones, la invención proporciona una molécula de ácido nucleico recombinante que comprende una o más secuencias de nucleótidos, donde dichas secuencias de nucleótidos comprenden, están constituidas esencialmente por o están constituidas por: (a) una secuencia de nucleótidos de cualquiera de **SEQ ID NOs:1-28**, **SEQ ID NOs:43-134**, **SEQ ID NOs:210-242, SEQ ID NOs:261-644**; (b) una secuencia de nucleótidos que codifica un polipéptido que comprende, está constituido esencialmente por o está constituido por la secuencia de aminoácidos de cualquiera de **SEQ ID NOs:29-42**, **SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046**; (c) una secuencia de nucleótidos que presenta una identidad secuencial significativa respecto a una secuencia de nucleótidos de (a), (b) anteriores; (d) una secuencia de nucleótidos que se aparea en condiciones rigurosas de hibridación con la secuencia de nucleótidos de (a)-(c) anteriores; (e) una secuencia de nucleótidos que difiere de las secuencias de nucleótidos de (a)-(d) anteriores debido a la degeneración del código genético; o (f) cualquier combinación de las secuencias de nucleótidos de (a)-(e).

En algunas realizaciones de la invención, se proporcionan secuencias de nucleótidos que presentan una identidad secuencial significativa respecto a las secuencias de nucleótidos de la invención. La expresión "identidad secuencial significativa" o "similitud secuencial significativa" se refiere a al menos aproximadamente un 70%, 75%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% y/o 100% de identidad o similitud con otra secuencia de nucleótidos. De este modo, en realizaciones adicionales, la "identidad secuencial significativa" o "similitud secuencial significativa" se refiere a un intervalo comprendido entre aproximadamente un 70% y aproximadamente un 100%, entre aproximadamente un 75% y aproximadamente un 100%, entre aproximadamente un 80% y aproximadamente un 100%, entre aproximadamente un 81% y aproximadamente un 100%, entre aproximadamente un 82% y aproximadamente un 100%, entre aproximadamente un 83% y aproximadamente un 100%, entre aproximadamente un 84% y aproximadamente un 100%, entre aproximadamente un 85% y aproximadamente un 100%, entre aproximadamente un 86% y aproximadamente un 100%, entre aproximadamente un 87% y aproximadamente un 100%, entre aproximadamente un 88% y aproximadamente un 100%, entre aproximadamente un 89% y aproximadamente un

100%, entre aproximadamente un 90% y aproximadamente un 100%, entre aproximadamente un 91% y aproximadamente un 100%, entre aproximadamente un 92% y aproximadamente un 100%, entre aproximadamente un 93% y aproximadamente un 100%, entre aproximadamente un 94% y aproximadamente un 100%, entre aproximadamente un 95% y aproximadamente un 100%, entre aproximadamente un 96% y aproximadamente un 100%, entre aproximadamente un 97% y aproximadamente un 100%, entre aproximadamente un 98% y aproximadamente un 100% y/o entre aproximadamente un 99% y aproximadamente un 100% de identidad o similitud con otra secuencia de nucleótidos. Por consiguiente, en algunas realizaciones, una secuencia de nucleótidos de la invención es una secuencia de nucleótidos que presenta una identidad secuencial significativa respecto a la secuencia de nucleótidos de cualquiera de **SEQ ID NOs:1-28**, **SEQ ID NOs:43-134**, **SEQ ID NOs:210-242, SEQ ID NOs:261-644.** En algunas realizaciones particulares, una secuencia de nucleótidos de la invención es una secuencia de nucleótidos que presenta una identidad secuencial significativa respecto a la secuencia de nucleótidos de cualquiera de **SEQ ID NOs:15, 17, 20, 22, 23, 24, 26, 226, 227, 228, 230, 232** y/o **233.**

En algunas realizaciones de la invención, las secuencias de nucleótidos y/o las moléculas de ácido nucleico de la invención se pueden expresar para producir polipéptidos, cada uno de los cuales, cuando es producido en una planta, da como resultado una mayor resistencia a una plaga de nematodos que atacan plantas. De este modo, en otros aspectos de la invención, se proporciona un polipéptido, donde el polipéptido comprende, está constituido esencialmente por o está constituido por una secuencia de aminoácidos de cualquiera de **SEQ ID NOs:29-42**, **SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046,** donde la producción de dicho polipéptido en una planta da como resultado una mayor resistencia de la planta frente a una plaga de nematodos que atacan plantas.

Un aspecto adicional más de la invención es una composición nematicida que comprende uno o más polipéptidos de la invención. En algunas realizaciones, la composición comprende un polipéptido que comprende, está constituido esencialmente por o está constituido por una secuencia de aminoácidos de cualquiera de **SEQ ID NOs:29-42**, **SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046** o cualquier combinación de estas.

En algunas realizaciones, un polipéptido de la invención comprende, está constituido esencialmente por o está constituido por una secuencia de aminoácidos que presenta una identidad de al menos un 70%, p. ej., una identidad de al menos un 70%, 75%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%,

94%, 95%, 96%, 97%, 98%, 99% y/o 100% respecto a una secuencia de aminoácidos de cualquiera de **SEQ ID NOs:29-42**, **SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046**.

Los polipéptidos de la invención se pueden producir en, y obtener a partir de, células transformadas con las moléculas de ácido nucleico que comprenden las secuencias de nucleótidos de la invención. Por consiguiente, los polipéptidos se pueden aislar y proporcionar en una composición de la invención como un polipéptido de longitud completa parcial o totalmente purificado, o como un fragmento o variante activa de este, o el polipéptido se puede proporcionar como un extracto celular o lisado celular a partir de la célula o células de un organismo que produce dicho(s) polipéptido(s). En cualquier caso, no se requiere que la purificación sea completa. El polipéptido, variante o fragmento de este puede tener una pureza de al menos aproximadamente un 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% (p/p) o superior.

En algunas realizaciones, un polipéptido o una secuencia de nucleótidos de la invención puede ser una variante modificada de forma conservativa. La expresión "variante modificada de forma conservativa", tal como se utiliza en la presente, se refiere a polipéptidos y secuencias de nucleótidos que contienen sustituciones, deleciones o adiciones individuales que modifican, añaden o suprimen un único aminoácido o nucleótido o un pequeño porcentaje de aminoácidos o nucleótidos en la secuencia, donde la modificación da como resultado la sustitución de un aminoácido por un aminoácido químicamente similar. En la técnica se conocen bien las tablas de sustituciones conservativas que proporcionan aminoácidos funcionalmente similares.

Tal como se utiliza en la presente, una variante modificada de forma conservativa de un polipéptido es biológicamente activa y, por consiguiente, posee la actividad deseada del polipéptido de referencia (p. ej., confiere una mayor resistencia a una plaga de nematodos que atacan plantas, reduce el crecimiento de una plaga de nematodos que atacan plantas, reduce el desarrollo de quistes inducidos por nematodos), según se describe en la presente. La variante puede ser el resultado, por ejemplo, de un polimorfismo genético o manipulación humana. Una variante biológicamente activa del polipéptido de referencia puede tener una identidad o similitud secuencial de al menos un 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% o superior (p. ej., una identidad o similitud secuencial comprendida entre aproximadamente un 40% y aproximadamente un 99% o superior, y cualquier intervalo comprendido en el anterior) respecto a la secuencia de aminoácidos del polipéptido de referencia según se determine con programas de alineamiento de

secuencias y parámetros que se describen en otras secciones de la presente. Una variante activa puede diferir de la secuencia del polipéptido de referencia en solamente 1-15 residuos aminoacídicos, solamente 1-10 residuos aminoacídicos, tal como 6-10, solamente 5, solamente 4, 3, 2 o incluso 1 residuo aminoacídico.

En una población pueden existir variantes naturales. Estas variantes se pueden identificar utilizando técnicas de biología molecular muy conocidas, como la reacción en cadena de la polimerasa (PCR) e hibridación, tal como se describe más adelante. Las secuencias de nucleótidos obtenidas sintéticamente, por ejemplo, secuencias generadas por mutagénesis dirigida o mutagénesis mediada por PCR, las cuales siguen codificando un polipéptido de la invención, también se incluyen como variantes. Se pueden introducir una o más sustituciones, adiciones o deleciones de nucleótidos o aminoácidos en una secuencia de nucleótidos o aminoácidos descrita en la presente, de tal modo que las sustituciones, adiciones o deleciones se introduzcan en la proteína codificada. Las adiciones (inserciones) o deleciones (truncaciones) se pueden realizar en el extremo N-terminal o C-terminal de la proteína nativa, o en uno o más sitios en la proteína nativa. De forma análoga, se puede realizar una sustitución de uno o más nucleótidos o aminoácidos en uno o más sitios en la proteína nativa.

Por ejemplo, se pueden realizar sustituciones conservativas de aminoácidos en uno o más residuos aminoacídicos predichos, preferentemente no esenciales. Un residuo aminoacídico "no esencial" es un residuo que puede ser modificado a partir de la secuencia natural de una proteína sin alterar la actividad biológica, mientras que un aminoácido "esencial" es necesario para la actividad biológica. Una "sustitución conservativa de un aminoácido" es aquella en la que el residuo aminoacídico se reemplaza por un residuo aminoacídico que tiene una cadena lateral similar. En la técnica se conocen las familias de residuos aminoacídicos con cadenas laterales similares. Estas familias incluyen aminoácidos con cadenas laterales básicas (p. ej., lisina, arginina, histidina), cadenas laterales ácidas (p. ej., ácido aspártico, ácido glutámico), cadenas laterales polares no cargadas (p. ej., glicina, asparagina, glutamina, serina, treonina, tirosina, cisteína), cadenas laterales apolares (p. ej., alanina, valina, leucina, isoleucina, prolina, fenilalanina, metionina, triptófano), cadenas laterales beta-ramificadas (p. ej., treonina, valina, isoleucina) y cadenas laterales aromáticas (p. ej., tirosina, fenilalanina, triptófano, histidina). Estas sustituciones no se llevarían a cabo para residuos aminoacídicos conservados ni para residuos aminoacídicos que residan en un motivo conservado, donde dichos residuos son esenciales para la actividad de la proteína.

Por ejemplo, las variantes de secuencias de aminoácidos del polipéptido de referencia se pueden preparar mutando la secuencia de nucleótidos que codifica la

enzima. Los mutantes resultantes se pueden expresar recombinantemente en plantas y se pueden detectar aquellos que retengan la actividad biológica realizando ensayos que determinen la actividad contra nematodos y plantas mediante técnicas de ensayo estándares, según se describe en la presente. En la técnica se conocen métodos de mutagénesis y para alterar secuencias de nucleótidos. Remítase, p. ej., a Kunkel (1985) *Proc. Natl. Acad. Sci. USA* 82:488-492; Kunkel *et al.* (1987) *Methods in Enzymol.* 154:367-382; y *Techniques in Molecular Biology* (Walker & Gaastra eds., MacMillan Publishing Co. 1983) y las referencias citadas en dichos documentos; así como también la Patente de EE. UU. N.º 4.873.192. Evidentemente, las mutaciones realizadas en el ADN que codifica la variante no deben alterar el marco de lectura y preferentemente no crearán regiones complementarias que pudieran producir una estructura de ARNm secundaria. Remítase a la Publicación de Solicitud de Patente Europea N.º 75.444. Se pueden encontrar instrucciones sobre sustituciones de aminoácidos adecuadas que no afectan a la actividad biológica de la proteína de interés en el modelo de Dayhoff *et al.* (1978) *Atlas of Protein Sequence and Structure* (National Biomedical Research Foundation, Washington, D.C.), incorporado a la presente por referencia.

No se espera que las deleciones, inserciones y sustituciones en los polipéptidos que se describen en la presente produzcan cambios radicales en las características del polipéptido (p. ej., la actividad del polipéptido). Sin embargo, cuando resulte difícil predecir el efecto exacto de la sustitución, deleción o inserción antes de llevarla a cabo, un experto en la técnica apreciará que el efecto se puede evaluar mediante ensayos de detección rutinarios que pueden detectar las actividades de interés de los polipéptidos particulares (p. ej., conferir una mayor resistencia a una plaga de nematodos que atacan plantas, reducir el crecimiento de una plaga de nematodos que atacan plantas, reducir el desarrollo de quistes inducidos por nematodos).

En algunas realizaciones, las composiciones de la invención pueden comprender fragmentos activos del polipéptido. El término "fragmento", tal como se utiliza en la presente, se refiere a una porción del polipéptido de referencia que retiene la actividad del polipéptido de conferir una mayor resistencia a una plaga de nematodos que atacan plantas, reducir el crecimiento de una plaga de nematodos que atacan plantas o reducir el desarrollo de quistes. Un fragmento también se refiere a una porción de una molécula de ácido nucleico que codifica el polipéptido de referencia. Un fragmento activo del polipéptido se puede preparar, por ejemplo, aislando una porción de una molécula de ácido nucleico codificante de dicho polipéptido que exprese el fragmento codificado del polipéptido (p. ej., mediante expresión recombinante *in vitro*) y evaluando la actividad del fragmento. Las moléculas de ácido nucleico que codifican tales fragmentos pueden estar

constituidas por al menos aproximadamente 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800, 1900 o 2000 nucleótidos contiguos, o por hasta el número de nucleótidos que estén presentes en una molécula de ácido nucleico codificante del polipéptido de longitud completa. Como tales, los fragmentos polipeptídicos pueden estar constituidos por al menos aproximadamente 50, 60, 70, 80, 90, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, 525, 550, 525, 550, 600, 625, 650, 675 o 700 residuos aminoacídicos contiguos, o por hasta el número total de residuos aminoacídicos que estén presentes en el polipéptido de longitud completa.

De este modo, en algunas realizaciones, una variante o un fragmento funcional de un polipéptido de esta invención o una variante o un fragmento funcional que presente una identidad sustancial respecto a una secuencia de polipéptido de esta invención (p. ej., **SEQ ID NOs:29-42**, **SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046**) cuando se produce en una planta transgénica reduce la capacidad de las plagas de nematodos para sobrevivir, desarrollarse y reproducirse en/sobre o alrededor de la planta transgénica, o reduce los daños o pérdidas relacionados con los nematodos en las plantas transgénicas que producen dichos polipéptidos.

En algunas realizaciones, la composición nematicida comprende además un portador agrícolamente aceptable. La expresión "portador agrícolamente aceptable", tal como se utiliza en la presente, puede incluir material orgánico y/o inorgánico natural y/o sintético que se combina con el componente activo para facilitar su aplicación en la planta o parte de esta. Un portador agrícolamente aceptable incluye, sin carácter limitante, componentes inertes, dispersantes, surfactantes, adyuvantes, adherentes, adhesivos, aglutinantes o combinaciones de estos, que se puedan emplear en formulaciones agrícolas. En otras realizaciones, una planta o parte de planta transgénica puede actuar como portador agrícolamente aceptable.

En algunas realizaciones, la composición nematicida puede comprender además uno o más compuestos nematicidas y/o insectidicas adicionales. Estos compuestos nematicidas incluyen, sin carácter limitante, cloropicrina, metam sódico, metam potásico, dazomet, yodometano, disulfuro de dimetilo (DMDS), fluoruro de sulfurilo, oxamilo y fostiazato.

En otras realizaciones, la composición nematicida puede comprender además polipéptidos con actividad insecticida. Estos polipéptidos insecticidas incluyen, sin carácter limitante, endotoxinas cristal (Cry) de *Bacillus thuringiensis* y proteínas insecticidas vegetativas (VIP) de *Bacillus* sp.

Los polipéptidos y sus composiciones de la invención se pueden aplicar a la superficie de una planta o parte de planta, incluidas, sin carácter limitante, las semillas, hojas, flores, tallos, tubérculos, raíces y similares. En algunas realizaciones, los polipéptidos y las composiciones de la invención se suministran oralmente a un nematodo, donde el nematodo ingiere una o más partes de una planta a la que se ha aplicado una composición que comprende los polipéptidos de la invención. La aplicación de las composiciones de la invención a una planta se puede llevar a cabo empleando cualquier método conocido por los expertos en la técnica para aplicar compuestos, composiciones, formulaciones y similares a superficies de plantas. Algunos ejemplos no limitantes de aplicación incluyen pulverización, espolvoreación, aspersión, dispersión, nebulización, atomización, difusión, remojo, inyección al suelo, incorporación al suelo, empapamiento (p. ej., tratamiento del suelo o las raíces), inmersión, vertido, recubrimiento, infiltración en el tallo o las hojas, recubrimiento lateral o tratamiento de semillas y similares, y combinaciones de estos. Estos y otros procedimientos para aplicar uno o más compuestos, composiciones o formulaciones a una planta o parte de esta son de uso común para los expertos en la técnica. En algunas realizaciones, los polipéptidos se suministran oralmente a un nematodo en forma de una planta transgénica que comprende una o más secuencias de nucleótidos que codifican uno o más polipéptidos de la invención.

Los términos "expresar", "que expresa", "expresado" o "expresión" y similares, tal como se utilizan en la presente, con relación a una molécula de ácido nucleico y/o una secuencia de nucleótidos (p. ej., ARN o ADN) indican que la molécula de ácido nucleico y/o la secuencia de nucleótidos se transcribe y, opcionalmente, se traduce. De este modo, una molécula de ácido nucleico y/o una secuencia de nucleótidos puede expresar un polipéptido de interés o un ARN no traducido funcional.

Una secuencia de nucleótidos “heteróloga” es una secuencia de nucleótidos asociada de forma no natural con una célula huésped en la que se introduce, incluidas las copias múltiples que no son de origen natural de una secuencia de nucleótidos de origen natural.

Un ácido nucleico, una secuencia de nucleótidos, un polipéptido o una secuencia de aminoácidos "nativo/a" o "natural" se refiere a un ácido nucleico, una secuencia de nucleótidos, un polipéptido o una secuencia de aminoácidos de origen natural o endógeno/a. De este modo, por ejemplo "un ARNm natural" es una ARNm de origen natural presente en el organismo o endógeno a este. Una secuencia de ácido nucleico "homóloga" es una secuencia de nucleótidos que se asocia de forma natural con una célula huésped en la que se introduce.

Además, las expresiones "ácido nucleico", "molécula de ácido nucleico", "secuencia de nucleótidos" y "polinucleótido", tal como se utilizan en la presente, se pueden emplear indistintamente y engloban tanto el ARN como el ADN, incluidos el ADNc, ADN genómico, ARNm, ADN o ARN sintético (p. ej., sintetizado con métodos químicos) y quimeras de ADN y ARN. Los términos "polinucleótido", "secuencia de nucleótidos" o "ácido nucleico" se refieren a una cadena de nucleótidos, independientemente de la longitud de la cadena. El ácido nucleico puede ser bicatenario o monocatenario. Cuando es monocatenario, el ácido nucleico puede ser una hebra sentido o una hebra antisentido. El ácido nucleico se puede sintetizar empleando derivados o análogos oligonucleotídicos (p. ej., nucleótidos de tipo fosforotioato o inosina). Estos oligonucleótidos se pueden emplear, por ejemplo, para preparar ácidos nucleicos que presenten una capacidad modificada para aparear las bases o una mayor resistencia a nucleasas. La presente invención proporciona además un ácido nucleico que es el complemento (el cual puede ser un complemento completo o un complemento parcial) de un ácido nucleico, una secuencia de nucleótidos o un polinucleótido de esta invención. En la presente las moléculas de ácido nucleico y/o secuencias de nucleótidos proporcionadas en la presente se presentan en la dirección 5’ a 3’, de izquierda a derecha y se representan empleando el código estándar para representar los caracteres de nucleótidos según se indica en las reglas de secuencias de los EE. UU., 37 CFR §§1.821 - 1.825, y la Organización Mundial de la Propiedad Intelectual (WIPO), Norma ST.25.

La expresión "secuencia de nucleótidos antisentido" u "oligonucleótido antisentido", tal como se utiliza en la presente, se refiere a una secuencia de nucleótidos que es complementaria a una secuencia de ADN o ARN especificada. Los oligonucleótidos antisentido y los ácidos nucleicos que los expresan se pueden obtener de acuerdo con técnicas convencionales. Remítase, p. ej., a la Patente de EE. UU. N.º 5.023.243 concedida a Tullis; Patente de EE. UU. N.º 5.149.797 concedida a Pederson *et al.* La secuencia de nucleótidos antisentido puede ser complementaria a la secuencia de nucleótidos completa que codifica el polipéptido o a una porción de esta de al menos 10, 20, 40, 50, 75, 100, 150, 200, 300 o 500 bases contiguas y reducirá el nivel de producción del polipéptido.

Los expertos en la técnica se darán cuenta de que no es necesario que la secuencia de nucleótidos antisentido sea totalmente complementaria a la secuencia diana, siempre que el grado de similitud secuencial sea suficiente para que la secuencia de nucleótidos antisentido se hibride con su diana y reduzca la producción del polipéptido o transcripto. Tal como es sabido en la técnica, para secuencias de nucleótidos antisentido cortas generalmente se requiere un grado más elevado de similitud

secuencial, mientras que las secuencias de nucleótidos antisentido más largas tolerarán un grado más elevado de bases no coincidentes.

Por ejemplo, la hibridación de estas secuencias de nucleótidos se puede llevar a cabo en condiciones de rigurosidad reducida, rigurosidad media o incluso en condiciones rigurosas (p. ej., condiciones representadas por una rigurosidad del lavado de un 35-40% de formamida con 5x solución de Denhardt, un 0.5% de SDS y 1x SSPE a 37 °C; condiciones representadas por una rigurosidad del lavado de un 40-45% de formamida con 5x solución de Denhardt, un 0.5% de SDS y 1x SSPE a 42 °C; y/o condiciones representadas por una rigurosidad del lavado de un 50% de formamida con 5x solución de Denhardt, un 0.5% de SDS y 1x SSPE a 42 °C, respectivamente) para las secuencias de nucleótidos descritas específicamente en la presente. Remítase, p. ej., a Sambrook *et al.*, Molecular Cloning: A Laboratory Manual 2.ª Ed. (Cold Spring Harbor, NY, 1989).

En otras realizaciones, las secuencias de nucleótidos antisentido de la invención presentan una similitud secuencial de al menos aproximadamente un 70%, 80%, 90%, 95%, 97%, 98% o superior con el complemento de las secuencias codificantes descritas específicamente en la presente y reducirán el nivel de producción del polipéptido.

En otras realizaciones, la secuencia de nucleótidos antisentido se puede dirigir a cualquier secuencia codificante, el silenciamiento de la cual da como resultado una modulación de un polipéptido de esta invención (p. ej., **SEQ ID NOs: 29-42, 135-209, 243-260 y/o 665-1046**).

La longitud de la secuencia de nucleótidos antisentido (es decir, el número de nucleótidos en ella) no es crítica, siempre que se una selectivamente al lugar deseado y reduzca la transcripción y/o traducción de la secuencia diana, y se pueda determinar de acuerdo con procedimientos rutinarios. En general, la secuencia de nucleótidos antisentido tendrá una longitud comprendida entre aproximadamente ocho, diez o doce nucleótidos hasta aproximadamente 20, 30, 50, 75, 100, 200, 300, 400 o más nucleótidos.

Una secuencia de nucleótidos antisentido se puede construir empleando síntesis química y reacciones de unión enzimática con procedimientos conocidos en la técnica. Por ejemplo, una secuencia de nucleótidos antisentido se puede sintetizar con métodos químicos empleando nucleótidos de origen natural o varios nucleótidos modificados diseñados para aumentar la estabilidad biológica de las moléculas o para aumentar la estabilidad física del dúplex formado entre las secuencias de nucleótidos sentido y antisentido, p. ej., se pueden emplear derivados de tipo fosforotioato y nucleótidos sustituidos con acridina. Los ejemplos de nucleótidos modificados que se pueden emplear para generar la secuencia de nucleótidos antisentido incluyen 5-fluorouracilo, 5-bromouracilo, 5-clorouracilo, 5-yodouracilo, hipoxantina, xantina, 4-acetilcitosina, 5-

(carboxihidroxilmetil)uracilo, 5-carboximetilaminometil-2-tiouridina, 5-carboximetilaminometiluracilo, dihidrouracilo, beta-D-galactosilqueosina, inosina, *N*6-isopenteniladenina, 1-metilguanina, 1-metilinosina, 2,2-dimetilguanina, 2-metiladenina, 2-metilguanina, 3-metilcitosina, 5-metilcitosina, *N*6-adenina, 7-metilguanina, 5-metilaminometiluracilo, 5-metoxiaminometil-2-tiouracilo, beta-D-manosilqueosina, 5'-metoxicarboximetiluracilo, 5-metoxiuracilo, 2-metiltio-*N*6-isopenteniladenina, ácido uracil-5-oxiacético (v), wibutoxosina, pseudouracilo, queosina, 2-tiocitosina, 5-metil-2-tiouracilo, 2-tiouracilo, 4-tiouracilo, 5-metiluracilo, éster metílico del ácido uracil-5-oxiacético, ácido uracil-5-oxiacético (v), 5-metil-2-tiouracilo, 3-(3-amino-3-*N*-2-carboxipropil)uracilo, (acp3)w y 2,6-diaminopurina. Como alternativa, la secuencia de nucleótidos antisentido se puede producir empleando un vector de expresión en el que se haya clonado un ácido nucleico en una orientación antisentido (es decir, el ARN transcrito a partir del ácido nucleico insertado será de orientación antisentio respecto al ácido nucleico diana de interés).

Las secuencias de nucleótidos antisentido de la invención incluyen además secuencias de nucleótidos en las que al menos uno de los residuos de tipo fosfato que actúan como puente entre nucleótidos, o todos ellos, son fosfatos modificados tales como fosfonatos metílicos, fosfonotioatos metílicos, fosforomorfolidatos, fosforopiperazidatos y fosforoamidatos. Por ejemplo, cada uno de los residuos de tipo fosfato que actúa como puente entre nucleótidos puede estar modificado según se ha descrito. En otro ejemplo sin carácter limitante, la secuencia de nucleótidos antisentido es una secuencia de nucleótidos en la que uno de los nucleótidos, o todos ellos, contienen un resto de tipo alquilo inferior en la posición 2' (p. ej., alquilo C_1-C_4, lineal o ramificado, saturado o insaturado, tal como metilo, etilo, etenilo, propilo, 1-propenilo, 2-propenilo e isopropilo). Por ejemplo, cada uno de los nucleótidos puede estar modificado según se ha descrito. Remítase también a Furdon *et al.*, *Nucleic Acids Res. 17*:9193 (1989); Agrawal *et al.*, *Proc. Natl. Acad. Sci. USA 87*:1401 (1990); Baker *et al.*, *Nucleic Acids Res.* 18:3537 (1990); Sproat *et al.*, *Nucleic Acids Res. 17*:3373 (1989); Walder y Walder, *Proc. Natl. Acad. Sci. USA 85*:5011 (1988); que se incorporan a la presente a modo de referencia por su contenido acerca de métodos para preparar moléculas antisentido, incluidas aquellas que contienen bases de nucleótidos modificadas.

También se pueden emplear métodos de apareamiento de bases de triple hélice para inhibir la producción de los polipéptidos de esta invención (p. ej., **SEQ ID NOs: 29-42, 135-209, 243-260 y/o 665-1046**). Se cree que el apareamiento de triple hélice tiene lugar mediante la inhibición de la capacidad de la doble hélice de abrirse suficientemente para que se puedan unir las polimerasas, factores de transcripción o moléculas reguladoras. En la bibliografía se han descrito avances terapéuticos recientes empleando

ADN de triple hélice (p. ej., Gee *et al.*, (1994) En: Huber *et al.*, *Molecular and Immunologic Approaches*, Futura Publishing Co., Mt. Kisco, NY).

Las proteínas o ácidos nucleicos diferentes que presentan homología se denominan en la presente "homólogos". El término "homólogo" incluye secuencias homólogas de la misma especie y de especies diferentes y secuencias ortólogas de la misma especie y de especies diferentes. El término "homología" se refiere al nivel de similitud entre dos o más ácidos nucleicos y/o secuencias de aminoácidos en cuanto al porcentaje de identidad posicional (es decir, similitud o identidad secuencial). La homología también se refiere al concepto de propiedades funcionales similares entre los diferentes ácidos nucleicos o proteínas. De este modo, las composiciones y los métodos de la invención comprenden además homólogos respecto a las secuencias de nucleótidos y secuencias de polipéptidos de esta invención. El término "ortólogo", tal como se utiliza en la presente, se refiere a secuencias de nucleótidos y/o secuencias de aminoácidos homólogas en diferentes especies que se forman a partir de un gen ancestral común durante la especiación. Un homólogo de esta invención tiene una identidad secuencial significativa (p. ej., de un 70%, 75%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% y/o 100%) respecto a las secuencias de nucleótidos de la invención.

Un homólogo, tal como se describe en la presente, se puede utilizar con cualquier composición o método de la invención, junto o combinado con otro y/o con una o más secuencias de nucleótidos o secuencias de polipéptidos de la invención. De este modo, en una realización, la invención proporciona una molécula de ácido nucleico que comprende, está constituida esencialmente por o está constituida por una o más secuencias de nucleótidos de la invención y/o uno o más homólogos de cualquier secuencia de nucleótidos de la invención. En una realización adicional, la invención proporciona composiciones de polipéptidos que comprenden, están constituidas esencialmente por o están constituidas por uno o más de los polipéptidos de esta invención y/o un homólogo de estos.

La expresión "identidad secuencial", tal como se utiliza en la presente, se refiere a la medida en que dos secuencias de polinucleótidos o péptidos alineadas de forma óptima son invariables a través de una ventana de alineación de componentes, por ejemplo, nucleótidos o aminoácidos. La "identidad" se puede calcular fácilmente mediante métodos conocidos que incluyen, sin carácter limitante, los que se describen en: *Computational Molecular Biology* (Lesk, A. M., ed.) Oxford University Press, Nueva York (1988); *Biocomputing: Informatics and Genome Projects* (Smith, D. W., ed.) Academic Press, Nueva York (1993); *Computer Analysis of Sequence Data, Part I* (Griffin, A. M. y

Griffin, H. G., eds.) Humana Press, Nueva Jersey (1994); *Sequence Analysis in Molecular Biology* (von Heinje, G., ed.) Academic Press (1987); y *Sequence Analysis Primer* (Gribskov, M. y Devereux, J., eds.) Stockton Press, Nueva York (1991).

La expresión "porcentaje de identidad secuencial" o "porcentaje de identidad", tal como se utiliza en la presente, se refiere al porcentaje de nucleótidos idénticos en una secuencia de polinucleótido lineal de una molécula de polinucleótido de referencia ("búsqueda") (o su cadena complementaria) en comparación con una molécula de polinucleótido de prueba ("sujeto") (o su cadena complementaria) cuando las dos secuencias están alineadas de forma óptima. En algunas realizaciones, el "porcentaje de identidad" puede referirse al porcentaje de aminoácidos idénticos en la secuencia de aminoácidos.

La expresión "sustancialmente idéntico/a", tal como se utiliza en la presente, en el contexto de dos moléculas de ácido nucleico, secuencias de nucleótidos o secuencias proteicas, se refiere a dos o más secuencias o subsecuencias que presentan una identidad de los nucleótidos o los residuos aminoacídicos de al menos aproximadamente un 70%, al menos aproximadamente un 75%, al menos aproximadamente un 80%, al menos aproximadamente un 81%, al menos aproximadamente un 82%, al menos aproximadamente un 83%, al menos aproximadamente un 84%, al menos aproximadamente un 85%, al menos aproximadamente un 86%, al menos aproximadamente un 87%, al menos aproximadamente un 88%, al menos aproximadamente un 89%, al menos aproximadamente un 90%, al menos aproximadamente un 95%, al menos aproximadamente un 96%, al menos aproximadamente un 97%, al menos aproximadamente un 98% o al menos aproximadamente un 99%, cuando se comparan y alinean para una correspondencia máxima, según se determina empleando uno de los siguientes algoritmos de comparación de secuencias o por inspección visual. En algunas realizaciones de la invención, existe identidad sustancial en una región de las secuencias que tiene una longitud comprendida entre al menos aproximadamente 50 residuos y aproximadamente 150 residuos. De este modo, en algunas realizaciones de la invención, existe identidad sustancial en una región de las secuencias que tiene una longitud de al menos aproximadamente 50, aproximadamente 60, aproximadamente 70, aproximadamente 80, aproximadamente 90, aproximadamente 100, aproximadamente 110, aproximadamente 120, aproximadamente 130, aproximadamente 140, aproximadamente 150 o más residuos. En algunas realizaciones particulares, la secuencias son sustancialmente idénticas en al menos aproximadamente 150 residuos. En una realización adicional, las secuencias son sustancialmente idénticas a lo largo de toda la longitud de las regiones codificantes.

Además, en realizaciones representativas, las secuencias proteicas o de nucleótidos sustancialmente idénticas realizan sustancialmente la misma función (p. ej., conferir una mayor resistencia a una plaga de nematodos que atacan plantas, reducir el crecimiento de una plaga de nematodos que atacan plantas, reducir el desarrollo de quistes inducidos por nematodos).

A la hora de comparar secuencias, normalmente una secuencia actúa como secuencia de referencia con la que se comparan las secuencias de prueba. Cuando se utiliza un algoritmo para la comparación de secuencias, se introducen las secuencias de prueba y de referencia en una computadora, se designan las coordenadas de las subsecuencias, en caso necesario, y se designan los parámetros del programa para el algoritmo de las secuencias. El algoritmo para la comparación de las secuencias calcula entonces el porcentaje de identidad secuencial para una o más secuencias de prueba en relación con la secuencia de referencia, en función de los parámetros del programa designados.

La alineación óptima de las secuencias para alinear una ventana de comparación es bien conocida por los expertos en la técnica y puede llevarse a cabo mediante herramientas tales como el algoritmo de homología local de Smith y Waterman, el algoritmo de alineación de homología de Needleman y Wunsch, el método de búsqueda de similitudes de Pearson y Lipman, y opcionalmente mediante implementaciones computarizadas de estos algoritmos tales como GAP, BESTFIT, FASTA y TFASTA disponibles como parte de GCG® Wisconsin Package® (Accelrys Inc., San Diego, CA). Una "fracción de identidad" para los segmentos alineados de una secuencia de prueba y una secuencia de referencia es el número de componentes idénticos que comparten las dos secuencias alineadas dividido por el número total de componentes en el segmento de la secuencia de referencia, es decir, la secuencia de referencia completa o una parte definida más pequeña de la secuencia de referencia. El porcentaje de identidad secuencial se representa como la fracción de identidad multiplicada por 100. La comparación de una o más secuencias de polinucleótidos se puede realizar respecto a una secuencia de polinucleótido de longitud completa o una porción de esta, o respecto a una secuencia de polinucleótido más larga. A los efectos de esta invención, el "porcentaje de identidad" también se puede determinar empleando BLASTX versión 2.0 para secuencias de nucleótidos traducidas y BLASTN versión 2.0 para secuencias de nucleótidos.

Se dispone de un software de acceso público para la realización de los análisis BLAST en el Centro Nacional de Información Biotecnológica. Este algoritmo incluye identificar en primer lugar pares de secuencias de puntuación elevada (HSP) mediante la

identificación de palabras cortas de longitud W en la secuencia de búsqueda que igualen o satisfagan cierta puntuación umbral T evaluada positivamente cuando se alinean con una palabra de la misma longitud en una secuencia de la base de datos. Se hace referencia a T como el umbral de puntuación de la palabra vecina (Altschul *et al.*, 1990). Estas coincidencias de palabras vecinas iniciales actúan como semillas para iniciar búsquedas con el fin de encontrar HSP más largas que las contengan. Las coincidencias de las palabras se extienden posteriormente en ambas direcciones a lo largo de cada secuencia en la medida en que se pueda aumentar la puntuación de alineación acumulada. Las puntuaciones acumuladas se calculan utilizando, para las secuencias de nucleótidos, los parámetros M (puntuación de recompensa para un par de residuos coincidentes; siempre > 0) y N (puntuación de penalización para residuos no coincidentes; siempre < 0). Para secuencias de aminoácidos, se utiliza una matriz de puntuación para calcular la puntuación acumulada. La extensión de las coincidencias de las palabras en cada dirección se ve interrumpida cuando la puntuación de alineación acumulada disminuye una cantidad X respecto a su valor máximo alcanzado, la puntuación acumulada tiende a cero o por debajo de cero debido a la acumulación de una o más alineaciones de residuos con puntuación negativa, o se alcanza el final de la secuencia. Los parámetros W, T y X del algoritmo BLAST determinan la sensibilidad y la velocidad de la alineación. El programa BLASTN (para las secuencias de nucleótidos) utiliza por defecto una longitud de palabra (W) de 11, una expectativa (E) de 10, un corte de 100, M = 5, N = -4, y una comparación de las dos hebras. Para las secuencias de aminoácidos, el programa BLASTP utiliza por defecto una longitud de palabra (W) de 3, una expectativa (E) de 10 y la matriz de puntuación BLOSUM62 (remítase a Henikoff y Henikoff, *Proc. Natl. Acad. Sci. USA* 89: 10915 (1989)).

Además de calcular el porcentaje de identidad secuencial, el algoritmo BLAST también lleva a cabo un análisis estadístico de la similitud entre dos secuencias (remítase, por ejemplo, a Karlin y Altschul, *Proc. Nat'l. Acad. Sci. USA* 90: 5873-5787 (1993)). Una medida de la similitud proporcionada por el algoritmo BLAST es la probabilidad de la suma más pequeña (P(N)), que proporciona una indicación de la probabilidad de que una coincidencia entre dos secuencias de nucleótidos o de aminoácidos se produzca por casualidad. Por ejemplo, una secuencia de ácido nucleico de prueba se considera similar a una secuencia de referencia si la probabilidad de la suma más pequeña en una comparación de la secuencia de nucleótidos de prueba con la secuencia de nucleótidos de referencia está comprendida entre menos de aproximadamente 0.1 y menos de aproximadamente 0.001. De este modo, en algunas realizaciones de la invención, la probabilidad de la suma más pequeña en una comparación de la secuencia de

nucleótidos de prueba con la secuencia de nucleótidos de referencia es inferior a aproximadamente 0.001.

También se puede considerar que dos secuencias de nucleótidos son sustancialmente idénticas cuando las dos secuencias se hibridan entre sí en condiciones rigurosas. En algunas realizaciones representativas, dos secuencias de nucleótidos que se consideran sustancialmente idénticas se hibridan entre sí en condiciones muy rigurosas.

Las "condiciones de hibridación rigurosas" y "condiciones del lavado de hibridación rigurosas", en el contexto de los experimentos de hibridación de ácidos nucleicos, tales como las hibridaciones de Southern y Northern, dependen de la secuencia y son diferentes con parámetros ambientales distintos. Se puede consultar una amplia guía sobre la hibridación de ácidos nucleicos en Tijssen, *Laboratory Techniques in Biochemistry and Molecular Biology-Hybridization with Nucleic Acid Probes,* parte I, capítulo 2 “Overview of principles of hybridization and the strategy of nucleic acid probe assays”, Elsevier, Nueva York (1993). En general, se seleccionan condiciones de lavado y de hibridación muy rigurosas que estén aproximadamente 5 ºC por debajo del punto de fusión térmico (T_m) para la secuencia específica a un pH y una fuerza iónica definidos.

La T_m es la temperatura (a un pH y una fuerza iónica definidos) en la que el 50% de la secuencia diana se hibrida con una sonda perfectamente coincidente. Las condiciones muy rigurosas se seleccionan de modo que sean iguales a la T_m para una sonda particular. Un ejemplo de condiciones de hibridación rigurosas para la hibridación de secuencias de nucleótidos complementarias que tengan más de 100 residuos complementarios sobre un filtro en un ensayo de inmunotransferencia de Southern o Northern es formamida al 50% con 1 mg de heparina a 42 ºC, llevando a cabo la hibridación durante toda la noche. Un ejemplo de condiciones de lavado muy rigurosas es NaCl 0.15 M a 72 ºC durante aproximadamente 15 minutos. Un ejemplo de condiciones de lavado rigurosas es un lavado con 0.2x SSC a 65 ºC durante 15 minutos (remítase a Sambrook, *infra*, para obtener una descripción del tampón SSC). A menudo, un lavado de rigurosidad alta va precedido por un lavado de rigurosidad baja para eliminar la señal de fondo de la sonda. Un ejemplo de lavado de rigurosidad media para un dúplex de, por ejemplo, más de 100 nucleótidos, es 1x SSC a 45 ºC durante 15 minutos. Un ejemplo de lavado de rigurosidad baja para un dúplex de, por ejemplo, más de 100 nucleótidos, es 4-6x SSC a 40 ºC durante 15 minutos. Para sondas cortas (p. ej., de aproximadamente 10 a 50 nucleótidos), las condiciones rigurosas normalmente incluyen concentraciones salinas inferiores a aproximadamente 1.0 M de ión Na, normalmente una concentración de ión Na de aproximadamente 0.01 a 1.0 M (u otras sales) a un pH de 7.0 a 8.3 y la

temperatura es normalmente de al menos aproximadamente 30 ºC. También se pueden lograr condiciones rigurosas con la adición de agentes desestabilizantes tales como la formamida. En general, una relación entre la señal y el ruido de 2x (o superior) respecto a la observada para una sonda no relacionada en el ensayo de hibridación particular indica la detección de una hibridación específica. Las secuencias de nucleótidos que no se hibridan entre sí en condiciones rigurosas seguirán siendo sustancialmente idénticas si las proteínas que estas codifican son sustancialmente idénticas. Esto puede ocurrir, por ejemplo, cuando se crea una copia de una secuencia de nucleótidos utilizando la degeneración máxima del codón permitida por el código genético.

Los siguientes son ejemplos de conjuntos de condiciones de hibridación/lavado que se pueden utilizar para clonar secuencias de nucleótidos homólogas que son sustancialmente idénticas a las secuencias de nucleótidos de referencia de la invención. En una realización, una secuencia de nucleótidos de referencia se hibrida con la secuencia de nucleótidos "de prueba" en un 7% de dodecilsulfato sódico (SDS), $NaPO_4$ 0.5 M, EDTA 1 mM a 50 °C con lavado en 2X SSC y un 0.1% de SDS a 50 °C. En otra realización, la secuencia de nucleótidos de referencia se hibrida con la secuencia de nucleótidos "de prueba" en un 7% de dodecilsulfato sódico (SDS), $NaPO_4$ 0.5 M, EDTA 1 mM a 50 °C con lavado en 1X SSC y un 0.1% de SDS a 50 °C, o en un 7% de dodecilsulfato sódico (SDS), $NaPO_4$ 0.5 M, EDTA 1 mM a 50 °C con lavado en 0.5X SSC y un 0.1% de SDS a 50 °C. En otras realizaciones más, la secuencia de nucleótidos de referencia se hibrida con la secuencia de nucleótidos "de prueba" en un 7% de dodecilsulfato sódico (SDS), $NaPO_4$ 0.5 M, EDTA 1 mM a 50 °C con lavado en 0.1X SSC y un 0.1% de SDS a 50 °C, o en un 7% de dodecilsulfato sódico (SDS), $NaPO_4$ 0.5 M, EDTA 1 mM a 50 °C con lavado en 0.1X SSC y un 0.1% de SDS a 65 °C.

En realizaciones particulares, una indicación adicional de que dos secuencias de nucleótidos o dos secuencias de polipéptidos son sustancialmente idénticas puede ser que la proteína codificada por el primer ácido nucleico presente reactividad cruzada inmunológicamente con la proteína codificada por el segundo ácido nucleico o se una específicamente a esta. De este modo, en algunas realizaciones, un polipéptido puede ser sustancialmente idéntico a un segundo polipéptido, por ejemplo, si los dos polipéptidos se diferencian únicamente por sustituciones conservativas.

En algunas realizaciones, las moléculas de ácido nucleico recombinante, secuencias de nucleótidos y polipéptidos de la invención se "aislan". Una molécula de ácido nucleico "aislada", una secuencia de nucleótidos "aislada" o un polipéptido "aislado" es una molécula de ácido nucleico, secuencia de nucleótidos o polipéptido que, debido a la intervención humana, existe en un entorno diferente de su entorno nativo y, por lo tanto,

no es un producto natural. Una molécula de ácido nucleico, secuencia de nucleótidos o polipéptido aislado puede existir en una forma purificada, es decir, al menos parcialmente separado de al menos algunos de los demás componentes del organismo o virus de origen natural, por ejemplo, la célula o los componentes estructurales virales u otros polipéptidos o ácidos nucleicos que se encuentran asociados de forma habitual con el polinucleótido. En realizaciones específicas, la molécula de ácido nucleico aislada, la secuencia de nucleótidos aislada y/o el polipéptido aislado presenta una pureza de al menos aproximadamente un 1%, 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% o superior.

En otras realizaciones, una molécula de ácido nucleico, secuencia de nucleótidos o polipéptido aislado puede existir en un entorno no nativo tal como, por ejemplo, una célula huésped recombinante. De este modo, por ejemplo, con respecto a las secuencias de nucleótidos, el término "aisladas" se refiere a que están separadas del cromosoma y/o la célula en los que se encuentran de forma natural. Un polinucleótido también está aislado cuando se separa del cromosoma y/o la célula en los que se encuentra de forma natural y se inserta a continuación en un contexto genético, un cromosoma y/o una célula en los que no se encuentra de forma natural (p. ej., una célula huésped diferente, secuencias reguladoras diferentes y/o una posición diferente en el genoma de la que se encuentra de forma natural). Por consiguiente, las moléculas de ácido nucleico recombinante, secuencias de nucleótidos y sus polipéptidos codificados están "aislados" en el sentido de que, debido a la intervención humana, existen en un entorno diferente de su entorno nativo y, por lo tanto, no son productos naturales, sin embargo, en algunas realizaciones, se pueden introducir en una célula huésped recombinante y existir en ella.

En algunas realizaciones, las secuencias de nucleótidos y/o moléculas de ácido nucleico de la invención se pueden asociar operativamente con varios promotores para expresarse en células huésped (p. ej., células vegetales). De este modo, en algunas realizaciones, la invención proporciona células huésped transformadas y organismos transformados que comprenden las células huésped transformadas, donde las células huésped y los organismos se transforman con una o más moléculas de ácido nucleico/secuencias de nucleótidos de la invención. La expresión "asociado/a operativamente con", tal como se utiliza en la presente, cuando se refiere a una primera secuencia de ácido nucleico que está unida operativamente a una segunda secuencia de ácido nucleico, se refiere a una situación en la que la primera secuencia de ácido nucleico se sitúa en una relación funcional respecto a la segunda secuencia de ácido nucleico. Por ejemplo, un promotor está asociado operativamente con una secuencia codificante si el promotor realiza la transcripción o expresión de la secuencia codificante.

Un "promotor" de ADN es una secuencia de ADN no traducida situada antes de la región codificante que contiene el sitio de unión para la ARN polimerasa e inicia la transcripción del ADN. Una "región promotora" también puede incluir otros elementos que actúan como reguladores de la expresión génica. Los promotores pueden incluir, por ejemplo, promotores constitutivos, inducibles, regulados temporalmente, regulados por el desarrollo, regulados químicamente, con preferencia tisular y especificidad tisular, para ser empleados en la preparación de moléculas de ácido nucleico recombinante, es decir, genes quiméricos. En aspectos particulares, un "promotor" útil con la invención es un promotor capaz de iniciar la transcripción de una secuencia de nucleótidos en una célula de una planta.

Un "gen quimérico" es una molécula de ácido nucleico recombinante en la cual un promotor o secuencia de nucleótidos reguladora está asociada operativamente con una secuencia de nucleótidos que codifica un ARNm o que se expresa como una proteína, de tal modo que la secuencia de nucleótidos reguladora sea capaz de regular la transcripción o expresión de la secuencia de nucleótidos asociada. La secuencia de nucleótidos reguladora del gen quimérico no suele estar unida operativamente a la secuencia de nucleótidos asociada tal como se encuentra en la naturaleza.

La selección del promotor variará dependiendo de los requisitos temporales y espaciales para la expresión y también dependiendo de la célula huésped que se ha de transformar. De este modo, por ejemplo, la expresión de las secuencias de nucleótidos de la invención se puede realizar en cualquier planta y/o parte de planta (p. ej., en hojas, en briznas o tallos, en mazorcas, en inflorescencias (p. ej., espigas, panojas, olotes, etc.), en raíces, semillas y/o plántulas, y similares). En muchos casos, sin embargo, se busca la protección contra más de un tipo de plaga y, por lo tanto, se desea la expresión en múltiples tejidos. Aunque se ha demostrado que muchos promotores dicotiledóneos son operativos en monocotiledóneas y viceversa, los promotores dicotiledóneos se seleccionan idealmente para la expresión en dicotiledóneas y los promotores monocotiledóneos para la expresión en monocotiledóneas. Sin embargo, no existe ninguna restricción sobre la procedencia de los promotores seleccionados; es suficiente con que sean operativos a la hora de dirigir la expresión de las secuencias de nucleótidos en la célula deseada.

Los promotores útiles con la invención incluyen, sin carácter limitante, aquellos que dirigen la expresión de una secuencia de nucleótidos de forma constitutiva, aquellos que dirigen la expresión cuando son inducidos y aquellos que dirigen la expresión con especificidad por un tejido o por el desarrollo. Estos tipos de promotores son conocidos en la técnica.

Los ejemplos de promotores constitutivos incluyen, sin carácter limitante, el promotor del virus de Cestrum (cmp) (Patente de los EE. UU. N.º 7.166.770), el promotor de la actina 1 del arroz (Wang *et al.* (1992) *Mol. Cell. Biol.* 12:3399-3406; así como también la Patente de EE. UU. N.º 5.641.876), el promotor CaMV 35S (Odell *et al.* (1985) *Nature* 313:810-812), el promotor CaMV 19S (Lawton *et al.* (1987) *Plant Mol. Biol.* 9:315-324), el promotor nos (Ebert *et al.* (1987) *Proc. Natl. Acad. Sci USA* 84:5745-5749), el promotor Adh (Walker *et al.* (1987) *Proc. Natl. Acad. Sci. USA* 84:6624-6629), el promotor de la sacarosa-sintasa (Yang & Russell (1990) *Proc. Natl. Acad. Sci. USA* 87:4144-4148) y el promotor de la ubiquitina. El promotor constitutivo derivado de la ubiquitina se acumula en muchos tipos de células. Se han clonado promotores de la ubiquitina a partir de varias especies vegetales para su uso en plantas transgénicas, por ejemplo, girasol (Binet *et al.*, 1991. *Plant Science* 79: 87-94), maíz (Christensen *et al*., 1989. *Plant Molec. Biol.* 12: 619-632) y arabidopsis (Norris *et al.* 1993. *Plant Molec. Biol.* 21:895-906). El promotor de la ubiquitina del maíz (*UbiP*) se ha desarrollado en sistemas monocotiledóneos transgénicos y su secuencia y los vectores construidos para la transformación de monocotiledóneas se describen en la publicación de patente EP 0 342 926. El promotor de la ubiquitina es adecuado para la expresión de las secuencias de nucleótidos de la invención en plantas transgénicas, especialmente monocotiledóneas. Además, los casetes de expresión promotores descritos por McElroy *et al.* (*Mol. Gen. Genet.* 231: 150-160 (1991)) se pueden modificar fácilmente para la expresión de las secuencias de nucleótidos de la invención y son particularmente adecuados para emplear en huéspedes monocotiledóneos.

En algunas realizaciones, se pueden utilizar promotores con especificidad tisular/preferencia tisular. Los patrones de expresión con especificidad o preferencia tisular incluyen, sin carácter limitante, los que presentan especificidad o preferencia por el tejido verde, especificidad o preferencia por las raíces, especificidad o preferencia por el tallo y especificidad o preferencia por las flores. Los promotores adecuados para la expresión en el tejido verde incluyen muchos que regulan los genes implicados en la fotosíntesis y muchos de estos han sido clonados a partir de monocotiledóneas y dicotiledóneas. En una realización, un promotor útil con la invención es el promotor PEPC del maíz del gen de la fosfoenol-carboxilasa (Hudspeth & Grula, *Plant Molec. Biol.* 12:579-589 (1989)). Los ejemplos no limitantes de promotores con especificidad tisular incluyen aquellos asociados con genes que codifican las proteínas de reserva en la semilla (tales como β-conglicinina, cruciferina, napina y faseolina), zeína o proteínas de cuerpos grasos (tales como la oleosina) o proteínas implicadas en la biosíntesis de ácidos grasos (que incluyen la proteína portadora de acilo, estearoilo-ACP-desaturasa y desaturasas de

ácidos grasos (fad 2-1)) y otros ácidos nucleicos expresados durante el desarrollo embrionario (tales como Bce4, remítase, p. ej., a Kridl *et al.* (1991) *Seed Sci. Res.* 1:209-219; así como también la Patente Europea N.º 255378). Los promotores con especificidad tisular o preferencia tisular útiles para la expresión de las secuencias de nucleótidos de la invención en plantas, particularmente el maíz, incluyen, sin carácter limitante, aquellos que dirigen la expresión en la raíz, médula, hojas o polen. Los promotores de este tipo se describen, por ejemplo, en WO 93/07278, que se incorpora a la presente en su totalidad a modo de referencia. Otros ejemplos no limitantes de promotores con especificidad tisular o preferencia tisular útiles con la invención son el promotor de rubisco del algodón descrito en la Patente de EE. UU. 6.040.504; el promotor de la sacarosa-sintasa del arroz descrito en la Patente de EE. UU. 5.604.121; el promotor con especificidad por las raíces descrito por de Framond (FEBS 290:103-106 (1991); EP 0 452 269 concedida a Ciba- Geigy); el promotor con especificidad por el tallo descrito en la Patente de EE. UU. 5.625.136 (concedida a Ciba-Geigy) y que dirige la expresión del gen trpA del maíz; y el promotor del virus del enrollamiento de las hojas del Cestrum amarillo descrito en WO 01/73087, todos ellos incorporados a modo de referencia.

Ejemplos adicionales de promotores con especificidad tisular/preferencia tisular incluyen, sin carácter limitante, los promotores con especificidad por las raíces *RCc3* (Jeong *et al. Plant Physiol.* 153:185-197 (2010)) y RB7 (Patente de EE. UU. N.º 5459252), el promotor de la lectina (Lindstrom *et al.* (1990) *Der. Genet.* 11:160-167; y Vodkin (1983) *Prog. Clin. Biol. Res.* 138:87-98), el promotor de la alcohol-deshidrogenasa 1 del maíz (Dennis *et al.* (1984) *Nucleic Acids Res.* 12:3983-4000), S-adenosil-L-metionina-sintetasa (SAMS) (Vander Mijnsbrugge *et al.* **(**1996) *Plant and Cell Physiology*, 37(8):1108-1115), el promotor del complejo colector de luz del maíz (Bansal *et al.* (1992) *Proc. Natl. Acad. Sci. USA* 89:3654-3658), el promotor de la proteína de choque térmico del maíz (O'Dell *et al.* (1985) *EMBO J.* 5:451-458; y Rochester *et al.* (1986) *EMBO J.* 5:451-458), el promotor de la RuBP-carboxilasa de subunidad pequeña del chícharo (Cashmore, "Nuclear genes encoding the small subunit of ribulose-l,5-bisphosphate carboxylase" 29-39 en: *Genetic Engineering of Plants* (Hollaender ed., Plenum Press 1983); y Poulsen *et al.* (1986) *Mol. Gen. Genet.* 205:193-200), el promotor de la manopina-sintasa del plásmido Ti (Langridge *et al.* (1989) *Proc. Natl. Acad. Sci. USA 86:3219-3223*), el promotor de la nopalina-sintasa del plásmido Ti (Langridge *et al.* (1989), mencionado anteriormente), el promotor de la chalcona-isomerasa de la petunia (van Tunen *et al.* (1988) *EMBO J.* 7:1257-1263), el promotor de la proteína 1 rica en glicina del frijol (Keller *et al.* (1989) *Genes Dev.* 3:1639-1646), el promotor CaMV 35S truncado (O'Dell *et al.* (1985) *Nature* 313:810-812), el promotor de la patatina de la papa (Wenzler *et al.* (1989) *Plant Mol. Biol.* 13:347-354), el

promotor de células de las raíces (Yamamoto *et al.* (1990) *Nucleic Acids Res.* 18:7449), el promotor de la zeína del maíz (Kriz *et al.* (1987) *Mol. Gen. Genet.* 207:90-98; Langridge *et al.* (1983) *Cell* 34:1015-1022; Reina *et al.* (1990) *Nucleic Acids Res.* 18:6425; Reina *et al.* (1990) *Nucleic Acids Res.* 18:7449; y Wandelt *et al.* (1989) *Nucleic Acids Res.* 17:2354), el promotor de la globulina-1 (Belanger *et al.* (1991) *Genetics* 129:863-872), el promotor cab de la α-tubulina (Sullivan *et al.* (1989) *Mol. Gen. Genet.* 215:431-440), el promotor de la PEPCasa (Hudspeth & Grula (1989) *Plant Mol. Biol.* 12:579-589), promotores asociados con el complejo de genes R (Chandler *et al.* (1989) *Plant Cell* 1:1175-1183) y promotores de la chalcona-sintasa (Franken *et al.* (1991) *EMBO J.* 10:2605-2612). En algunas realizaciones particulares, las secuencias de nucleótidos de la invención están asociadas operativamente con un promotor que presenta preferencia por las raíces.

Para la expresión con especificidad por las semillas, es particularmente útil el promotor de la vicilina del chícharo (Czako *et al.* (1992) *Mol. Gen. Genet.* 235:33-40; así como también los promotores con especificidad por las semillas descritos en la Patente de EE. UU. N.º 5.625.136. Los promotores útiles para la expresión en hojas maduras son aquellos que se activan al inicio de la senescencia, tales como el promotor SAG de *Arabidopsis* (Gan *et al.* (1995) *Science* 270:1986-1988).

Además, se pueden utilizar promotores que sean funcionales en los plástidos. Los ejemplos no limitantes de estos promotores incluyen la región 5' UTR del gen 9 del bacteriófago T3 y otros promotores que se describen en la Patente de EE. UU. N.º 7.579.516. Otros promotores útiles con la invención incluyen, sin carácter limitante, el promotor de la RuBP-carboxilasa de subunidad pequeña S-E9 y el promotor del gen inhibidor de la tripsina de Kunitz (Kti3).

En algunas realizaciones de la invención, se pueden utilizar promotores inducibles. De este modo, por ejemplo, se pueden utilizar promotores regulados por agentes químicos para modular la expresión de un gen en una planta mediante la aplicación de un regulador químico exógeno. La regulación de la expresión de las secuencias de nucleótidos de la invención mediante promotores que se regulan químicamente hace posible que los polipéptidos de la invención se sinteticen solo cuando las plantas del cultivo se tratan con los agentes químicos inductores. Dependiendo del objetivo, el promotor puede ser un promotor inducible con un agente químico, donde la aplicación de un agente químico induce la expresión génica, o un promotor reprimible con un agente químico, donde la aplicación del agente químico reprime la expresión génica.

Los promotores inducibles con un agente químico son conocidos en la técnica e incluyen, sin carácter limitante, el promotor *In2*-2 del maíz, el cual se activa por acción de protectores de herbicidas de tipo bencenosulfonamida, el promotor GST del maíz, el cual

se activa por acción de compuestos electrófilos hidrófobos que se utilizan como herbicidas de preemergencia, y el promotor *PR-1* del tabaco, el cual se activa por acción del ácido salicílico (p. ej., el sistema PR1a), promotores que responden a esteroides (remítase, p. ej., al promotor inducible por glucocorticoides en Schena *et al.* (1991) *Proc. Natl. Acad. Sci. USA* 88, 10421-10425 y McNellis *et al.* (1998) *Plant J.* 14, 247-257) y promotores inducibles con tetraciclinas y reprimibles con tetraciclinas (remítase, p. ej., a Gatz *et al.* (1991) *Mol. Gen. Genet.* 227, 229-237, y las Patentes de EE. UU. N.ºs 5.814.618 y 5.789.156), promotores del sistema represor Lac, promotores del sistema incucible con cobre, promotores del sistema inducible con salicilato (p. ej., el sistema PR1a), promotores inducibles con glucocorticoides (Aoyama *et al.* (1997) *Plant J.* 11:605-612) y promotores del sistema inducible con ecdisona.

Otros ejemplos no limitantes de promotores inducibles incluyen promotores inducibles con ABA y turgor, el promotor de los genes de proteínas de unión a auxina (Schwob *et al.* (1993) *Plant J.* 4:423-432), el promotor de la UDP-glucosa-flavonoide-glicosil-transferasa (Ralston *et al.* (1988) *Genetics* 119:185-197), el promotor del inhibidor MPI-proteinasa (Cordero *et al.* (1994) *Plant J.* 6:141-150) y el promotor de la gliceraldehido-3-fosfato-deshidrogenasa (Kohler *et al.* (1995) *Plant Mol. Biol.* 29:1293-1298; Martínez *et al.* (1989) *J. Mol. Biol.* 208:551-565; y Quigley *et al.* (1989) *J. Mol. Evol.* 29:412-421). También se incluyen los promotores de los sistemas inducibles con bencenosulfonamida (Patente de EE. UU. N.º 5.364.780) e inducibles con alcohol (Publicaciones de Solicitud de Patente Internacional N.^{os} WO 97/06269 y WO 97/06268) y de la glutationa-S-transferasa. Asimismo, se puede utilizar cualquiera de los promotores inducibles descritos en Gatz (1996) *Current Opinion Biotechnol.* 7:168-172 y Gatz (1997) *Annu. Rev. Plant Physiol. Plant Mol. Biol.* 48:89-108. En la Patente de EE. UU. 5.614.395, la cual se incorpora a la presente en su totalidad a modo de referencia, se describen otros promotores inducibles químicamente útiles para dirigir la expresión de las secuencias de nucleótidos de esta invención en plantas. La inducción química de la expresión génica también se describe con detalle en la solicitud publicada EP 0 332 104 (concedida a Ciba-Geigy) y la Patente de EE. UU. 5.614.395. En algunas realizaciones, un promotor para inducción química puede ser el promotor PR-1a del tabaco.

En otros aspectos, las secuencias de nucleótidos de la invención pueden estar asociadas operativamente a un promotor que sea inducible con heridas o inducible con infecciones de patógenos o plagas (p. ej., una plaga de nematodos que atacan plantas). Se han descrito muchos promotores que se expresan en los sitios de heridas y/o en los sitios de ataque de plagas (p. ej., donde se alimentan los nematodos/insectos) o de infección por fitopatógenos. Idealmente, un promotor de este tipo debería ser activo solo

localmente en los sitios de ataque o adyacentes, y de este modo la expresión de las secuencias de nucleótidos de la invención se centraría en las células que están siendo invadidas. Los promotores de este tipo incluyen, sin carácter limitante, los descritos por Stanford *et al.*, *Mol. Gen. Genet.* 215:200-208 (1989), Xu *et al. Plant Molec. Biol.* 22:573-588 (1993), Logemann *et al*. *Plant Cell* 1:151-158 (1989), Rohrmeier y Lehle, *Plant Molec. Biol.* 22:783-792 (1993), Firek *et al*. *Plant Molec. Biol.* 22:129-142 (1993), Warner *et al*. *Plant J.* 3:191-201 (1993), la Patente de EE. UU. N.º 5.750.386, la Patente de EE. UU. N.º 5.955.646, la Patente de EE. UU. N.º 6.262.344, la Patente de EE. UU. N.º 6.395.963, la Patente de EE. UU. N.º 6.703.541, la Patente de EE. UU. N.º 7.078.589, la Patente de EE. UU. N.º 7.196.247, la Patente de EE. UU. N.º 7.223.901 y la Publicación de Solicitud de Patente de EE. UU. 2010043102.

La expresión "casete de expresión", tal como se utiliza en la presente, se refiere a una molécula de ácido nucleico que comprende una secuencia de nucleótidos de interés (p. ej., las secuencias de nucleótidos de la invención), donde dicha secuencia de nucleótidos está asociada operativamente con al menos una secuencia de control (p. ej., un promotor). De este modo, algunas realizaciones de la invención proporcionan casetes de expresión diseñados para expresar las secuencias de nucleótidos de la invención. De este modo, por ejemplo, se proporcionan uno o más promotores vegetales asociados operativamente con una o más secuencias de nucleótidos de la invención (p. ej., **SEQ ID NOs:1-28**, **SEQ ID NOs:43-134**, **SEQ ID NOs:210-242, SEQ ID NOs:261-644**) en casetes de expresión para la expresión en un organismo o una de sus células (p. ej., una planta, parte de planta y/o célula vegetal).

Un casete de expresión que comprende una secuencia de nucleótidos de interés puede ser quimérico, lo que significa que al menos uno de sus componentes es heterólogo con respecto a al menos uno de sus demás componentes. Un casete de expresión también puede ser de los de origen natural, pero que se ha obtenido en una forma recombinante útil para la expresión heteróloga. Sin embargo, normalmente el casete de expresión es heterólogo con respecto al huésped, es decir, la secuencia de ácido nucleico particular del casete de expresión no se encuentra de forma natural en la célula huésped y se debe haber introducido en la célula huésped o en un antecesor de la célula huésped mediante un evento de transformación.

Además de los promotores unidos operativamente a las secuencias de nucleótidos de la invención, un casete de expresión de la invención también puede incluir otras secuencias reguladoras. La expresión "secuencias reguladoras", tal como se utiliza en la presente, se refiere a secuencias de nucleótidos situadas antes (secuencias no codificantes 5’), en o después (secuencias no codificantes 3’) de una secuencia

codificante y que afectan a la transcripción, el procesamiento o la estabilidad del ARN, o la traducción de la secuencia codificante asociada. Las secuencias reguladoras incluyen, sin carácter limitante, promotores, potenciadores, intrones, secuencias líder de la traducción, señales de terminación y secuencias señal de la poliadenilación.

A los efectos de la invención, las regiones o secuencias reguladoras pueden ser nativas/análogas respecto a la planta, parte de planta y/o célula vegetal y/o las secuencias reguladoras pueden ser nativas/análogas respecto a las otras secuencias reguladoras. Como alternativa, las secuencias reguladoras pueden ser heterólogas respecto a la planta (y/o parte de plata y/o célula vegetal) y/o unas respecto a otras (es decir, respecto a las secuencias reguladoras). De este modo, por ejemplo, un promotor puede ser heterólogo si está unido operativamente a un polinucleótido de una especie diferente de la especie de la cual se derivó el polinucleótido. Como alternativa, un promotor también puede ser heterólogo respecto a una secuencia de nucleótidos seleccionada si el promotor es de la misma especie/una especie análoga respecto a la especie de la cual se deriva el polinucleótido, pero uno de ellos o ambos (es decir, el promotor y/o el polinucleótido) están modificados sustancialmente respecto a su locus genómico y/o forma original, y/o el promotor no es el promotor nativo para el polinucleótido unido operativamente.

Existe constancia de que cierto número de secuencias líder no traducidas derivadas de virus mejoran la expresión génica. Específicamente, se ha demostrado que las secuencias líder del virus del mosaico del tabaco (TMV, la "secuencia ω"), del virus del moteado clorótico del maíz (MCMV) y del virus del mosaico de la alfalfa (AMV) son eficaces para incrementar la expresión (Gallie *et al.* (1987) *Nucleic Acids Res.* 15:8693-8711; y Skuzeski *et al.* (1990) *Plant Mol. Biol.* 15:65-79). Otras secuencias líder conocidas en la técnica incluyen, sin carácter limitante, secuencias líder de picornavirus tales como una secuencia líder de la región no codificante 5' de encefalomiocarditis (EMCV) (Elroy-Stein *et al.* (1989) *Proc. Natl. Acad. Sci. USA* 86:6126-6130); secuencias líder de potivirus tales como la secuencia líder del virus del grabado del tabaco (TEV) (Allison *et al.* (1986) *Virology* 154:9-20); secuencia líder del virus del mosaico enanizante del maíz (MDMV) (Allison *et al.* (1986), mencionado anteriormente); secuencia líder de la proteína de unión a la cadena pesada de inmunoglobulinas humanas (BiP) (Macejak & Samow (1991) *Nature* 353:90-94); secuencia líder no traducida del ARNm de las proteínas de revestimiento de AMV (AMV RNA 4; Jobling & Gehrke (1987) *Nature* 325:622-625); secuencia líder del virus del mosaico del tabaco TMV (Gallie *et al.* (1989) *Molecular Biology of RNA* 237-256); y secuencia líder MCMV (Lommel *et al.* (1991)

Virology 81:382-385). Remítase también a Della-Cioppa *et al.* (1987) *Plant Physiol.* 84:965-968.

Un casete de expresión también puede incluir opcionalmente una región de terminación de la transcripción y/o traducción (es decir, región de terminación) que sea funcional en plantas. Se dispone de varios terminadores de la transcripción que se pueden utilizar en casetes de expresión y que son responsables de la terminación de la transcripción más allá de la secuencia de nucleótidos heteróloga de interés y la correcta poliadenilación del ARNm. La región de terminación puede ser nativa respecto a la región de iniciación de la transcripción, puede ser nativa respecto a la secuencia de nucleótidos de interés unida operativamente, puede ser nativa respecto a la planta huésped o puede derivarse de otra fuente (es decir, exógena o heteróloga respecto al promotor, la secuencia de nucleótidos de interés, la planta huésped o cualquier combinación de estos). Los terminadores de la transcripción adecuados incluyen, sin carácter limitante, el terminador CAMV 35S, el terminador tml, el terminador de la nopalina-sintasa y/o el terminador rbcs E9 del chícharo. Estos pueden utilizarse tanto en plantas monocotiledóneas como en dicotiledóneas. Además, puede utilizarse un terminador de la transcripción nativo de la secuencia codificante.

Un casete de expresión de la invención también puede incluir una secuencia de nucleótidos para un marcador seleccionable, que se puede utilizar para seleccionar una planta, parte de planta y/o célula vegetal transformada. La expresión "marcador seleccionable", tal como se utiliza en la presente, se refiere a una secuencia de nucleótidos que, cuando se expresa, imparte un fenotipo distintivo a la planta, parte de planta y/o célula vegetal que expresa el marcador y, de este modo, permite diferenciar tales plantas, partes de planta y/o células vegetales transformadas de aquellas que no tienen el marcador. Tal secuencia de nucleótidos puede codificar un marcador seleccionable o detectable, dependiendo de si el marcador confiere un rasgo que se pueda seleccionar de un modo químico, tal como utilizando un agente selectivo (p. ej., un antibiótico, herbicida o similar), o de si el marcador es simplemente un rasgo que se pueda identificar mediante observación o análisis, tal como mediante detección selectiva (p. ej., el rasgo del locus R). Por supuesto, existen muchos ejemplos de marcadores seleccionables adecuados en la técnica, los cuales se pueden utilizar en los casetes de expresión descritos en la presente.

Los ejemplos de marcadores seleccionables incluyen, sin carácter limitante, una secuencia de nucleótidos que codifica *neo* o *nptII*, que confiere resistencia a la kanamicina, G418 y similares (Potrykus *et al.* (1985) *Mol. Gen. Genet.* 199:183-188); una secuencia de nucleótidos que codifica *bar,* que confiere resistencia a fosfinotricina; una

secuencia de nucleótidos que codifica una 5-enolpiruvilshikimato-3-fosfato(EPSP)-sintasa alterada, que confiere resistencia a glifosato (Hinchee *et al.* (1988) *Biotech.* 6:915-922); una secuencia de nucleótidos que codifica una nitrilasa tal como *bxn* de *Klebsiella ozaenae* que confiere resistencia a bromoxinilo (Stalker *et al.* (1988) *Science* 242:419-423); una secuencia de nucleótidos que codifica una acetolactato-sintasa (ALS) alterada que confiere resistencia a imidazolinona, sulfonilurea u otros productos químicos que inhiben ALS (Solicitud de Patente Europea N.º 154204); una secuencia de nucleótidos que codifica una dihidrofolato-reductasa (DHFR) resistente a metotrexato (Thillet *et al.* (1988) *J. Biol. Chem.* 263:12500-12508); una secuencia de nucleótidos que codifica una dalapón-deshalogenasa que confiere resistencia a dalapón; una secuencia de nucleótidos que codifica una manosa-6-fosfato-isomerasa (denominada también fosfomanosa-isomerasa (PMI)) que confiere una capacidad para metabolizar manosa (Patentes de EE. UU. N.os 5.767.378 y 5.994.629); una secuencia de nucleótidos que codifica una antranilato-sintasa alterada que confiere resistencia a 5-metiltriptófano; y/o una secuencia de nucleótidos que codifica *hph* que confiere resistencia a higromicina. Un experto en la técnica será capaz de elegir un marcador seleccionable adecuado para utilizar en un casete de expresión de la invención.

Los marcadores seleccionables adicionales incluyen, sin carácter limitante, una secuencia de nucleótidos que codifica β-glucuronidasa o *uidA* (GUS) que codifica una enzima para la que se conocen varios sustratos cromogénicos; una secuencia de nucleótidos del locus R que codifica un producto que regula la producción de pigmentos de antocianina (color rojo) en tejidos vegetales (Dellaporta *et al.*, "Molecular cloning of the maize R-nj allele by transposon-tagging with Ac", págs. 263-282 en: *Chromosome Structure and Function: Impact of New Concepts,* 18.º Simposio sobre Genética de Stadler (Gustafson & Appels eds., Plenum Press 1988)); una secuencia de nucleótidos que codifica β-lactamasa, una enzima para la que se conocen varios sustratos cromogénicos (p. ej., PADAC, una cefalosporina cromogénica) (Sutcliffe (1978) *Proc. Natl. Acad. Sci. USA* 75:3737-3741); una secuencia de nucleótidos que codifica *xylE* que codifica una catecol-dioxigenasa (Zukowsky *et al.* (1983) *Proc. Natl. Acad. Sci. USA* 80:1101-1105); una secuencia de nucleótidos que codifica tirosinasa, una enzima capaz de oxidar tirosina a DOPA y dopaquinona, que a su vez condensa para formar melanina (Katz *et al.* (1983) *J. Gen. Microbiol.* 129:2703-2714); una secuencia de nucleótidos que codifica β-galactosidasa, una enzima para la cual se conocen sustratos cromogénicos; una secuencia de nucleótidos que codifica luciferasa (lux) que permite la detección de bioluminescencia (Ow *et al.* (1986) *Science* 234:856-859); una secuencia de nucleótidos que codifica aequorina, que se puede emplear en la detección de bioluminescencia

sensible al calcio (Prasher *et al.* (1985) *Biochem. Biophys. Res. Comm.* 126:1259-1268); o una secuencia de nucleótidos que codifica proteína fluorescente verde (Niedz *et al.* (1995) *Plant Cell Reports* 14:403-406). Un experto en la técnica será capaz de elegir un marcador seleccionable adecuado para utilizar en un casete de expresión de la invención.

Un casete de expresión de la invención también puede incluir secuencias de nucleótidos que codifiquen otros rasgos deseados. Estos rasgos deseados pueden ser otras secuencias de nucleótidos que confieran resistencia a nematodos, resistencia a insectos o que confieran otros rasgos deseables desde un punto de vista agrícola. Tales secuencias de nucleótidos se pueden agrupar con cualquier combinación de secuencias de nucleótidos para crear plantas, partes de plantas o células vegetales con el fenotipo deseado. Se pueden crear combinaciones agrupadas mediante cualquier método, incluido, sin carácter limitante, el cultivo selectivo de plantas mediante metodología convencional o transformación genética. Si se agrupan mediante transformación genética de las plantas, las secuencias de nucleótidos que codifican rasgos deseados adicionales se pueden combinar en cualquier momento y en cualquier orden. Por ejemplo, se puede utilizar una planta transgénica que comprenda uno o más rasgos deseados como diana para introducir otros rasgos mediante una transformación posterior. Las secuencias de nucleótidos adicionales se pueden introducir simultáneamente en un protocolo de cotransformación con una secuencia de nucleótidos, molécula de ácido nucleico, constructo de ácido nucleico y/o composición de la invención, proporcionados por cualquier combinación de casetes de expresión. Por ejemplo, si se introducen dos secuencias de nucleótidos, estas se pueden incorporar en casetes separados (*trans*) o se pueden incorporar en el mismo casete (*cis*). La expresión de las secuencias de nucleótidos puede estar controlada por el mismo promotor o por promotores diferentes. Se reconoce además que las secuencias de nucleótidos se pueden agrupar en un sitio genómico deseado usando un sistema de recombinación específico para un sitio. Remítase, p. ej., a las Publicaciones de Solicitud de Patente Internacional N.^{os} WO 99/25821, WO 99/25854, WO 99/25840, WO 99/25855 y WO 99/25853.

De este modo, un casete de expresión puede incluir una secuencia codificadora de uno o más polipéptidos para rasgos agronómicos que sean beneficiosos principalmente para una empresa de semillas, un agricultor o procesador de grano. Un polipéptido de interés puede ser cualquier polipéptido codificado por una secuencia de nucleótidos de interés. Los ejemplos no limitantes de polipéptidos de interés que son adecuados para la producción en plantas incluyen aquellos que dan como resultado rasgos agronómicamente importantes tales como resistencia a herbicidas (también denominada en ocasiones "tolerancia a herbicidas"), resistencia a virus, resistencia a patógenos

bacterianos, resistencia a insectos, resistencia a nematodos y/o resistencia a hongos. Remítase, p. ej., a las Patentes de EE. UU. N.os 5.569.823, 5.304.730, 5.495.071, 6.329.504 y 6.337.431. De este modo, en algunas realizaciones, el casete de expresión o vector de expresión de la invención puede comprender una o más secuencias de nucleótidos que confieren resistencia a insectos y/o resistencia a nematodos adicional.

En otras realizaciones, un polipéptido de interés también puede ser uno que aumente el vigor o rendimiento de la planta (incluidos los rasgos que permiten que una planta se desarrolle a temperaturas, condiciones de suelo y niveles de luz solar y precipitación diferentes) o uno que permita identificar una planta que exhiba un rasgo de interés (p. ej., un marcador seleccionable, color del revestimiento de la semilla, etc.). Se describen varios polipéptidos de interés, así como también métodos para producir estos polipéptidos en una planta, por ejemplo, en las Patentes de EE. UU. N.os 4.761.373, 4.769.061, 4.810.648; 4.940.835, 4.975.374, 5.013.659, 5.162.602, 5.276.268, 5.304.730, 5.495.071, 5.554.798, 5.561.236, 5.569.823, 5.767.366, 5.879.903, 5.928.937, 6.084.155, 6.329.504 y 6.337.431, así como también la Publicación de Patente de EE. UU. N.o 2001/0016956. Remítase también a la red informática mundial en lifesci.sussex.ac.uk/home/Neil_Crickmore/Bt/.

En algunas realizaciones particulares de la invención, una secuencia de nucleótidos de interés incluye, sin carácter limitante, iARN (ARNip, ARN antisentido) y/o miARN, que se asocia con la resistencia a nematodos, y/o secuencias de nucleótidos que codifican resistencia a insectos, que incluyen, sin carácter limitante, secuencias de nucleótidos que codifican toxinas de *Bacillus thuringiensis* (Bt), por ejemplo, los genes de varias delta-endotoxias tales como *Cry1Aa*, *Cry1Ab*, *Cry1Ac*, *Cry1B*, *Cry1C*, *Cry1D*, *Cry1Ea*, *Cry1Fa*, *Cry3A*, *Cry9A*, *Cry9C* y *Cry9B*; así como también genes que codifican proteínas insecticidas vegetativas tales como *Vip1*, *Vip2* y *Vip3*. Se puede consultar una lista exhaustiva de toxinas de Bt en Internet, en la base de datos para la nomenclatura de toxinas de *Bacillus thuringiensis* de cuyo mantenimiento se encarga la Universidad de Sussex (remítase también a Crickmore *et al.* (1998) *Microbiol. Mol. Biol. Rev.* 62:807-813).

Además de los casetes de expresión, las moléculas de ácido nucleico y secuencias de nucleótidos que se describen en la presente se pueden emplear junto con vectores. El término "vector" se refiere a una composición para transferir, suministrar o introducir un ácido nucleico (o ácidos nucleicos) en una célula. Un vector comprende una molécula de ácido nucleico que comprende la(s) secuencia(s) de nucleótidos que se ha(n) de transferir, suministrar o introducir. Los vectores que se emplean en la transformación de plantas y otros organismos son muy conocidos en la técnica. Los ejemplos no limitantes de clases generales de vectores incluyen un vector viral, incluido, sin carácter

limitante, un vector de adenovirus, un vector retroviral, un vector viral adenoasociado, un vector plasmídico, un vector derivado de fago, un vector fagémido, un cósmido, un fósmido, un bacteriófago o un cromosoma artificial. La selección de un vector dependerá de la técnica de transformación preferida y de la especie diana de la transformación. Por consiguiente, en otras realizaciones, una molécula de ácido nucleico recombinante de la invención puede estar comprendida en un vector recombinante. El tamaño de un vector puede variar considerablemente dependiendo de si el vector comprende uno o múltiples casetes de expresión (p. ej., para agrupación molecular). De este modo, el tamaño de un vector puede estar comprendido entre aproximadamente 3 kb y aproximadamente 30 kb. De este modo, en algunas realizaciones, el vector tiene un tamaño de aproximadamente 3 kb, 4 kb, 5 kb, 6 kb, 7 kb, 8 kb, 9 kb, 10 kb, 11 kb, 12 kb, 13 kb, 14 kb, 15 kb, 16 kb, 17 kb, 18 kb, 19 kb, 20 kb, 21 kb, 22 kb, 23 kb, 24 kb, 25 kb, 26 kb, 27 kb, 28 kb, 29 kb, 30 kb o cualquier intervalo comprendido entre estos valores. En algunas realizaciones particulares, el vector puede tener un tamaño comprendido entre aproximadamente 3 kb y aproximadamente 10 kb.

En realizaciones adicionales de la invención, se proporciona un método para producir una célula vegetal transgénica, comprendiendo dicho método introducir en una célula vegetal una molécula de ácido nucleico recombinante/secuencia de nucleótidos de la invención, con lo que se produce una célula vegetal transgénica que puede regenerar una planta transgénica con mayor resistencia a una plaga de nematodos que atacan plantas, en comparación con una planta regenerada a partir de una célula vegetal que no comprende dicha molécula de ácido nucleico. En algunas realizaciones, la célula vegetal transgénica comprende más de una (p. ej., 2, 3, 4, 5, 6, 7, 8, 9, 10, etc.) molécula de ácido nucleico/secuencia de nucleótidos de la invención. De este modo, en algunos aspectos de la invención, las plantas transgénicas, o partes de estas, comprenden y expresan una o más moléculas de ácido nucleico/secuencias de nucleótidos de la invención, con la que producen uno o más polipéptidos de la invención.

En realizaciones representativas, se proporciona un método para producir una célula vegetal transgénica, comprendiendo dicho método introducir en una célula vegetal una molécula de ácido nucleico recombinante de la invención, comprendiendo dicha molécula de ácido nucleico recombinante una secuencia de nucleótidos unida operativamente a un promotor que, cuando se expresa en una planta, confiere una mayor resistencia a una plaga de nematodos en plantas, donde la secuencia de nucleótidos comprende, está constituida esencialmente por o está constituida por: (a) una secuencia de nucleótidos de cualquiera de **SEQ ID NOs:1-28**, **SEQ ID NOs:43-134**, **SEQ ID NOs:210-242, SEQ ID NOs:261-644**; (b) una secuencia de nucleótidos que codifica un polipéptido que

comprende, está constituido esencialmente por o está constituido por la secuencia de aminoácidos de cualquiera de **SEQ ID NOs:29-42**, **SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046**; (c) una secuencia de nucleótidos que presenta una identidad secuencial significativa respecto a la secuencia de nucleótidos de (a) y (b) anteriores; (d) una secuencia de nucleótidos que se aparea en condiciones rigurosas de hibridación con la secuencia de nucleótidos de (a), (b) o (c); (e) una secuencia de nucleótidos que difiere de las secuencias de nucleótidos de (a), (b), (c) o (d) anteriores debido a la degeneración del código genético; o (f) cualquier combinación de las secuencias de nucleótidos de (a)-(e), con lo que se produce una célula vegetal transgénica que puede regenerar una planta con una mayor resistencia a una plaga de nematodos que atacan plantas, en comparación con una planta regenerada a partir de una célula vegetal que no comprende dicha molécula de ácido nucleico recombinante. En realizaciones adicionales, se proporciona un método para producir una célula vegetal transgénica, comprendiendo dicho método introducir en una célula vegetal una molécula de ácido nucleico recombinante de la invención, comprendiendo dicha molécula de ácido nucleico recombinante una secuencia de nucleótidos unida operativamente a un promotor que, cuando se expresa en una planta, confiere una mayor resistencia a una plaga de nematodos que atacan plantas, donde la secuencia de nucleótidos comprende, está constituida esencialmente por o está constituida por: (a) una secuencia de nucleótidos de cualquiera de **SEQ ID NOs: 15, 17, 20, 22, 23, 24, 26, 226, 227, 228, 230, 232** y/o **233**; (b) una secuencia de nucleótidos que codifica un polipéptido que comprende, está constituido esencialmente por o está constituido por la secuencia de aminoácidos de cualquiera de **SEQ ID NOs: 29, 31, 34, 36-38, 40, 244-246, 250, 251**; (c) una secuencia de nucleótidos que presenta una identidad secuencial significativa respecto a la secuencia de nucleótidos de (a) y (b) anteriores; (d) una secuencia de nucleótidos que se aparea en condiciones rigurosas de hibridación con la secuencia de nucleótidos de (a), (b) o (c); (e) una secuencia de nucleótidos que difiere de las secuencias de nucleótidos de (a), (b), (c) o (d) anteriores debido a la degeneración del código genético; o (f) cualquier combinación de las secuencias de nucleótidos de (a)-(e), con lo que se produce una célula vegetal transgénica que puede regenerar una planta con una mayor resistencia a una plaga de nematodos que atacan plantas, en comparación con una planta regenerada a partir de una célula vegetal que no comprende dicha molécula de ácido nucleico recombinante.

De este modo, en algunas realizaciones, la invención proporciona una planta transgénica o parte de esta que se regenera a partir de una célula vegetal transgénica de la invención, donde la planta o parte de planta transgénica presenta una mayor resistencia a una plaga de nematodos que atacan plantas, en comparación con una planta o parte de

planta de control que se regenera a partir de una célula vegetal que no comprende dicha molécula de ácido nucleico recombinante.

Los términos "aumentar", "que aumenta", "mayor", "mejorar", "superior", "que mejora" y "aumento" (y sus variaciones gramaticales), tal como se utilizan en la presente, describen un aumento de la resistencia de una planta a una plaga de nematodos que atacan plantas (p. ej., una planta de soja que presenta una mayor resistencia al nematodo que induce quistes en la soja) mediante la introducción de una molécula de ácido nucleico recombinante de la invención en la planta, con lo que se produce una planta transgénica que presenta una mayor resistencia a la plaga. Este aumento de la resistencia se puede observar comparando la resistencia de la planta transformada con la molécula de ácido nucleico recombinante de la invención con la resistencia de una planta que carece de (es decir, que no ha sido transformada con) la molécula de ácido nucleico recombinante de la invención (es decir, un control).

Los términos "reducir", "reducido", "que reduce", "reducción", "disminuir", "suprimir" y "atenuar" (y sus variaciones gramaticales), tal como se utilizan en la presente, describen, por ejemplo, una reducción del crecimiento de una plaga de nematodos que atacan plantas, una reducción de la capacidad del nematodo para sobrevivir, desarrollarse, alimentarse y/o reproducirse, una reducción de la capacidad infecciosa de una plaga de nematodos que atacan plantas, una reducción de la infestación de una planta por parte de una plaga de nematodos que atacan plantas y/o una reducción del desarrollo de quistes inducidos por nematodos de una plaga de nematodos que atacan plantas en las raíces de una planta en comparación con un control, según se describe en la presente.

Un aspecto adicional de la invención proporciona células huésped no humanas transformadas y organismos no humanos transformados que comprenden células no humanas transformadas, donde las células transformadas y los organismos transformados comprenden moléculas de ácido nucleico que comprenden una o más secuencias de nucleótidos de la invención. En algunas realizaciones, la célula huésped no humana transformada incluye, sin carácter limitante, una célula bacteriana transformada y/o una célula vegetal transformada. De este modo, en algunas realizaciones, el organismo no humano transformado que comprende la célula huésped no humana transformada incluye, sin carácter limitante, una bacteria transformada y/o una planta transformada.

En algunas realizaciones particulares, la invención proporciona una célula vegetal transformada que comprende una molécula de ácido nucleico de la invención y/o una planta transgénica regenerada a partir de dicha célula vegetal transgénica. Por

consiguiente, en algunas realizaciones de la invención, se proporciona una planta transgénica que presenta una mayor resistencia a una plaga de nematodos que atacan plantas, donde dicha planta transgénica se regenera a partir de una célula vegetal transgénica que comprende al menos una molécula de ácido nucleico recombinante/secuencia de nucleótidos de la invención.

Aspectos adicionales de la invención incluyen un producto recolectado producido a partir de las plantas transgénicas y/o partes de estas de la invención, así como también un producto procesado producido a partir de dicho producto recolectado. Un producto recolectado puede ser una planta entera o cualquier parte de la planta, según se describe en la presente, donde dicho producto recolectado comprende una molécula de ácido nucleico recombinante/secuencia de nucleótidos de la invención. De este modo, en algunas realizaciones, los ejemplos no limitantes de un producto recolectado incluyen una semilla, una fruta, una flor o una de sus partes (p. ej., una antera, un estigma y similares), una hoja, un tallo y similares. En otras realizaciones, un producto procesado incluye, sin carácter limitante, harina, pienso, aceite, almidón, cereales y similares, producidos a partir de una semilla recolectada de la invención, donde dicha semilla comprende una molécula de ácido nucleico recombinante/secuencia de nucleótidos de la invención.

Los ejemplos no limitantes de plantas pueden incluir cultivos de verduras, que incluyen alcachofas, colinabo, rúcula, puerros, espárragos, lechuga (p. ej., arrepollada, criolla, romana), bok choy, malanga, melones (p. ej., almizcle, sandía, melón amarillo, melón verde, cantalupo), cultivos de coles (p. ej., coles de Bruselas, repollo, coliflor, brócoli, berzas, col crespa, col china, bok choy) cardo, zanahorias, col napa, ocra, cebollas, apio, perejil, chícharos, chirivías, endibias, pimientos, papas, cucurbitáceas (p. ej., tuétano, pepino, calabacín, cidra cayote, calabaza), rábanos, cebollas de bulbo seco, rutabaga, berenjena (también denominada brinjal), salsifí, escarola, chalotas, endivias, ajo, espinacas, ajos tiernos, cidra cayote, verduras de hoja, remolacha (remolacha azucarera y remolacha forrajera), batatas, acelgas, rábano picante, tomates, nabos y especies; un cultivo frutal y/o de la vid tal como manzanas, damascos, cerezas, nectarinas, duraznos, peras, ciruelas, prunas, cerezas, membrillo, almendras, castañas, avellanas, nuez pecana, pistachos, nueces, cítricos, arándanos, bayas boysenas, arándanos rojos, grosellas, bayas loganas, frambuesas, frutillas, moras, uvas, aguacates, plátanos, kiwis, caquis, granada, piña, frutas tropicales, pomos, melón, mango, papaya y lichi; una planta de un cultivo de campo tal como trébol, alfalfa, onagra, Limnanthes alba, maíz (de campo, dulce, palomitas de maíz), lúpulos, jojoba, maníes, arroz, cártamo, granos pequeños (cebada, avena, centeno, trigo, etc.), sorgo, tabaco, pochote, una planta leguminosa (alubias, lentejas, arvejas, soja), una planta oleaginosa (colza, mostaza,

amapola, oliva, girasol, coco, planta de aceite de ricino, cacao, maní), *Arabidopsis*, una planta que produce fibra (algodón, lino, cáñamo, yute), lauráceas (canela, alcanfor) o una planta tal como café, caña de azúcar, té y plantas que producen goma natural; y/o una planta de parterre tal como una planta floral, un cactus, una planta ornamental y/o exhuberante, así como también árboles tales como árboles forestales (árboles latifolios y perennifolios tales como las coníferas), árboles frutales, ornamentales y que producen frutos secos, así como también arbustos y otros productos de vivero.

En algunas realizaciones, una planta puede ser cualquier especie vegetal o variedad vegetal que sea vulnerable a la infección de nematodos que inducen quistes en la soja, que incluye, sin carácter limitante, clavel chino, alubias comestibles, lespedeza, *Vicia* (común, vellosa o de invierno), lupino, trébol (carmesí, escarlata o híbrido), trébol de olor amarillo, loto corniculado, coronilla rosa, arveja, chícharo salvaje, frijol cabecita negra, soja (natural y cultivada), robinia negra, robinia de la miel, portulaca, Campanas de Irlanda, álsine, oreja de ratón, *Vervascum*, *Senna obtusifolia*, *Digitalis penstemon*, ombú, verdolaga, berro amargo, *Cleome serrulata*, *Geranium maculatum*, linaria, *Cycloloma*, *Psoralea* spp*., Cleome serrulata, Vicia* (americana, caroliniana), trébol carretilla (*Medicago minima*), oreja de ratón (*Cerastium vulgatum*), dalea, *Astragalus canadensis*, *Sesbania herbacea*, borraja, flor del canario, *Nierembergia*, alcaravea, *Physalis alkekengi*, Viscaria de gema azul, campana de coral, clavel de flor doble de Margaret, *Rosa multiflora*, reina rosada, geranio (*Geranium maculatum*), *Nierembergia*, *Delphinium*, digitales, *Geum*, marrubio, amapola, salvia, *Antirrhinum*, lengua vellosa (*Penstemon digitalis*), *Desmodium nudifolorum, D. marilandicum, D. viridiflorum,* neguilla, albahaca, arvejilla de olor, *Verbena*, ortiga mansa (*Lamium amplexicaule*), lamio púrpura (*Lamium purpureum*), (carraspique (*Thlaspi arvense*), zurrón de pastor (*Capsella bursa-pastoris*), tréboles amarillos, *Desmodium*, neguilla, *Amphicarpaea bracteata*, *Galactia spiciformis* y pallar (*Strophostyles helvola*).

En algunas realizaciones particulares, una planta transgénica de la invención incluye, sin carácter limitante, una planta de soja transgénica, una planta de remolacha azucarera transgénica, una planta de maíz transgénica, una planta de algodón transgénica, una planta de canola transgénica, una planta de trigo transgénica o una planta de arroz transgénica. En otras realizaciones, una célula vegetal transgénica de la invención incluye, sin carácter limitante, una célula de soja transgénica, una célula de remolacha azucarera transgénica, una célula de maíz transgénica, una célula de algodón transgénica, una célula de canola transgénica, una célula de caña de azúcar transgénica, una célula de trigo transgénica o una célula de arroz transgénica.

La expresión "parte de planta", tal como se utiliza en la presente, incluye, sin carácter limitante, embriones, polen, óvulos, semillas, hojas, flores, ramas, fruto, granos, mazorcas, olotes, vainas, tallos, raíces, ápices de las raíces, anteras, células vegetales, incluidas las células vegetales que están intactas en plantas y/o partes de plantas, protoplastos vegetales, tejidos vegetales, cultivos de tejidos de células vegetales, callos de plantas, agregados vegetales y similares. Además, la expresión "célula vegetal", tal como se utiliza en la presente, se refiere a una unidad estructural y fisiológica de la planta que comprende una pared celular y también se puede denominar protoplasto. Una célula vegetal de la invención puede estar en forma de una única célula aislada o puede ser una célula cultivada o puede formar parte de una unidad más organizada tal como, por ejemplo, un tejido vegetal o un órgano vegetal. Un "protoplasto" es una célula vegetal aislada sin una pared celular o solamente con partes de la pared celular. De este modo, en algunas realizaciones de la invención, una célula transgénica que comprende una molécula de ácido nucleico y/o una secuencia de nucleótidos de la invención es una célula de cualquier planta o parte de planta, que incluye, sin carácter limitante, una célula de la raíz, una célula de una hoja, una célula de un cultivo tisular, una célula de una semilla, una célula de una flor, una célula de una fruta, una célula del polen y similares.

En algunas realizaciones particulares, la invención proporciona una semilla transgénica producida a partir de una planta transgénica de la invención, donde la semilla transgénica comprende una molécula de ácido nucleico/secuencia de nucleótidos de la invención.

La expresión "cultivo de células vegetales" se refiere a los cultivos de unidades vegetales tales como, por ejemplo, protoplastos, células de cultivo celular, células en los tejidos vegetales, polen, tubos polínicos, óvulos, sacos embrionarios, cigotos y embriones en diferentes etapas de desarrollo. En algunas realizaciones de la invención, se proporciona un cultivo de tejidos transgénicos o un cultivo de células vegetales transgénicas, donde el cultivo de células o tejidos transgénicos comprende una molécula de ácido nucleico/secuencia de nucleótidos de la invención.

La expresión "órgano vegetal", tal como se utiliza en la presente, se refiere a una parte distinta y visiblemente diferenciada y estructurada de una planta tal como una raíz, tallo, hoja, brote de la flor o embrión.

La expresión "tejido vegetal", tal como se utiliza en la presente, se refiere a un grupo de células vegetales organizadas en una unidad estructural y funcional. Queda incluido cualquier tejido vegetal *in planta* o en cultivo. Este término incluye, sin carácter limitante, plantas enteras, órganos vegetales, semillas de las plantas, el cultivo tisular y cualquier grupo de células vegetales organizado en unidades estructurales y/o

funcionales. El uso de este término junto con, o en ausencia de, cualquier tipo específico de tejido vegetal, como el que se indica anteriormente o que esté contemplado por esta definición, no pretende ser exclusivo para cualquier otro tipo de tejido vegetal.

La expresión "plaga de nematodos que atacan plantas", tal como se utiliza en la presente, incluye cualquier especie de nematodos que sea una plaga para una planta. Los ejemplos no limitantes de plagas de nematodos incluyen los nematodos que inducen quistes (*Heterodera* spp.), especialmente los nematodos que inducen quistes en la soja (*Heterodera glycines*), nematodos noduladores de raíz (*Meloidogyne* spp.), nematodos lanza (*Hoplolaimus* spp.), nematodos estilete (*Tylenchorhynchus* spp.), nematodos en espiral (*Helicotylenchus* spp.), nematodos lesionadores (*Pratylenchus* spp.), nematodos de aguijón (*Belonoluimus* spp.), nematodos reniformes (*Rotylenchulus reniformis*), nematodos barrenadores (*Radopholus similis*), nematodos de los cítricos (*Tylenchulus semipenetrans*) y nematodos anillados (*Criconema* spp.).

El término "introducir", en el contexto de una secuencia de nucleótidos de interés (p. ej., las secuencias de nucleótidos y moléculas de ácido nucleico de la invención), se refiere a presentar la secuencia de nucleótidos de interés a la planta, parte de planta y/o célula vegetal de forma tal que la secuencia de nucleótidos tenga acceso al interior de la célula. Cuando deba introducirse más de una secuencia de nucleótidos, estas secuencias de nucleótidos se pueden agrupar como parte de un único constructo de polinucleótido o de ácido nucleico o como constructos separados de polinucleótidos o de ácidos nucleicos, y pueden estar situadas en el mismo vector de transformación o en vectores diferentes. Por consiguiente, estos polinucleótidos se pueden introducir en células vegetales en un único evento de transformación, en eventos de transformación separados o, por ejemplo, como parte de un protocolo de cultivo selectivo. Por lo tanto, el término "transformación", tal como se utiliza en la presente, se refiere a la introducción de un ácido nucleico heterólogo en una célula. La transformación de una célula puede ser estable o transitoria. De este modo, en algunas realizaciones, una célula vegetal de la invención se transforma de forma estable con una molécula de ácido nucleico de la invención. En otras realizaciones, una planta de la invención se transforma de forma transitoria con una molécula de ácido nucleico de la invención.

La expresión "transformación transitoria", en el contexto de un polinucleótido, se refiere a que el polinucleótido se introduce en la célula pero no se integra en el genoma de la célula.

Se pretende que la expresión "introducir de forma estable" o "introducido de forma estable", en el contexto de un polinucléotido introducido en una célula, se refiera a que el

polinucleótido introducido se incorpora de forma estable en el genoma de la célula y, por consiguiente, la célula se transforma de forma estable con el polinucleótido.

La expresión "transformación estable" o "transformado de forma estable", tal como se utiliza en la presente, se refiere a que se introduce un ácido nucleico en una célula y se integra en el genoma de la célula. En este sentido, el ácido nucleico integrado puede ser heredado por su progenie, más particularmente, por la progenie de generaciones sucesivas múltiples. El término "genoma", tal como se utiliza en la presente, también incluye el genoma plastídico y el nuclear y, por lo tanto, incluye la integración del ácido nucleico en, por ejemplo, el genoma cloroplástico. La transformación estable, tal como se utiliza en la presente, también se puede referir a un transgén que se mantiene extracromosómicamente, por ejemplo, como un minicromosoma.

La transformación transitoria puede detectarse mediante, por ejemplo, un ensayo inmunoabsorbente ligado a enzimas (ELISA) o inmunotransferencia Western, que pueden detectar la presencia de un péptido o polipéptido codificado por uno o más transgenes introducidos en un organismo. La transformación estable de una célula puede detectarse mediante, por ejemplo, un ensayo de hibridación de inmunotransferencia Southern de ADN genómico de la célula con secuencias de ácidos nucleicos que se hibridan específicamente con una secuencia de nucleótidos de un transgén introducido en un organismo (por ejemplo, una planta). La transformación estable de una célula puede detectarse mediante, por ejemplo, un ensayo de hibridación de inmunotransferencia Northern de ARN de la célula con secuencias de ácidos nucleicos que se hibridan específicamente con una secuencia de nucleótidos de un transgén introducido en una planta u otro organismo. La transformación estable de una célula también puede detectarse mediante, p. ej., la reacción en cadena de la polimerasa (PCR) u otras reacciones de amplificación que son muy conocidas en la técnica, utilizando secuencias de cebadores específicas que se hibridan con la(s) secuencia(s) diana de un transgén, lo cual da como resultado la amplificación de la secuencia del transgén, que puede detectarse de acuerdo con métodos estándar. La transformación también puede detectarse mediante protocolos de secuenciación directa y/o hibridación de uso común en la técnica.

Un ácido nucleico de la invención (p. ej., una o más de las secuencias de nucleótidos de **SEQ ID NOs:1-28**, **SEQ ID NOs:43-134**, **SEQ ID NOs:210-242, SEQ ID NOs:261-644** o una secuencia de nucleótidos que codifica uno o más polipéptidos que presentan la secuencia de aminoácidos de cualquiera de **SEQ ID NOs:29-42**, **SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046**) se puede introducir en una célula mediante cualquier método conocido por los expertos en la técnica. En algunas

realizaciones de la invención, la transformación de una célula comprende una transformación nuclear. En otras realizaciones, la transformación de una célula comprende una transformación plastídica (p. ej., transformación de cloroplastos).

Los procedimientos para transformar plantas son muy conocidos y de uso rutinario en la técnica y se describen en la bibliografía. Los ejemplos no limitantes de métodos para transformar plantas incluyen la transformación mediante el suministro de ácidos nucleicos mediado por bacterias (p. ej., mediante *Agrobacteria*), suministro de ácidos nucleicos mediado por virus, suministro de ácidos nucleicos mediado por carburo de silicio o filamentos finos de ácidos nucleicos, suministro de ácidos nucleicos mediado por liposomas, microinyección, bombardeo de micropartículas, transformación mediada por fosfato de calcio, transformación mediada por ciclodextrinas, electroporación, transformación mediada por nanopartículas, sonicación, infiltración, captación de ácidos nucleicos mediada por polietilenglicol, así como cualquier otro mecanismo eléctrico, químico, físico (mecánico) y/o biológico que de como resultado la introducción de ácido nucleico en la célula vegetal, incluidas cualquiera de sus combinaciones. Las directrices generales para varios métodos de transformación de plantas conocidos en la técnica incluyen Miki *et al*. ("Procedures for Introducing Foreign DNA into Plants" en *Methods in Plant Molecular Biology and Biotechnology*, Glick, B. R. y Thompson, J. E., Eds. (CRC Press, Inc., Boca Ratón, 1993), páginas 67-88) y Rakowoczy-Trojanowska (*Cell. Mol. Biol. Lett*. 7:849-858 (2002)).

La transformación mediada por *Agrobacterium* es un método empleado habitualmente para la transformación de plantas, en particular, plantas dicotiledóneas, debido a su elevada eficacia de transformación y a su gran utilidad con muchas especies diferentes. La transformación mediada por *Agrobacterium* normalmente implica la transferencia del vector binario portador de ADN exógeno de interés a una cepa de *Agrobacterium* adecuada que puede depender del complemento de genes *vir* portados por la cepa huésped de *Agrobacterium* en un plásmido Ti corresidente o cromosómicamente (Uknes *et al.* (1993) *Plant Cell* 5:159-169). La transferencia del vector binario recombinante a *Agrobacterium* se puede realizar mediante un procedimiento de apareamiento triparental utilizando *Escherichia coli* portadora del vector binario recombinante, una cepa adyuvante de *E. coli* portadora de un plásmido que es capaz de movilizar el vector binario recombinante hasta la cepa de *Agrobacterium* diana. Como alternativa, el vector binario recombinante se puede transferir a *Agrobacterium* por transformación con ácidos nucleicos (Höfgen & Willmitzer (1988) *Nucleic Acids Res.* 16:9877).

La transformación de una planta por *Agrobacterium* recombinante suele implicar el cultivo conjunto de *Agrobacterium* con explantes de la planta y sigue métodos muy conocidos en la técnica. El tejido transformado se regenera en un medio de selección portador de un marcador de resistencia a antibióticos o herbicidas presente entre los bordes del ADN-T plasmídico binario.

Otro método para transformar plantas, partes de plantas y/o células vegetales implica la introducción propulsada de partículas inertes o biológicamente activas en tejidos y células vegetales. Remítase, p. ej., a las Patentes de EE. UU. N.ºs 4.945.050, 5.036.006 y 5.100.792. En general, este método implica propulsar partículas inertes o biológicamente activas hacia las células vegetales en condiciones eficaces para que atraviesen la superficie externa de la célula y consigan incorporarse en el interior de esta. Cuando se utilizan partículas inertes, el vector puede introducirse en la célula recubriendo las partículas con el vector que contiene el ácido nucleico de interés. Como alternativa, la célula o células pueden estar rodeadas por el vector de tal manera que el vector sea introducido en la célula por la estela de la partícula. También se pueden propulsar partículas biológicamente activas (p. ej., células de levadura desecadas, bacterias desecadas o un bacteriófago, cada uno de los cuales contiene uno o más ácidos nucleicos que se desean introducir) en tejido vegetal.

De este modo, en realizaciones particulares de la invención, una célula vegetal se puede transformar mediante cualquier método conocido en la técnica y según se describe en la presente y se pueden regenerar plantas intactas a partir de estas células transformadas empleando cualquiera de las diferentes técnicas conocidas. La regeneración de plantas a partir de células vegetales, cultivos de tejidos vegetales y/o protoplastos cultivados se describe, por ejemplo, en Evans *et al.* (*Handbook of Plant Cell Cultures,* Vol. 1, MacMilan Publishing Co. Nueva York (1983)); y Vasil I. R. (ed.) (*Cell Culture and Somatic Cell Genetics of Plants,* Acad. Press, Orlando, Vol. I (1984) y Vol. II (1986)). Los métodos para seleccionar plantas, células vegetales y/o cultivos de tejidos vegetales transgénicos transformados son de uso rutinario en la técnica y pueden emplearse en los métodos de la invención proporcionados en la presente.

Asimismo, las propiedades genéticas modificadas por ingeniería en las semillas y plantas, partes de plantas y/o células vegetales transgénicas de la invención anteriormente descritas se pueden transmitir por reproducción sexual o crecimiento vegetativo y, por lo tanto, pueden mantenerse y propagarse en las plantas de la progenie. Generalmente, el mantenimiento y la propagación hacen uso de métodos conocidos en agricultura desarrollados para adaptarse a propósitos específicos tales como la recolección, siembra o labranza.

Por consiguiente, una secuencia de nucleótidos se puede introducir en la planta, parte de planta y/o célula vegetal de varias formas muy conocidas en la técnica. Los métodos de la invención no dependen de un método particular para introducir una o más secuencias de nucleótidos en una planta, sino únicamente de que consigan acceder al interior de al menos una célula de la planta. Cuando deba introducirse más de una secuencia de nucleótidos, estas se pueden agrupar como parte de un único constructo de ácido nucleico o como constructos separados de ácidos nucleicos, y pueden estar situadas en el mismo constructo de ácido nucleico o en constructos diferentes. Por consiguiente, las secuencias de nucleótidos pueden introducirse en la célula de interés en un único evento de transformación, en eventos de transformación separados o, por ejemplo, en plantas, como parte de un protocolo de cultivo selectivo.

De este modo, en realizaciones adicionales, la invención proporciona un método para producir una planta con mayor resistencia a la infestación por parte de una plaga de nematodos que atacan plantas, comprendiendo el método los pasos de (a) cruzar una planta transgénica de la invención consigo misma o con otra planta para producir una semilla que comprenda un vector o una molécula de ácido nucleico recombinante de la invención; y (b) cultivar una planta de la progenie a partir de dicha semilla para producir una planta con mayor resistencia a la infestación por parte de plagas de nematodos que atacan plantas. En algunas realizaciones, el método comprende además (c) cruzar la planta de la progenie de (b) consigo misma o con otra planta y (d) repetir los pasos (b) y (c) durante 0-7 (p. ej., 0, 1, 2, 3, 4, 5, 6, 7) generaciones adicionales para producir una planta con mayor resistencia a la infestación por parte de plagas de nematodos que atacan plantas.

En realizaciones adicionales, se proporciona un método para producir una planta de soja con mayor resistencia a la infestación por parte de una plaga de nematodos que atacan plantas, comprendiendo el método los pasos de (a) cruzar una planta de soja transgénica de la invención consigo misma o con otra planta de soja para producir una semilla de soja que comprenda un vector o una molécula de ácido nucleico recombinante de la invención; y (b) cultivar una planta de soja de la progenie a partir de dicha semilla para producir una planta de soja con mayor resistencia a la infestación por parte de plagas de nematodos que atacan plantas. En algunas realizaciones, el método comprende además (c) cruzar la planta de soja de la progenie de (b) consigo misma o con otra planta de soja y (d) repetir los pasos (b) y (c) durante 0-7 (p. ej., 0, 1, 2, 3, 4, 5, 6, 7) generaciones adicionales para producir una planta de soja con mayor resistencia a la infestación por parte de plagas de nematodos que atacan plantas.

La invención proporciona además un cultivo vegetal que comprende una pluralidad

de plantas transgénicas de la invención plantadas conjuntamente en un campo agrícola.

Además, se proporciona un método para mejorar el rendimiento de un cultivo vegetal cuando dicho cultivo vegetal se pone en contacto con una plaga de nematodos que atacan plantas, comprendiendo el método cultivar una pluralidad de plantas que comprenden una molécula de ácido nucleico recombinante de la invención como cultivo vegetal, donde la pluralidad de plantas de dicho cultivo vegetal presentan una mayor resistencia a la infección por parte de nematodos, con lo que se mejora el rendimiento de dicho cultivo vegetal en comparación con un cultivo vegetal de control puesto en contacto con dicha plaga de nematodos que atacan plantas, donde el cultivo vegetal de control se produce a partir de una pluralidad de plantas que carecen de dicha molécula de ácido nucleico. En algunas realizaciones particulares de la invención, el cultivo es un cultivo de soja.

En algunas realizaciones, se proporciona un método para mejorar el rendimiento de un cultivo cuando dicho cultivo se pone en contacto con una plaga de nematodos que atacan plantas, comprendiendo el método poner en contacto la plaga de nematodos que atacan plantas con una cantidad eficaz de un polipéptido de la invención o una composición nematicida de la invención, donde se mejora el rendimiento del cultivo en comparación con un cultivo vegetal puesto en contacto con una plaga de nematodos que atacan plantas que no se ha puesto en contacto con dicho polipéptido y/o composición nematicida. En algunas realizaciones particulares de la invención, el cultivo es un cultivo de soja.

En otras realizaciones más, la invención proporciona además métodos para controlar una plaga de nematodos que atacan plantas, métodos para reducir la capacidad infecciosa para una planta de una plaga de nematodos que atacan plantas, métodos para reducir la infestación de una planta por parte de una plaga de nematodos que atacan plantas, métodos para reducir el desarrollo de quistes inducidos por nematodos y métodos para reducir el crecimiento de una plaga de nematodos que atacan plantas que comprenden poner en contacto la plaga de nematodos que atacan plantas con una composición de la invención, donde dicha composición comprende una molécula de ácido nucleico recombinante, una secuencia de nucleótidos y/o un polipéptido de esta invención. En algunas realizaciones particulares, la composición de la invención es una célula vegetal transgénica, planta transgénica o parte de planta transgénica que comprende y expresa una molécula de ácido nucleico recombinante/secuencia de nucleótidos de la invención.

Por consiguiente, en una realización, la invención proporciona un método para controlar una plaga de nematodos que atacan plantas, que comprende poner en contacto

la plaga de nematodos que atacan plantas con una cantidad eficaz de un polipéptido de la invención o una composición de este, con lo que se controla la plaga de nematodos que atacan plantas en comparación con el control de una plaga de nematodos que atacan plantas que no se ha puesto en contacto con dicho polipéptido o composición de este.

De este modo, en una realización adicional, la invención proporciona un método para controlar una plaga de nematodos que atacan plantas, que comprende poner en contacto la plaga de nematodos que atacan plantas con una planta transgénica y/o una parte de esta que comprende una molécula de ácido nucleico recombinante de la invención, con lo que se controla la plaga de nematodos que atacan plantas en comparación con el control de una plaga de nematodos que atacan plantas que se ha puesto en contacto con una planta o parte de planta de control, careciendo dicha planta de control de dicha molécula de ácido nucleico recombinante.

El hecho de "poner en contacto" una plaga de nematodos que atacan plantas con un polipéptido de la invención y/o una composición de este o de "suministrar" a una plaga de nematodos que atacan plantas un polipéptido de la invención y/o una composición de este se refiere a que la plaga de nematodos que atacan plantas entra en contacto con, se expone a, los polipéptidos de esta invención y/o composiciones de estos, lo cual da como resultado un efecto tóxico sobre el nematodo y un control de este (p. ej., control, menor capacidad infecciosa, menor infestación, menor formación de quistes, menor crecimiento y similares). Una plaga de nematodos que atacan plantas se puede poner en contacto con un polipéptido de la invención o composición nematicida de la invención empleando cualquier método conocido en la técnica. Por ejemplo, la puesta en contacto incluye, sin carácter limitante, (1) proporcionar el o los polipéptidos de la invención en una planta transgénica, donde el nematodo consume (ingiere) una o más partes de la planta transgénica, (2) en una(s) composicion(es) proteica(s) que se puede(n) aplicar a la superficie de una planta o parte de planta, por ejemplo, por pulverización sobre la superficie de la planta, o se puede(n) aplicar empapando la tierra cerca de las raíces de la planta, o sumergiendo toda la planta o partes de esta (p. ej., las raíces) o (3) cualquier otro sistema de suministro reconocido en la técnica.

La expresión "cantidad eficaz" se refiere a la concentración o cantidad de un polipéptido o una composición nematicida que inhibe o reduce la capacidad de una plaga de nematodos que atacan plantas para sobrevivir, desarrollarse, alimentarse y/o reproducirse, o que limita los daños o pérdidas relacionadas con los nematodos en las plantas de cultivo. De este modo, en algunas realizaciones de la invención, una "cantidad eficaz" puede significar que extermina el nematodo. En otras realizaciones, una "cantidad eficaz" no significa que extermine el nematodo.

El término "controlar", en el contexto de un efecto sobre un organismo (p. ej., una plaga de nematodos que atacan plantas), se refiere a inhibir o reducir, mediante un efecto tóxico, la capacidad del organismo para sobrevivir, desarrollarse, alimentarse y/o reproducirse, o limitar los daños o las pérdidas en las plantas de cultivo que se relacionan con la actividad del organismo. El hecho de "controlar" un organismo puede o no significar exterminar el organismo, aunque en algunas realizaciones "controlar" significa exterminar el organismo.

De este modo, en realizaciones particulares, la sobreexpresión de una molécula de ácido nucleico de la invención en una planta da como resultado la producción del polipéptido codificado, con lo que se confiere resistencia a la planta frente a una plaga de nematodos que atacan plantas. Sin pretender vincularse a ninguna teoría particular, los polipéptidos de esta invención pueden ejercer un efecto "tóxico directo" sobre los nematodos o, en su lugar, pueden activar la producción de otras proteínas o metabolitos o pueden activar una o más vías diferentes, cualquiera de las cuales puede ejercer un efecto tóxico sobre la plaga de nematodos que atacan plantas.

En otras realizaciones de la invención, se proporciona un método para reducir la capacidad infecciosa para una planta de una plaga de nematodos que atacan plantas, comprendiendo el método poner en contacto la plaga de nematodos que atacan plantas con una cantidad eficaz de un polipéptido de la invención, con lo que se reduce la capacidad infecciosa de la plaga de nematodos que atacan plantas en comparación con la capacidad infecciosa de una plaga de nematodos que atacan plantas a la que no se ha suministrado dicho polipéptido.

Los términos "infectar" y "capacidad infecciosa", tal como se utilizan en la presente, se refieren a la capacidad de la plaga de nematodos que atacan plantas para infectar, infestar o parasitar un huésped vegetal. Los términos "infestar" e "infestación" se refieren a una plaga de nematodos que habitan o invaden una planta en números o cantidades que son suficientemente elevados para ser perjudiciales para la planta.

En algunas realizaciones de la invención, se proporciona un método para reducir la capacidad infecciosa para una planta de una plaga de nematodos que atacan plantas, comprendiendo el método poner en contacto la plaga de nematodos que atacan plantas con una planta transgénica que comprende una molécula de ácido nucleico recombinante de la invención, con lo que se reduce la capacidad infecciosa de la plaga de nematodos que atacan plantas en comparación con la de una plaga de nematodos que atacan plantas que se ha puesto en contacto con una planta o parte de planta de control, donde dicha planta de control carece de dicha molécula de ácido nucleico recombinante.

En otras realizaciones, la invención proporciona un método para reducir el desarrollo de quistes de nematodos producidos por una plaga de nematodos que atacan plantas en las raíces de una planta, que comprende poner en contacto una plaga de nematodos que atacan plantas con una cantidad eficaz del polipéptido de la invención, donde el desarrollo de quistes de nematodos producidos por la plaga de nematodos que atacan plantas en las raíces de dicha planta se reduce en comparación con el desarrollo de quistes en las raíces de una planta producidos por una plaga de nematodos que atacan plantas que no se ha puesto en contacto con dicho polipéptido.

En realizaciones adicionales, se proporciona un método para reducir el desarrollo de quistes de nematodos producidos por una plaga de nematodos que atacan plantas en las raíces de una planta, comprendiendo el método poner en contacto una plaga de nematodos que atacan plantas con las raíces de una planta transgénica que comprende una molécula de ácido nucleico recombinante de la invención, donde el desarrollo de quistes producidos por una plaga de nematodos que atacan plantas en las raíces de la planta transgénica se reduce en comparación con el desarrollo de quistes en las raíces de una planta de control que carece de dicha molécula de ácido nucleico recombinante.

En otras realizaciones de la invención, se proporciona un método para reducir el crecimiento de la población de una plaga de nematodos que atacan plantas, comprendiendo el método poner en contacto la población de la plaga de nematodos que atacan plantas con una cantidad eficaz de un polipéptido de la invención, donde se reduce el crecimiento de la población de la plaga de nematodos que atacan plantas en comparación con el crecimiento de la población de una plaga de nematodos que atacan plantas de control que no se ha puesto en contacto con el polipéptido.

En otras realizaciones más, se proporciona un método para reducir el crecimiento de la población de una plaga de nematodos que atacan plantas, comprendiendo el método poner en contacto la población de la plaga de nematodos que atacan plantas con una planta transgénica que comprende una molécula de ácido nucleico recombinante de la invención, donde se reduce el crecimiento de la población de la plaga de nematodos que atacan plantas en comparación con el crecimiento de la población de una plaga de nematodos que atacan plantas que se ha puesto en contacto con una planta o parte de planta de control, careciendo dicha planta o parte de planta de control de la molécula de ácido nucleico recombinante.

De este modo, cuando una planta transgénica que comprende una molécula de ácido nucleico recombinante de la invención, o una parte de esta, se expone a o se pone en contacto con una plaga de nematodos que atacan plantas, por ejemplo, el nematodo se alimenta de o se pone en contacto con la planta transgénica o una parte de esta, la

capacidad de la plaga de nematodos que atacan plantas para sobrevivir, desarrollarse, alimentarse y/o reproducirse junto con la planta se inhibe o reduce, con lo que se controla el nematodo/la población de nematodos y/o se reduce la capacidad de la plaga de nematodos que atacan plantas para infectar o infestar la planta o producir quistes en la planta. Además, uno o más polipéptidos de la invención o composiciones que comprenden uno o más polipéptidos de la invención se pueden utilizar directamente para controlar o reducir el crecimiento de una plaga de nematodos que atacan plantas, con lo que se reduce la capacidad de la plaga de nematodos que atacan plantas para infectar o infestar una planta o producir quistes en una planta.

A continuación, la invención se describirá haciendo referencia a los siguientes ejemplos. Cabe destacar que no se pretende que estos ejemplos limiten el alcance de las reivindicaciones de la invención, sino que se pretende que sirvan de ejemplo de ciertas realizaciones. Se pretende que cualquier variación de los métodos ejemplificados que se le ocurra a un experto quede englobada en el alcance de la invención.

EJEMPLOS

Ejemplo 1: Construcción de casetes de expresión para la transformación de raíz pilosa

Al menos un ácido nucleico de la invención que comprende una secuencia de nucleótidos de cualquiera de las secuencias de nucleótidos de **SEQ ID NOs:1-28**, **SEQ ID NOs:43-134**, **SEQ ID NOs:210-242, SEQ ID NOs:261-644** o una secuencia de nucleótidos que codifica cualquiera de los polipéptidos que presentan las secuencias de aminoácidos de **SEQ ID NOs:29-42**, **SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046** se clona en un casete de expresión que tiene la estructura básica de 5' a 3' de: 5'-promotor-ácido nucleico de la invención-terminador-3'. Los casetes de expresión también pueden comprender potenciadores, intrones, secuencias líder y similares. Un casete de expresión de este tipo tiene la estructura: prActin2(incluido el intrón Act2):cEVO18010081 (**SEQ ID NO:24**):tNOS o prActin2(incluido el intrón Act2):cEVO18010044 (**SEQ ID NO:224**):tNOS. Otros ácidos nucleicos de la invención se pueden sustituir por la secuencia codificante cEVO18010081 o EVO18010044 para crear diferente casetes de expresión. A continuación, el casete de expresión se clona en un vector de expresión binario para crear un vector de transformación de raíz pilosa (RP). Se creó un vector de transformación de RP cEVO18010081 (**SEQ ID NO:24**) o cEVO18010044 (**SEQ ID NO: 224**) mediante la clonación del casete de expresión cEVO18010081 (**SEQ ID NO:24**) o cEVO18010044 (**SEQ ID NO: 224**), respectivamente, y un segundo casete de expresión que codifica un marcador puntuable en un vector binario.

A modo de ejemplo, el vector de transformación de RP resultante 20844 que comprende cEVO18010081 (**SEQ ID NO:24**) se muestra en la **Figura 1**.

Ejemplo 2: Expresión en raíces de soja transgénica

El vector de expresión binario descrito en el Ejemplo 1 que contiene un ácido nucleico de la invención y un vector vacío (sin un ácido nucleico de la invención) que se muestra en la Figura 2 se transformaron en raíces de soja con el fin de evaluar la capacidad del vector binario para expresar una proteína que sea capaz de reducir los quistes producidos por los nematodos que inducen quistes en la soja (SCN). Se empleó el cultivar de soja Williams 82 como germoplasma para la transformación de raíz pilosa. Se germinaron semillas de soja en agar al 1% que contiene sacarosa al 0.5% en placas de Petri a aproximadamente 27 °C durante 5 días. A continuación se cortaron las plántulas de las cotiledóneas y la superficie dañada se inoculó con cultivos de una cepa de *Agrobacterium rhizogenes* (p. ej., K599) portadora del vector de expresión binario o el vector vacío. Las cotiledóneas se colocaron en agar al 1% durante 6 días y después se transfieren a un medio de selección. En aproximadamente dos semanas, los eventos de raíz pilosa transgénicos independientes inducidos a partir de las cotiledóneas se recolectaron y transfirieron a un medio de cultivo y se cultivaron en la oscuridad a aproximadamente 27 °C. Narayanan *et al*. (*Crop Science* 39, 1680-1686 (1999)) indican que los fenotipos de resistencia a SCN en una planta de soja entera se conservan en las raíces pilosas transgénicas, por consiguiente, el sistema de raíz pilosa transgénica es útil para evaluar los genes candidatos de resistencia a SCN y predecir la actividad en las plantas de soja enteras.

Aproximadamente dos semanas después de la transferencia a las placas de cultivo, las raíces pilosas transformadas se inocularon con nematodos que inducen quistes en la soja en la etapa J2 con superficie esterilizada (SCN J2) y las raíces se cultivaron en la oscuridad a aproximadamente 27 °C, lo que permite la formación de quistes en los eventos de raíz pilosa. Un mes después de inocular los nematodos, se determinó el número de quistes para las raíces que expresan los polinucleótidos de **SEQ ID NOs: 15-28, 31, 35, 225, 227, 228, 230-234** o **238-240** (es decir, que producen los polipéptidos de **SEQ ID NOs: 29-38, 40-42, 52, 243, 244, 246, 248-252, 25** o **256-259**) o para las raíces que expresan los polinucleótidos de **SEQ ID NOs: 1047-1062** y para las raíces que expresan el vector vacío (como control negativo). Los experimentos se repitieron al menos una vez.

Los resultados de los experimentos se muestran en las **Tablas 1-25** a continuación.

Tabla 1

ID del plásmido	Secuencia de nucleótidos	Número medio de quistes (media)	Número de eventos de raíz pilosa (n)	Error estándar (EE)
SCNBHR10	SEQ ID NO:15	22.1	17	2.5
SCNBHR25	SEQ ID NO:21	24	3	5.6
SCNBHR52	SEQ ID NO:23	12. 2	11	3.4
SCNBHR81	SEQ ID NO:24	33.6	14	4
SCNBHRCK	Vector vacío	21.2	11	3

Tabla 2

ID del plásmido	Secuencia de nucleótidos	Media	n	EE
SCNBHR18	SEQ ID NO:18	10.8	16	2.4
SCNBHR21	SEQ ID NO:20	6.4	18	1.2
SCNBHR25	SEQ ID NO:21	10.5	13	1.1
SCNBHR36	SEQ ID NO:22	12	8	1.7
SCNBHR52	SEQ ID NO:23	2	1	
SCNBHR84	SEQ ID NO:27	14.1	20	1.4
SCNBHRCK	Vector vacío	13.3	9	1.7

Tabla 3

ID del plásmido	Secuencia de nucleótidos	Media	n	EE
SCNBHR15	SEQ ID NO:17	15	9	3.6
SCNBHR82	SEQ ID NO:25	16.9	15	2.5
SCNBHRCK	Vector vacío	10.4	12	1.6

Tabla 4

ID del plásmido	Secuencia de nucleótidos	Media	n	EE
SCNBHR10	SEQ ID NO:15	15	2	2
SCNBHR15	SEQ ID NO:17	12.3	7	2.4
SCNBHR36	SEQ ID NO:22	14.5	10	2.6
SCNBHR52	SEQ ID NO:23	6	1	
SCNBHR81	SEQ ID NO:24	5	3	0
SCNBHR82	SEQ ID NO:25	8	1	
SCNBHRCK	Vector vacío	20.5	2	2.5

Tabla 5

ID del plásmido	Secuencia de nucleótidos	Media	n	EE
SCNBHR11	SEQ ID NO:16	27.6	16	2.3
SCNBHR19	SEQ ID NO:19	24.1	16	3
SCNBHR83	SEQ ID NO:26	17.8	14	2.2
SCNBHR88	SEQ ID NO:28	21.6	13	2.7
SCNBHRCK	Vector vacío	18.5	10	2.5

Tabla 6

ID del plásmido	Secuencia de nucleótidos	Media	n	EE
SCNBHR10	SEQ ID NO:15	43	1	
SCNBHR15	SEQ ID NO:17	41.3	3	12.4
SCNBHR21	SEQ ID NO:20	27.9	7	2.9
SCNBHR36	SEQ ID NO:22	32	3	11.9
SCNBHR52	SEQ ID NO:23	42.7	7	4.2
SCNBHR81	SEQ ID NO:24	19	1	
SCNBHR83	SEQ ID NO:26	31.5	2	1.5
SCNBHRCK	Vector vacío	60.8	5	4

Tabla 7

ID del plásmido	Secuencia de nucleótidos	Media	n	EE
SCNBHR40	SEQ ID NO:1047	34.5	12	6
SCNBHR44	SEQ ID NO:225	29.6	12	3.5
SCNBHR47	SEQ ID NO:227	29.1	13	3.5
SCNBHR50	SEQ ID NO:1048	31.1	13	3.2
SCNBHR55	SEQ ID NO:1049	36.5	15	3.8
SCNBHR57	SEQ ID NO:1050	40.1	14	3.2
SCNBHR60	SEQ ID NO:232	20.7	11	3.2
SCNBHR65	SEQ ID NO:1051	33.8	11	5.9
SCNBHRCK	Vector vacío	39.9	11	4.3

Tabla 8

ID del plásmido	Secuencia de nucleótidos	Media	n	EE
SCNBHR43	SEQ ID NO:1052	70.9	7	4.8
SCNBHR48	SEQ ID NO:228	23.3	7	9.7
SCNBHR52	SEQ ID NO:23	24.8	4	6.2
SCNBHR71	SEQ ID NO:1053	66.6	8	11.1
SCNBHR72	SEQ ID NO:1054	71.6	9	5.2
SCNBHR79	SEQ ID NO:1055	108.8	4	32.6
SCNBHR91	SEQ ID NO:1056	48	4	12.2
SCNBHRCK	Vector vacío	72.7	3	22.3

Tabla 9

ID del plásmido	Secuencia de nucleótidos	Media	n	EE
SCNBHR58	SEQ ID NO:1057	43.6	8	6
SCNBHR59	SEQ ID NO:231	97	13	8.1
SCNBHR86	SEQ ID NO:1058	58.4	7	15.2
SCNBHR89	SEQ ID NO:1059	45.5	6	7
SCNBHRCK	Vector vacío	62.9	10	9.4

Tabla 10

ID del plásmido	Secuencia de nucleótidos	Media	n	EE
SCNBHR43	SEQ ID NO:1052	44.9	10	5.1
SCNBHR79	SEQ ID NO:1055	44.7	12	4.2
SCNBHR91	SEQ ID NO:1056	30.7	3	9.8
SCNBHRCK	Vector vacío	46.8	10	5.8

Tabla 11

ID del plásmido	Secuencia de nucleótidos	Media	n	EE
SCNBHR71	SEQ ID NO:1053	65	7	11
SCNBHR72	SEQ ID NO:1054	53.7	8	8.9
SCNBHR91	SEQ ID NO:1056	46	3	7.6
SCNBHRCK	Vector vacío	65.4	8	7.4

Tabla 12

ID del plásmido	Secuencia de nucleótidos	Media	n	EE
SCNBHR48	SEQ ID NO:228	34.6	8	7.4
SCNBHR61	SEQ ID NO:233	53.2	6	5.9
SCNBHR73	SEQ ID NO:238	44	7	8
SCNBHR77	SEQ ID NO:239	34.8	6	6.4
SCNBHRCK	Vector vacío	78	9	10.6

Tabla 13

ID del plásmido	Secuencia de nucleótidos	Media	n	EE
SCNBHR68	SEQ ID NO:1060	46.2	6	10.7
SCNBHR70	SEQ ID NO:1061	53.7	3	12.8
SCNBHR80	SEQ ID NO:240	34.5	2	7.5
SCNBHR85	SEQ ID NO:1062	45	2	5
SCNBHRCK	Vector vacío	55.2	6	6.3

Tabla 14

ID del plásmido	Secuencia de nucleótidos	Media	n	EE
SCNBHR15	SEQ ID NO:17	45.8	12	3.6
SCNBHR21	SEQ ID NO:20	51.1	14	4.1
SCNBHR36	SEQ ID NO:22	50.4	5	4.9
SCNBHR52	SEQ ID NO:23	45.5	13	4.1
SCNBHR66	SEQ ID NO:236	62	7	11.7
SCNBHR77	SEQ ID NO:239	57.2	12	6
SCNBHR81	SEQ ID NO:24	30.2	12	2.6
SCNBHRCK	Vector vacío	65.7	17	5.8

Tabla 15

ID del plásmido	Secuencia de nucleótidos	Media	n	EE
SCNBHR10	SEQ ID NO:15	63	11	3.9
SCNBHRCK	Vector vacío	97.4	14	8.3

Tabla 16

ID del plásmido	Secuencia de nucleótidos	Media	n	EE
SCNBHR59	SEQ ID NO:231	398.1	19	17.15435
SCNBHRCK	Vector vacío	312.4	11	29.17074

Tabla 17

ID del plásmido	Secuencia de nucleótidos	Media	n	EE
SCNBHR43	SEQ ID NO:1052	84.5	14	6.8
SCNBHR58	SEQ ID NO:1057	85.4	9	5.9
SCNBHRCK	Vector vacío	89.8	11	4.2

Tabla 18

ID del plásmido	Secuencia de nucleótidos	Media	n	EE
SCNBHR54	SEQ ID NO:230	69.9	13	4.9
SCNBHR61	SEQ ID NO:233	66.3	13	5.1
SCNBHR73	SEQ ID NO:238	96.5	13	11.6
SCNBHRCK	Vector vacío	103.2	13	9.6

Tabla 19

ID del plásmido	Secuencia de nucleótidos	Media	n	EE
SCNBHR60	SEQ ID NO:232	82.6	9	5.8
SCNBHRCK	Vector vacío	145.8	10	17.8

Tabla 20

ID del plásmido	Secuencia de nucleótidos	Media	n	EE
SCNBHR80	SEQ ID NO:240	65.3	19	4.6
SCNBHRCK	Vector vacío	61	14	5.4

Tabla 21

ID del plásmido	Secuencia de nucleótidos	Media	n	EE
SCNBHR47	SEQ ID NO:227	57.5	13	3.7
SCNBHR53	SEQ ID NO:229	61.9	16	3.4
SCNBHR92	SEQ ID NO:242	85.3	15	5.6
SCNBHRCK	Vector vacío	81.5	16	5

Tabla 22

ID del plásmido	Secuencia de nucleótidos	Media	n	EE
SCNBHR83	SEQ ID NO:26	75.7	15	5.9
SCNBHRCK	Vector vacío	104.7	14	8.

Tabla 23

ID del plásmido	Secuencia de nucleótidos	Media	n	EE
SCNBHR44	SEQ ID NO:225	97.9	20	5
SCNBHR60	SEQ ID NO:232	72.3	12	5.8
SCNBHR63	SEQ ID NO:234	102.5	19	5.7
SCNBHR82	SEQ ID NO:25	109.8	17	3.9
SCNBHRCK	Vector vacío	109.6	16	4.8

Tabla 24

ID del plásmido	Secuencia de nucleótidos	Quistes	n	EE
SCNBHR77	SEQ ID NO:239	63	18	3.3
SCNBHRCK	Vector vacío	71	13	4.4

Tabla 25

Vector	Secuencia de nucleótidos	Quistes	n	EE
SCNBHR54	SEQ ID NO:230	36	19	2.3
SCNBHR73	SEQ ID NO:238	40	11	1.5
SCNBHRCK	Vector vacío	33	19	2.3

Los resultados de estos experimentos muestran que el número de quistes formados en raíces de soja que expresan al menos una secuencia de polinucleótido que presenta la secuencia de nucleótidos de la **SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:230, SEQ ID NO:232** y/o **SEQ ID NO:233** fue significativamente inferior al de raíces de soja transgénicas que comprendían el control de vector vacío. Los expertos en la técnica comprenderán que también se podrían utilizar las secuencias genómicas y/o el ARNm más las secuencias de UTR y ORF correspondientes a las SEQ ID Nos anteriores que se han proporcionado en la presente para reducir el parasitismo de nematodos (p. ej., **SEQ ID NOs:1, 3, 6, 8, 9, 10, 12, 43, 45, 48, 50, 51, 53, 211, 212, 214, 216, 217**).

Los polinucleótidos que presentan una identidad secuencial sustancial (p. ej., una identidad de al menos un 80%) respecto a los polinucleótidos mostrados anteriormente que reducen el número de quistes en las raíces de soja también podrían ser útiles para

reducir la infestación por parte de nematodos, el número de quistes y similares en las plantas. Los ejemplos no limitantes de polinucleótidos que presentan una identidad sustancial respecto a la secuencia de nucleótidos de la **SEQ ID NO:15** incluyen las secuencias de nucleótidos de las **SEQ ID NOs: 56-60**; respecto a la secuencia de nucleótidos de la **SEQ ID NO:17** incluyen la secuencia de nucleótidos de la **SEQ ID NO:63**; respecto a la secuencia de nucleótidos de la **SEQ ID NO:20** incluyen las secuencias de nucleótidos de la **SEQ ID NO:66** y/o la **SEQ ID NO:67**; respecto a la secuencia de nucleótidos de la **SEQ ID NO:22** incluyen las secuencias de nucleótidos de las **SEQ ID NOs:68-112**; respecto a la secuencia de nucleótidos de la **SEQ ID NO:23** incluyen las secuencias de nucleótidos de las **SEQ ID NOs:113-118**; respecto a la secuencia de nucleótidos de la **SEQ ID NO:24** incluyen la secuencia de nucleótidos de la **SEQ ID NO:119**; respecto a la secuencia de nucleótidos de la **SEQ ID NO:26** incluyen las secuencias de nucleótidos de las **SEQ ID NOs:120-124**; respecto a la secuencia de nucleótidos de la **SEQ ID NO:227** incluyen las secuencias de nucleótidos de las **SEQ ID NOs:226, 389-398**; respecto a la secuencia de nucleótidos de la **SEQ ID NO:228** incluyen las secuencias de nucleótidos de las **SEQ ID NOs:399-401**; respecto a la secuencia de nucleótidos de la **SEQ ID NO:230** incluyen las secuencias de nucleótidos de las **SEQ ID NOs:408-633**; y/o respecto a la secuencia de nucleótidos de la **SEQ ID NO:232** incluyen las secuencias de nucleótidos de las **SEQ ID NOs:637-642**.

Ejemplo 3: Construcción de vectores y casetes de expresión para la transformación de soja

Los casetes de expresión descritos en el Ejemplo 1 se utilizan en experimentos de transformación de soja o se construyen diferentes casetes de expresión. Al menos un ácido nucleico que comprende una secuencia de nucleótidos seleccionada entre las secuencias de nucleótidos de cualquiera de **SEQ ID NOs:1-28, 43-134, 210-242, 261-664** o las secuencias de nucleótidos que codifican el polipéptido que presenta la secuencia de aminoácidos de cualquiera de **SEQ ID NOs:29-42, 135-209, 243-260, 665-1046** se clona en un casete de expresión y el casete de expresión se clona en un vector binario para generar plantas de soja transgénicas. El material genético que se ha de transferir a la planta de soja se clona entre el borde izquierdo y el borde derecho del vector binario. Un casete de expresión de este tipo tiene la estructura: eFMV:e35S:prAct2(incluido el intrón Act2): cEVO18010081 (**SEQ ID NO:24**):tNOS. El casete de expresión cEVO18010081 (**SEQ ID NO:24**) y un segundo casete de expresión que codifica un marcador seleccionable se clonan en un vector binario para crear 20944 EVO, que se muestra en la **Figura 3**. Otro casete de expresión a modo de ejemplo tiene la estructura: eFMV:e35S:prAct2(incluido el intrón Act2): cEVO18010044 (**SEQ ID NO:224**):tNOS.

El vector binario que comprende un casete de expresión descrito previamente se introduce en una cepa de *Agrobacterium tumefaciens* (p. ej., EHA101), empleando electroporación. Las colonias bacterianas individuales que contienen el vector binario se seleccionan para confirmar la presencia del vector intacto y se utilizan en otros experimentos.

Ejemplo 4: Producción de soja transgénica

La transformación de la soja para producir plantas de soja transgénicas se llevó a cabo empleando dianas preparadas a partir de semillas germinadas de la variedad Williams 82 mediante transformación mediada por *Agrobacterium tumefaciens*, según se describe en la presente. Las semillas de soja maduras se recolectaron, secaron y esterilizaron con cloro gaseoso. Las semillas esterilizadas se colocaron en vitrinas de flujo laminar durante 2 semanas antes de la germinación. Las semillas se colocaron en medio de germinación durante de 15 a 40 horas para realizar la germinación. Los explantes se prepararon según describe Khan (Solicitud de Patente de EE. UU. 20040034889) empleando semillas germinadas mediante la extracción de hipocólitos, un cotiledón y primordios foliares primarios. A continuación, los explantes se lesionaron provocando ligeras lesiones en la región nodal cotiledonaria y también en regiones apicales. A continuación, los explantes se infectaron con una cepa EHA101 de *Agrobacterium* que contenía un vector binario adecuado. Los explantes infectados se cocultivaron en medio de cocultivo, según se describe en Hwang *et al.* 2008 (WO08112044). A continuación, la suspensión de *A. tumefaciens* en exceso se eliminó mediante aspiración y los explantes se trasladaron a placas que contenían un medio de cocultivo no selectivo. Los explantes se cocultivaron con el *A. tumefaciens* remanente a 23 °C durante 4 días en la oscuridad. A continuación, los explantes se transfirieron a medio de recuperación complementado con una mezcla de antibióticos constituida por ticarcilina (75 mg/L), cefotaxima (75 mg/L) y vancomicina (75 mg/l) y se incubaron en la oscuridad durante siete días, según se describe en Hwang *et al.* 2008 (WO08112044). A continuación, los explantes se transfirieron a un medio de regeneración que contenía glifosato (de 75 a 100 uM) y una mezcla de antibióticos constituida por ticarcilina (75 mg/L), cefotaxima (75 mg/L) y vancomicina (75 mg/l) para inhibir y exterminar *A. tumefaciens*. La elongación de los tallos se llevó a cabo en un medio de elongación que contenía glifosato (50 uM). Se utilizó el gen EPSPS como marcador seleccionable durante el proceso de transformación. Las plántulas regeneradas se transplantaron en la tierra, según se describe en Que *et al.* (WO08112267), y se evaluaron para detectar la presencia de las secuencias tanto del gen marcador EPSPS como de resistencia a la espectinomicina (Espec) por análisis de PCR TaqMan (Ingham *et al.*, 2001). Este análisis permite seleccionar los eventos transgénicos

que tienen el ADN-T y que están exentos del ADN del esqueleto del vector. Las plantas que dieron un resultado positivo para las secuencias del gen EPSPS y negativo para el gen de Espec se transfirieron al invernadero para el análisis de la expresión del miARN y la fijación de las semillas. Empleando este método, los elementos genéticos dentro de las regiones de los bordes derecho e izquierdo del plásmido de transformación se transfieren de forma eficaz y se integran al genoma de la célula vegetal, mientras que los elementos genéticos fuera de estas regiones fronterizas generalmente no se transfieren.

Cuando las raíces tienen aproximadamente 2-3 pulgadas, se trasplantan a las macetas de 1 galón empleando tierra Fafard #3 y 30 gramos de Osmocote Plus 15–9–12 incorporado. Se riegan meticulosamente y se colocan en el cubículo con luz fluorescente configurada para un día de 16 horas. Las temperaturas son de aproximadamente 85 °F (29.4 °C) durante el día y aproximadamente 70 °F (21 °C) durante la noche. Las plantas se riegan al menos una vez al día.

Las plantas permanecen en el cubículo hasta que se realiza el muestreo Taqman secundario, generalmente de 1 a 2 semanas. A continuación, las plantas se colocan en un sistema de riego por goteo automático y se riegan dos veces al día. Se coloca una caja encima de la planta y esta puede podarse muy ligeramente si fuera necesario. La iluminación consiste en una combinación de lámparas de haluro metálico y de vapor de sodio con bombillas de 400 y 1000 vatios con un período de día de 10 horas. La pared exterior se oscurece para bloquear la luz que extendería la duración del día. Las temperaturas se configuran a aproximadamente 79 °F (26 °C) durante el día y aproximadamente 70 °F (21 °C) durante la noche. La humedad es ambiente.

Las plantas se mantienen de esta forma hasta que las vainas alcanzan la madurez, aproximadamente 100 días basándose en la fecha de la selección Taqman. A continuación, las vainas se recolectan, se colocan en una bolsa de papel, se secan al aire durante 2 días y después se secan a máquina a aproximadamente 80 °F (27 °C) durante aproximadamente 2 días adicionales. Las vainas se pelan y las semillas T1 se recolectan y se almacenan a aproximadamente 4 °C hasta la próxima prueba.

En el ensayo de SCN, se utiliza como control Williams 82 de origen natural o segregantes nulos de la generación T1. Como alternativa, un control en el ensayo de SCN puede ser una planta transformada con un vector vacío tal como el que se muestra en la Figura 4 (es decir, un casete de expresión idéntico pero sin ninguna secuencia de nucleótidos de **SEQ ID NOs:1-28**, **SEQ ID NOs: 43-134**, **SEQ ID NOs:210-242** ni **SEQ ID NOs:261-644**, ni ninguna secuencia de nucleótidos que codifique uno o más polipéptidos que presenten la secuencia de aminoácidos de **SEQ ID NOs: 29-42, SEQ ID NOs:135-209, SEQ ID NOs:243-260** ni **SEQ ID NOs:665-1046**.

Ejemplo 5: Evaluación de la formación de quistes en las plantas de soja transformadas

Las plantas de soja transformadas con el casete de expresión que contiene al menos una secuencia de nucleótidos de cualquiera de las secuencias de nucleótidos de **SEQ ID NOs:1-28**, **SEQ ID NOs: 43-134**, **SEQ ID NOs:210-242, SEQ ID NOs:261-644**, o una secuencia de nucleótidos que codifica cualquiera de los polipéptidos que presentan la secuencia de aminoácidos de cualquiera de **SEQ ID NOs: 29-42, SEQ ID NOs:135-209, SEQ ID NOs:243-260** o **SEQ ID NOs:665-1046** se inoculan con nematodos que inducen quistes en la soja en la etapa J2 (SCN J2). Las plántulas de soja transgénicas de generación T1 de 3 semanas de edad que se cultivaron en bolsas de germinación se inoculan individualmente con una suspensión de SCN J2 con una concentración de 500 J2 por planta. Las plantas de soja se cultivan a 27 °C en una cámara de crecimiento con 16 horas por día de periodo luminoso.

Un mes después de la inoculación de los nematodos, se determina el número de quistes para las plantas de soja transgénicas que comprenden dichas secuencias de nucleótidos que se han expuesto previamente y para los segregantes nulos (plantas que no tienen el ácido nucleico de la invención) de los mismos predecesores T0.

Ejemplo 6. Evaluación del efecto de los ácidos nucleicos recombinantes seleccionados sobre la resistencia y/o la tolerancia frente a nematodos

Para validar el efecto de los polinucleótidos seleccionados de la invención sobre la resistencia y/o la tolerancia de las plantas frente a nematodos, los polinucleótidos seleccionados se sobreexpresaron en plantas como se indica a continuación.

Estrategia de clonación: los polinucleótidos seleccionados con una secuencia de nucleótidos de la **SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:228** o **SEQ ID NO:1047** se clonaron en vectores binarios para generar plantas transgénicas.

Para la clonación, en primer lugar se identificó el marco de lectura abierto (ORF) de longitud completa. En el caso de agregados de ORF-EST y en algunos casos ARNm ya publicados, las secuencias se analizaron para identificar la totalidad del marco de lectura abierto comparando los resultados de varios algoritmos de traducción para conocer las proteínas de otras especies de plantas. Para clonar los ADNc de longitud completa, se llevó a cabo una transcripción inversa (RT) seguida de una reacción en cadena de la polimerasa (PCR; RT-PCR) en el ARN total extraído de raíces, hojas, flores, silicuas u otros tejidos vegetales que se cultivaron en condiciones normales y en diferentes condiciones de tratamiento. El ARN total se extrajo utilizando métodos de uso

común en la técnica. La producción de ADNc y la amplificación por PCR se llevaron a cabo utilizando protocolos estándar, que son conocidos por los expertos en la técnica (remítase, p. ej., a Sambrook J., E.F. Fritsch y T. Maniatis. 1989. *Molecular cloning: a laboratory manual*, 2.ª Ed. Cold Spring Harbor Laboratory Press, Nueva York). Los productos de PCR se purificaron utilizando el kit de purificación para PCR (Qiagen)**.** En los casos en los que no se identificó la totalidad de la secuencia codificante, se utilizó el kit RACE de Invitrogen (RACE = siglas en inglés que se refieren a la amplificación rápida de los extremos del ADNc) para acceder a la totalidad del transcrito de ADNc del gen procedente de las muestras de ARN descritas anteriormente. Los productos de RACE se clonaron en un vector con un número elevado de copias y a continuación se secuenciaron o bien se secuenciaron directamente. La información del procedimiento RACE se utilizó para clonar el ORF de longitud completa de los genes correspondientes.

Cuando se clonó ADN genómico, los genes se amplificaron mediante PCR directa sobre el ADN genómico extraído de tejido foliar utilizando el kit *DNAeasy* (Qiagen, N.º de cat. 69104). Normalmente, se sintetizaron 2 conjuntos de cebadores para la amplificación de cada gen a partir de un ADNc o una secuencia genómica: un conjunto externo de cebadores y un conjunto interno (cebadores para PCR anidada). Cuando fue necesario, se utilizó un cebador adicional (o dos) de los cebadores para PCR anidada.

Para facilitar la clonación de los ADNc/las secuencias genómicas, se añadió una extensión de 8-12 bp al extremo 5' de cada cebador. La extensión del cebador incluye un sitio de restricción de endonucleasas. Los sitios de restricción se seleccionaron utilizando dos parámetros: (a) el sitio no existe en la secuencia de ADNc y (b) los sitios de restricción en los cebadores directo e inverso se diseñan de modo que el ADNc digerido se inserte en la formación sentido en el vector binario que se utiliza para la transformación.

Cada producto de PCR digerido se insertó en un vector pUC19 (New England BioLabs Inc) con un número elevado de copias o en plásmidos que se originaron a partir de este vector. En algunos casos, el producto de PCR no digerido se puede insertar en pCR-Blunt II-TOPO (Invitrogen).

La secuenciación de los productos de PCR amplificados se realizó utilizando un secuenciador ABI 377 (Amersham Biosciences Inc). En algunos casos, después de confirmar las secuencias de los genes clonados, el ADNc clonado se introdujo en un vector binario pGI modificado que contenía el promotor At6669 (**SEQ ID NO:1063)** mediante la digestión con las endonucleasas de restricción adecuadas. Después de la inserción, se realizó una única copia del terminador NOS (Vancanneyt *et al. Molecular Genetics and Genomics* 220, 245-50, 1990). Los productos digeridos y el vector

plasmídico linearizado se ligaron utilizando la enzima ADN-ligasa T4 (Roche, Suiza). Los plásmidos con un número elevado de copias que contenían los genes clonados se digirieron con endonucleasas de restricción (New England BioLabs Inc) de acuerdo con los sitios diseñados en los cebadores y se clonaron en vectores binarios.

Varias secuencias de ADN de los genes seleccionados fueron sintetizadas por el proveedor comercial GeneArt (www.geneart.com). El ADN sintético se diseñó *in silico*. Se añadieron sitios adecuados para las enzimas de restricción a las secuencias clonadas en el extremo 5' y en el extremo 3' para permitir posteriormente la clonación en el vector binario pQFNc en una posición posterior al promotor At6669.

Vectores binarios utilizados para la clonación: El plásmido pPI se construyó insertando una secuencia sintética de la señal de poli-(A), que se originó a partir del vector plasmídico básico pGL3 (Promega, N.º de ac. U47295; 4658-4811 bp), en el sitio de restricción *Hind*III del vector binario pBI101.3 (Clontech, N.º de ac. U12640). pGI (pBXYN) es similar a pPI, pero el gen original en la estructura básica, el gen GUS, se reemplazó por el gen del intrón GUS seguido por el terminador NOS. En el pasado, pGI se ha utilizado para clonar las secuencias de polinucleótidos, inicialmente bajo el control del promotor 35S (Odell *et al. Nature* 313, 810 - 812 (28 de febrero de 1985)).

Los vectores pGI modificados (pQXNc (**Fig. 7**); o pQFN (**Fig. 6**), pQFNc (**Fig. 6**) o pQYN 6669 (**Fig. 5**) son versiones modificadas del vector pGI en las cuales el casete se ha invertido entre los bordes izquierdo y derecho de modo que el gen y su promotor correspondiente están cerca del borde derecho y el gen NPTII está cerca del borde izquierdo.

Se insertó At6669, la secuencia del promotor de *Arabidopsis thaliana* (**SEQ ID NO:1063**), en el vector binario pGI modificado, en una posición previa a los genes clonados, a continuación se ligó el ADN y se extrajo el plásmido binario a partir de colonias de *E. coli* positivas, según se ha descrito anteriormente.

Las colonias se analizaron por PCR utilizando los cebadores que cubrían la inserción, los cuales se diseñaron para que abarcaran el promotor y el gen introducidos. Se identificaron los plásmidos positivos, se aislaron y se secuenciaron.

Para la clonación de cada gen, se utilizaron al menos 2 cebadores: directo e inverso. En algunos casos, se utilizaron cuatro cebadores: directo externo, inverso externo, directo anidado o inverso anidado. Los genes se clonaron a partir del organismo indicado, excepto los genes producidos sintéticamente por GeneArt.

Ejemplo 7. Producción de plantas de Arabidopsis transgénicas que expresan polinucleótidos seleccionados

Producción de células de Agrobacterium tumefaciens que contienen los vectores binarios de acuerdo con algunas realizaciones de la invención. Se utilizó cada uno de los vectores binarios descritos en el Ejemplo 6 anteriormente para transformar células de *Agrobacterium*. Como control negativo, se utilizó un constructo binario adicional que contenía únicamente el promotor At6669. Los vectores binarios se introdujeron en células competentes LB4404 o GV301 de *Agrobacterium tumefaciens* (aproximadamente 10^9 células/mL) por electroporación. La electroporación se llevó a cabo utilizando un electroporador MicroPulser (Biorad), con cubetas de 0.2 cm (Biorad) y el programa de electroporación EC-2 (Biorad). Las células tratadas se cultivaron en medio líquido LB a 28 °C durante 3 horas, a continuación se colocaron en placas sobre agar LB suplementado con gentamicina (50 mg/L; para cepas GV301 de *Agrobacterium*) o estreptomicina (300 mg/L; para la cepa LB4404 de *Agrobacterium*) y kanamicina (50 mg/L) a 28 °C durante 48 horas. Las colonias de *Agrobacterium*, que se desarrollaron en el medio selectivo, se analizaron adicionalmente por PCR utilizando los cebadores diseñados para abarcar la secuencia insertada en el plásmido pPI. Los productos de PCR resultantes se aislaron y se secuenciaron para verificar que se habían introducido debidamente las secuencias de polinucleótidos correctas de la invención en las células de *Agrobacterium*.

Preparación de plantas de Arabidopsis para la transformación – Se transformaron *Arabidopsis thaliana* var Columbia (plantas T_0) de acuerdo con el procedimiento de inmersión floral (Clough *et al.* (1998) *Plant J.* 16(6): 735-43; y Desfeux *et al.* (2000) *Plant Physiol.* 123(3): 895-904) con pequeñas modificaciones. Resumiendo, las plantas T_0 de *Arabidopsis thaliana* Columbia (Col0) se sembraron en macetas de 250 mL rellenas de mezcla de cultivo a base de turba húmeda. Las macetas se cubrieron con papel de aluminio y una cúpula de plástico, se mantuvieron a 4 °C durante 3–4 días, a continuación se descubrieron y se incubaron en una cámara de crecimiento a 18–24 °C con ciclos de luz/oscuridad de 16/8 horas. Las plantas T_0 estaban listas para la transformación seis días antes de la floración.

Preparación de Agrobacterium que contiene los vectores binarios para la transformación en plantas de Arabidopsis – Se cultivaron colonias individuales de *Agrobacterium* que contenían los vectores binarios con los genes de algunas realizaciones de la invención en medio LB suplementado con kanamicina (50 mg/L) y gentamicina (50 mg/L). Los cultivos se incubaron a 28 °C durante 48 horas con agitación enérgica y se centrifugaron a 4000 rpm durante 5 minutos. Los pellets que contenían las células de *Agrobacterium* se volvieron a suspender en un medio de transformación que contenía Murashige-Skoog (Duchefa) con una concentración de la mitad (2.15 g/L);

bencilaminopurina 0.044 μM (Sigma); 112 μg/L de vitaminas B5 Gambourg (Sigma); sacarosa al 5%; y 0.2 mL/L de Silwet L-77 (OSI Specialists, CT) en agua destilada dos veces, a un pH de 5.7.

Transformación de plantas de Arabidopsis con Agrobacterium – La transformación de las plantas T_0 se llevó a cabo invirtiendo cada planta en una suspensión de *Agrobacterium* de modo que el tejido vegetal situado por encima del suelo se sumergiera durante 3-5 segundos. Cada planta T_0 inoculada se colocó inmediatamente en una bandeja de plástico, a continuación se cubrió con una cúpula de plástico transparente para conservar la humedad y se mantuvo en la oscuridad a temperatura ambiente durante 18 horas para propiciar la infección y la transformación. A continuación, las plantas transformadas (transgénicas) se descubrieron y se transfirieron a un invernadero para que se recuperasen y madurasen. Las plantas T_0 transgénicas se cultivaron en el invernadero durante 3-5 semanas hasta que las silicuas se volvieron marrones y se secaron, a continuación se recolectaron las semillas de las plantas y se mantuvieron a temperatura ambiente hasta que se plantaron.

Generación de plantas transgénicas T_1 y T_2 – Para generar las plantas transgénicas T_1 y T_2 que contenían los genes, se esterilizó la superficie de las semillas recolectadas de las plantas transgénicas T_0 empapándolas en etanol al 70% durante 1 minuto y a continuación empapándolas en hipoclorito de sodio al 5% y tritón al 0.05% durante 5 minutos. Las semillas con la superficie esterilizada se lavaron completamente en agua destilada estéril y a continuación se colocaron en placas de cultivo que contenían Murashig-Skoog (Duchefa) con una concentración de la mitad; sacarosa al 2%; agar vegetal al 0.8%; kanamicina 50 mM y carbenicilina 200 mM (Duchefa). Las placas de cultivo se incubaron a 4 °C durante 48 horas y a continuación se transfirieron a una cámara de crecimiento a 25 °C para una semana adicional de incubación. Las plantas vitales T_1 de *Arabidopsis* se transfirieron a placas de cultivo nuevas para otra semana de incubación. Tras la incubación, las plantas T_1 se retiraron de las placas de cultivo y se plantaron en una mezcla de crecimiento contenida en macetas de 250 mL. Se permitió que las plantas transgénicas crecieran en un invernadero hasta llegar a la madurez. Las semillas recolectadas de las plantas T_1 se cultivaron y desarrollaron hasta la madurez como plantas T_2 en las mismas condiciones que las utilizadas para cultivar y desarrollar las plantas T_1.

Ejemplo 8. Evaluación de Arabidopsis transgénicas para determinar si se reduce la infección por parte de nematodos.

El vector de expresión binario descrito anteriormente, pQFN o pQFNc, que incluía el promotor At6669 que contenía al menos un ácido nucleico de la invención o un vector

vacío (sin ningún ácido nucleico de la invención) se transformó en *Arabidopsis* para evaluar la capacidad del vector binario para expresar una proteína que fuera capaz de reducir los quistes provocados por nematodos que producen quistes en la remolacha azucarera (BCN, por sus siglas en inglés). Se utilizó el cultivar de *Arabidopsis* Columbia-0 como germoplasma para la transformación. Las semillas de *Arabidopsis* se germinaron en Phytagel al 3% que contenía sacarosa al 0.5% en tubos de 1.5 mL a aproximadamente 25 °C durante 10 días. A continuación, se transfirieron plantas individuales, de 5 a 10 plantas por evento y de 3 a 7 eventos por SEQ ID, a macetas de 0.25 litros que contenían arena y se cultivaron durante 10 días más en el invernadero. A continuación, las macetas se inocularon con nematodos que producen quistes en la remolacha azucarera en el estadio J2 (BCN J2) y las plantas se cultivaron en el invernadero a aproximadamente 25 °C, lo cual permite la formación de quistes en la raíz de las plantas. Un mes después de la inoculación de los nematodos, se determinó el número de quistes tanto para las raíces que expresaban al menos uno de los polinucleótidos de **SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:228** o **SEQ ID NO:1047** como para las raíces que expresaban el vector vacío (como control negativo). El experimento se repitió al menos una vez.

Tabla 26. Genes que presentan una reducción de la infección en la planta frente a nematodos.

		Quistes provocados por nematodos hembra por planta			
SEQ ID NO	N.º de evento	Media	EE (±)	Valor p	% de control
Control de vector vacío	Mezcla135	9.89	1.20	1.00	-
SEQ ID NO:1047	61990.12	2.90	0.75	<.0001	29
SEQ ID NO:1047	61991.13	7.10	1.67	0.34	72
SEQ ID NO:1047	61995.2	6.10	0.74	0.08	62
SEQ ID NO:228	60025.11	1.00	0.52	<.0001	10
SEQ ID NO:228	62025.7	6.50	0.79	0.15	66
SEQ ID NO:228	62026.11	6.67	1.81	0.22	67
SEQ ID NO:16	62118.11	3.09	0.59	<.0001	31
SEQ ID NO:16	62118.12	3.10	0.66	0.00	31
SEQ ID NO:16	62121.6	3.30	0.60	0.00	33
SEQ ID NO:16	62122.4	3.80	1.28	0.00	38

SEQ ID NO:16	62392.4	2.50	0.91	<.0001	25

Tabla 27. Genes que presentan una reducción de la infección en la planta frente a nematodos.

SEQ ID NO	N.º de evento	Quistes provocados por nematodos hembra por planta			% de control
		Media	EE (±)	Valor p	
Control de vector vacío	mezcla138-b	11.5	0.63	1	-
SEQ ID NO:18	61888.3	5.5556	1.11	0.012	48
SEQ ID NO:18	61888.4	2.8889	0.66	<.0001	25
SEQ ID NO:18	61889.1	4.8889	1.18	0.0033	43
SEQ ID NO:18	61890.4	5.8889	1.55	0.0219	51
SEQ ID NO:18	61891.2	7.1111	1.46	0.1417	62
SEQ ID NO:24	61895.1	4	1.02	0.0013	35
SEQ ID NO:24	61896.1	4.75	0.68	0.0036	41
SEQ ID NO:24	61896.3	6.4	1.3182	0.0418	56
SEQ ID NO:24	61896.5	4.9	0.836	0.0024	43
SEQ ID NO:24	61896.6	3.5	0.85	<.0001	30
SEQ ID NO:24	61897.1	5.2	1.96	0.033	45
SEQ ID NO:24	61897.3	3.8	1	0.0002	33
SEQ ID NO:24	61898.1	3.2857	0.81	0.0003	29
SEQ ID NO:17	62236.3	5.2	1.27	0.0045	45
SEQ ID NO:17	62237.2	2	0.67	<.0001	17
SEQ ID NO:17	62237.3	3.1111	0.93	<.0001	27
SEQ ID NO:17	62239.2	3.4	1.63	0.0018	30
SEQ ID NO:17	62240.4	6.1	1.83	0.0251	53

Tabla 28. Genes que presentan una reducción de la infección en la planta frente a nematodos.

SEQ ID NO	N.º de evento	Quistes provocados por nematodos hembra por planta			% de control
		Media	EE (±)	Valor p	
Control de vector vacío	Mezcla136	5.33	0.62	1	-

SEQ ID NO:15	61433.2	1.17	0.31	0.0241	22
SEQ ID NO:15	61454.2	1.83	0.75	0.1045	34
SEQ ID NO:15	61455.4	2.67	1.59	0.4177	50
SEQ ID NO:15	61457.2	2.5	0.85	0.3301	47
SEQ ID NO:19	61535.5	2.33	0.56	0.2553	44
SEQ ID NO:19	61536.5	2.17	0.6	0.1934	41
SEQ ID NO:19	61536.6	3.67	0.72	0.9621	69
SEQ ID NO:26	62570.3	1.33	0.49	0.0358	25
SEQ ID NO:26	62570.4	0.83	0.31	0.0104	16
SEQ ID NO:26	62570.5	0.75	0.75	0.0284	14
SEQ ID NO:26	62571.1	0.83	0.54	0.0104	16
SEQ ID NO:26	62573.5	0.17	0.17	0.0016	3
SEQ ID NO:26	62573.6	1.5	0.67	0.0522	28
SEQ ID NO:26	62873.3	0.67	0.33	0.0066	13
SEQ ID NO:26	62576.4	0.2	0.2	0.0035	4
SEQ ID NO:27	62578.1	0.83333	0.4	0.0104	16
SEQ ID NO:27	62578.3	0.8	0.8	0.0164	15
SEQ ID NO:27	62578.4	0.5	0.34	0.0042	9
SEQ ID NO:27	62579.1	1.16667	0.48	0.0241	22
SEQ ID NO:27	62579.2	0.66667	0.33	0.0066	13

Tabla 29. Genes que presentan una reducción de la infección en la planta frente a nematodos.

Nombre del gen (SEQ ID NO)	N.º de evento	Quistes provocados por nematodos hembra por planta			
		Media	EE (±)	Valor p	% de control
Control de vector vacío	Mezcla135	8.75	2.25	1	-
SEQ ID NO:23	61448.2	2.86	1	0.0003	33
SEQ ID NO:23	61448.3	1.43	0.65	<.0001	16
SEQ ID NO:23	61449.1	2.14	1.16	<.0001	24
SEQ ID NO:23	61449.3	2.14	0.8	<.0001	24
SEQ ID NO:23	61450.1	1.67	0.49	<.0001	19
SEQ ID NO:23	61450.2	0	0	<.0001	0
SEQ ID NO:23	61450.4	0.5	0.27	<.0001	6

SEQ ID NO:23	61452.4	1.75	0.85	0.0001	20
SEQ ID NO:20	61724.1	0	0	<.0001	0
SEQ ID NO:20	61724.4	0.71	0.57	<.0001	8
SEQ ID NO:20	61725.2	3	1.2	0.0004	34
SEQ ID NO:20	61725.3	0	0	<.0001	0
SEQ ID NO:20	61725.6	0	0	<.0001	0
SEQ ID NO:20	61726.2	2.3	0.7	<.0001	26
SEQ ID NO:20	61727.3	1.4	0.75	<.0001	16
SEQ ID NO:22	62124.3	3.5	2.22	0.0081	40
SEQ ID NO:22	62125.1	0.43	0.2	<.0001	5
SEQ ID NO:22	62125.3	0	0	<.0001	0
SEQ ID NO:22	62126.1	1.57	0.69	<.0001	18
SEQ ID NO:22	62126.3	4.33	1.67	0.0731	50
SEQ ID NO:22	62129.2	1	0.41	<.0001	11

Los resultados de estos experimentos (**Tablas 26-29**) indican que el número de quistes formados en raíces de *Arabidopsis* que expresan, por ejemplo, al menos un polinucleótido con la secuencia de nucleótidos de **SEQ ID NOs:16, 20, 22, 23, 24, 26, 27, 228** y/o **1047** fue significativamente inferior al de raíces de soja transgénicas que comprendían el control de vector vacío.

De modo similar a los polinucleótidos que se ha identificado que reducen el desarrollo de quistes provocados por nematodos en la raíz pilosa de la soja, los polinucleótidos que presentan una identidad secuencial sustancial (p. ej., una identidad de al menos un 80%) respecto a los polinucleótidos mostrados anteriormente que reducen el número de quistes en las raíces de *Arabidopsis* también podrían ser útiles para reducir la infestación por parte de nematodos, el número de quistes y similares en las plantas. Los ejemplos no limitantes de polinucleótidos que presentan una identidad sustancial respecto a la secuencia de nucleótidos de la **SEQ ID NO:16** incluyen la **SEQ ID NO:61** y/o la **SEQ ID NO:62**; respecto a la secuencia de nucleótidos de la **SEQ ID NO:20** incluyen las secuencias de nucleótidos de la **SEQ ID NO:66** y/o la **SEQ ID NO:67**; respecto a la secuencia de nucleótidos de la **SEQ ID NO:22** incluyen las secuencias de nucleótidos de las **SEQ ID NOs:68-112**; respecto a la secuencia de nucleótidos de la **SEQ ID NO:23** incluyen las secuencias de nucleótidos de las **SEQ ID NOs:113-118**; respecto a la secuencia de nucleótidos de la **SEQ ID NO:24** incluyen la **SEQ ID NO:119**; respecto a la secuencia de nucleótidos de la **SEQ ID NO:26** incluyen las secuencias de nucleótidos de

las **SEQ ID NOs:120-124**; respecto a la secuencia de nucleótidos de la **SEQ ID NO:27** incluyen las secuencias de nucleótidos de las **SEQ ID NOs:125-127**; y/o respecto a la secuencia de nucleótidos de la **SEQ ID NO:228** incluyen las secuencias de nucleótidos de las **SEQ ID NOs:399-401**.

En conjunto, los resultados de las **Tablas 1-29** muestran que los polinucleótidos/polipéptidos de la invención pueden ser útiles para incrementar la resistencia y/o la tolerancia a nematodos que atacan a las plantas.

Lo expuesto previamente es ilustrativo de la invención y no se debe interpretar como limitante de esta. La invención se define mediante las siguientes reivindicaciones y los equivalentes de las reivindicaciones deben incluirse en ella.

Se hace constar que con relación a esta fecha, el mejor método conocido por la solicitante para llevar a la práctica la citada invención, es el que resulta claro de la presente descripción de la invención.

REIVINDICACIONES

1. Un método para controlar una plaga de nematodos que atacan plantas, que comprende poner en contacto la plaga de nematodos que atacan plantas con una planta transgénica, o una de sus partes, que ha incorporado a su genoma una molécula de ácido nucleico recombinante que modula la expresión de uno o más polipéptidos seleccionados del grupo constituido por **SEQ ID NOs:29-42**, **SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046**, y cualquier combinación de estos, con lo que se controla la plaga de nematodos que atacan plantas.

2. El método de la reivindicación 1, donde la molécula de ácido nucleico recombinante comprende una secuencia de nucleótidos unida operativamente a un promotor que funciona en una planta o célula vegetal, y donde la secuencia de nucleótidos se selecciona del grupo constituido por:

(a) una secuencia de nucleótidos de cualquiera de **SEQ ID NOs:1-28**, **SEQ ID NOs: 43-134**, **SEQ ID NOs:210-242, SEQ ID NOs:261-644**;

(b) una secuencia de nucleótidos que codifica un polipéptido que comprende una secuencia de aminoácidos de cualquiera de **SEQ ID NOs:29-42, SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046**;

(c) una secuencia de nucleótidos que presenta al menos un 70% de identidad secuencial respecto a la secuencia de nucleótidos de (a) o (b);

(d) una secuencia de nucleótidos que se aparea en condiciones rigurosas de hibridación con la secuencia de nucleótidos de (a), (b) o (c), o un complemento de estas;

(e) una secuencia de nucleótidos que difiere de las secuencias de nucleótidos de (a), (b), (c) o (d) anteriores debido a la degeneración del código genético; y

(f) cualquier combinación de las secuencias de nucleótidos de (a)-(e).

3. El método de la reivindicación 1, donde la molécula de ácido nucleico recombinante es capaz de producir un ARN bicatenario que comprende una hebra antisentido y una hebra sentido, donde la hebra antisentido es complementaria respecto a una porción de una secuencia de nucleótidos que codifica dichos polipéptidos, comprendiendo la porción de aproximadamente 18 a aproximadamente 25 nucleótidos consecutivos con una identidad secuencial sustancial respecto a cualquiera de **SEQ ID NOs:1-28**, **SEQ ID NOs: 43-134**, **SEQ ID NOs:210-242, SEQ ID NOs:261-644** o cualquier combinación de estas.

4. El método de la reivindicación 1 o la reivindicación 2, donde la molécula de ácido nucleico recombinante modula la expresión provocando la sobreexpresión de dichos polipéptidos en la planta transgénica.

5. El método de la reivindicación 1 o la reivindicación 3, donde la molécula de ácido nucleico recombinante modula la expresión provocando la reducción de o reduciendo la expresión de dichos polipéptidos en la planta transgénica.

6. El método de cualquiera de las reivindicaciones 1 a 5, donde la planta o parte de planta transgénica es una planta de soja transgénica, una planta de remolacha azucarera transgénica, una planta de maíz transgénica, una planta de algodón transgénica, una planta de canola transgénica, una planta de trigo transgénica o una planta de arroz transgénica, o una de sus partes.

7. El método de cualquiera de las reivindicaciones 1 a 6, donde la plaga de nematodos se selecciona del grupo constituido por: un nematodo que induce quistes (*Heterodera* spp.), un nematodo nodulador de raíz (*Meloidogyne* spp.), un nematodo lanza (*Hoplolaimus* spp.), un nematodo estilete (*Tylenchorhynchus* spp.), un nematodo en espiral (*Helicotylenchus* spp.), un nematodo lesionador (*Pratylenchus* spp.), un nematodo de aguijón (*Belonoluimus* spp.), un nematodo reniforme (*Rotylenchulus reniformis*), un nematodo barrenador (*Radopholus similis*), un nematodo anillado (*Criconema* spp.) y cualquier combinación de estos.

8. El método de la reivindicación 7, donde el nematodo es un nematodo que induce quistes en la soja o un nematodo que induce quistes en la remolacha azucarera.

9. Una planta transgénica, o una de sus partes, que ha incorporado a su genoma una molécula de ácido nucleico recombinante que modula la expresión de uno o más polipéptidos seleccionados del grupo constituido por **SEQ ID NOs:29-42**, **SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046**, y cualquier combinación de estos, donde la planta transgénica es resistente a una plaga de nematodos.

10. Una semilla de la planta transgénica de la reivindicación 9.

11. Una molécula de ácido nucleico recombinante que comprende una secuencia de nucleótidos unida operativamente a un promotor que funciona en una planta, donde la secuencia de nucleótidos se selecciona del grupo constituido por:

(a) una secuencia de nucleótidos de cualquiera de **SEQ ID NOs:1-28**, **SEQ ID NOs: 43-134**, **SEQ ID NOs:210-242, SEQ ID NOs:261-644**;

(b) una secuencia de nucleótidos que codifica un polipéptido que comprende una secuencia de aminoácidos de cualquiera de **SEQ ID NOs:29-42, SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046**;

(c) una secuencia de nucleótidos que presenta al menos un 70% de identidad secuencial respecto a la secuencia de nucleótidos de (a) o (b);

(d) una secuencia de nucleótidos que se aparea en condiciones rigurosas de hibridación con la secuencia de nucleótidos de (a), (b) o (c), o un complemento de estas;

(e) una secuencia de nucleótidos que difiere de las secuencias de nucleótidos de (a), (b), (c) o (d) anteriores debido a la degeneración del código genético; y

(f) cualquier combinación de las secuencias de nucleótidos de (a)-(e).

12. Una molécula de ácido nucleico recombinante capaz de producir un ARN bicatenario que comprende una hebra antisentido y una hebra sentido, donde la hebra antisentido es complementaria respecto a una porción de una secuencia de nucleótidos que codifica un polipéptido que comprende una secuencia de aminoácidos de cualquiera de **SEQ ID NOs:29-42, SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046**, o cualquier combinación de estas, estando la porción constituida esencialmente por de aproximadamente 18 a aproximadamente 25 nucleótidos consecutivos de cualquiera de **SEQ ID NOs:1-28**, **SEQ ID NOs: 43-134**, **SEQ ID NOs:210-242, SEQ ID NOs:261-644** o cualquier combinación de estas.

13. Un vector que comprende la molécula de ácido nucleico recombinante de la reivindicación 11 o la reivindicación 12.

14. Una célula transgénica que comprende la molécula de ácido nucleico recombinante de la reivindicación 11 o la reivindicación 12.

15. La célula transgénica de la reivindicación 14, la cual es una célula vegetal transgénica.

16. La célula vegetal transgénica de la reivindicación 15, donde la célula vegetal es una célula vegetal de soja transgénica, una célula vegetal de remolacha azucarera transgénica, una célula vegetal de maíz transgénica, una célula vegetal de algodón transgénica, una célula vegetal de canola transgénica, una planta de caña de azúcar transgénica, una célula vegetal de trigo transgénica o una célula vegetal de arroz transgénica.

17. Una planta transgénica que comprende la célula vegetal transgénica de la reivindicación 15 o la reivindicación 16.

18. Una semilla de la planta transgénica de la reivindicación 17, donde la semilla comprende la molécula de ácido nucleico recombinante.

19. Una composición nematicida que comprende un polipéptido heterólogo que comprende una secuencia de aminoácidos de cualquiera de **SEQ ID NOs:29-42, SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046,** o cualquier combinación de estas, en un portador agrícolamente aceptable.

20. La composición nematicida de la reivindicación 19, que comprende además compuestos nematicidas o insecticidas adicionales.

21. La composición nematicida de la reivindicación 20, donde el compuesto nematicida adicional se selecciona del grupo constituido por cloropicrina, metam sódico, metam potásico, dazomet, yodometano, disulfuro de dimetilo (DMDS), fluoruro de sulfurilo, oxamilo y fostiazato.

22. Una composición nematicida que comprende el vector de la reivindicación 13.

23. Un método para producir una planta transgénica, comprendiendo el método introducir en una planta una molécula de ácido nucleico recombinante de la reivindicación 11 o la reivindicación 12, con lo que se produce una planta transgénica que presenta mayor resistencia a una plaga de nematodos que atacan plantas.

24. El método de la reivindicación 23, donde la introducción se lleva a cabo transformando una célula vegetal y regenerando una planta transgénica o mediante cultivo selectivo.

25. El método de la reivindicación 23 o la reivindicación 24, donde la plaga de nematodos que atacan plantas se selecciona del grupo constituido por: un nematodo que induce quistes (*Heterodera* spp.), un nematodo nodulador de raíz (*Meloidogyne* spp.), un nematodo lanza (*Hoplolaimus* spp.), un nematodo estilete (*Tylenchorhynchus* spp.), un nematodo en espiral (*Helicotylenchus* spp.), un nematodo lesionador (*Pratylenchus* spp.), un nematodo de aguijón (*Belonoluimus* spp.), un nematodo reniforme (*Rotylenchulus reniformis*), un nematodo barrenador (*Radopholus similis*), un nematodo anillado (*Criconema* spp.) y cualquier combinación de estos.

26. Una planta transgénica producida mediante el método de cualquiera de las reivindicaciones 23-25.

27. Una planta transgénica que presenta mayor resistencia a una plaga de nematodos que atacan plantas producida mediante el método de cualquiera de las reivindicaciones 23-25.

28. La planta transgénica de cualquiera de las reivindicaciones 23-27, donde la planta transgénica es una planta de soja transgénica, una planta de remolacha azucarera transgénica, una planta de maíz transgénica, una planta de algodón transgénica, una planta de canola transgénica, una planta de trigo transgénica o una planta de arroz transgénica.

29. Un método para reducir la capacidad infecciosa para una planta de una plaga de nematodos que atacan plantas, que comprende poner en contacto la plaga de nematodos que atacan plantas con la planta transgénica de la reivindicación 9 o la

composición nematicida de la reivindicación 19, con lo que se reduce la capacidad infecciosa para la planta de la plaga de nematodos que atacan plantas.

30. Un método para reducir el desarrollo de quistes de nematodos producidos por una plaga de nematodos que atacan plantas, que comprende poner en contacto la plaga de nematodos que atacan plantas con la planta transgénica de la reivindicación 9 o la composición nematicida de la reivindicación 19, donde se reduce el desarrollo de quistes de nematodos producidos por la plaga de nematodos que atacan plantas en las raíces de la planta.

31. Un método para reducir el crecimiento de la población de una plaga de nematodos que atacan plantas, que comprende poner en contacto la población de la plaga de nematodos que atacan plantas con la planta transgénica de la reivindicación 9 o la composición nematicida de la reivindicación 19, donde se reduce el crecimiento de la población de la plaga de nematodos que atacan plantas.

32. Un método para producir una planta de soja con mayor resistencia a la infestación por parte de una plaga de nematodos que atacan plantas, comprendiendo el método los pasos de (a) cruzar la planta transgénica de cualquiera de las reivindicaciones 9, 17 o 26-28 consigo misma o con otra planta para producir una semilla que comprenda la molécula de ácido nucleico de la reivindicación 11 o la reivindicación 12, o el vector de la reivindicación 13; (b) cultivar una planta de la progenie a partir de dicha semilla para producir una planta con mayor resistencia a la infestación por parte de plagas de nematodos que atacan plantas.

33. El método de la reivindicación 32, que comprende además (c) cruzar la planta de la progenie consigo misma o con otra planta y (d) repetir los pasos (b) y (c) durante 0-7 generaciones adicionales para producir una planta con mayor resistencia a la infestación por parte de plagas de nematodos que atacan plantas.

34. Un cultivo que comprende una pluralidad de las plantas transgénicas de cualquiera de las reivindicaciones 9, 17 o 26-28 plantadas conjuntamente en un campo agrícola.

35. Un método para mejorar el rendimiento de un cultivo vegetal que comprende: cultivar una pluralidad de las plantas de cualquiera de las reivindicaciones 9, 17 o 26-28 como cultivo vegetal, donde la pluralidad de plantas de dicho cultivo vegetal presenta mayor resistencia a la infección por parte de nematodos, con lo que se mejora el rendimiento de dicho cultivo vegetal.

36. Un producto tras la recolección derivado de la planta de cualquiera de las reivindicaciones 26-28.

37. El producto de la reivindicación 36, donde el producto es pienso de semillas, harina de semillas, aceite de semillas, azúcar o cereales producidos para contener productos secundarios vegetales en parte o en su totalidad.

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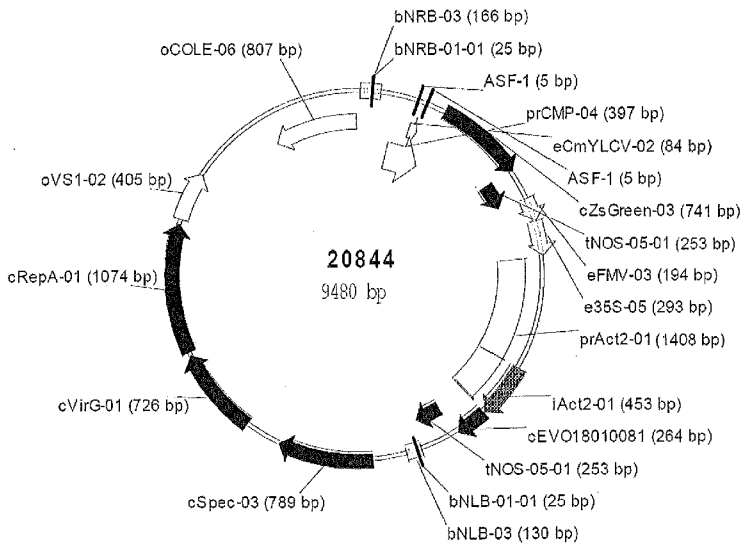
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[Continued on next page]

(54) **Title**: COMPOSITIONS AND METHODS FOR INCREASING NEMATODE RESISTANCE IN PLANTS

FIG. 1



(57) **Abstract**: The invention relates to methods and compositions for increasing resistance or tolerance to a nematode plant pest in a plant or part thereof. Nucleotide sequences that confer resistance or tolerance to nematode plant pests when expressed in a plant are provided as well as compositions comprising the polypeptides encoded by the nucleotide sequences, and transgenic plants and parts thereof comprising the nucleotide sequences.

WO 2013/078153 A1

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— *as to applicant's entitlement to apply for and be granted a patent (Rule 4.17(ii))*

— *as to the applicant's entitlement to claim the priority of the earlier application (Rule 4.17(iii))*

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COMPOSITIONS AND METHODS FOR INCREASING NEMATODE RESISTANCE IN PLANTS

STATEMENT REGARDING ELECTRONIC FILING OF A SEQUENCE LISTING

A Sequence Listing in ASCII text format, submitted under 37 C.F.R. § 1.821, entitled 9207-58WO_ST25.txt, 3,013,855 bytes in size, generated on November 14, 2012 and filed via EFS-Web, is provided in lieu of a paper copy. This Sequence Listing is hereby incorporated herein by reference into the specification for its disclosures.

STATEMENT OF PRIORITY

This application claims the benefit of U.S. Provisional Application No. 61/562,060, filed November 21, 2011 and U.S. Provisional Application No. 61/684,234, filed August 17, 2012, the entire contents of each of which are incorporated by reference herein.

FIELD OF THE INVENTION

The invention relates to compositions and methods for control of nematode pests in plants.

BACKGROUND

Nematodes are elongated symmetrical roundworms that constitute one of the largest and most successful phyla in the animal kingdom. Many nematode species are free-living and feed on bacteria, whereas others have evolved into pests or parasites of plants and animals, including humans.

Nematode pests of plants are responsible for many billions of dollars in economic losses annually. Nematode plant pests feed on stems, buds, leaves and, in particular, on roots of more than 2,000 vegetables, fruits, and ornamental plants, causing an estimated $100-125 billion crop loss worldwide. Nematodes are present throughout the United States (US), but are mostly a problem in warm, humid areas of the south and west, as well as in sandy soils. The most economically damaging plant nematode pest genera belong to the family Heterderidae of the order Tylenchida, and include the cyst nematodes [genera *Heterodera* and *Globodera*, e.g., soybean cyst nematode (*Heterodera glycines*, SCN) and potato cyst nematodes (*G. pallida* and G. *rostochiensis*)], and the root-knot nematodes (genus Meloidogyne).

Root-knot nematodes infest thousands of different plant species including vegetables, fruits, and row crops. Cyst nematodes are known to infest tobacco, cereals, sugar beets,

potato, rice, corn, soybeans and many other crops. *Heterodera schachtii* (BCN) principally attacks sugar beets, and *Heterodera avenae* is a pest of cereals. *Heterodera zeae* feeds on corn, and *Globodera rostochiensis* and *G. pallida* feed on potatoes. The soybean cyst nematode (SCN) is present in every soybean-producing state in the US, and causes total soybean yield losses estimated to be nearly $1 billion per year. Once SCN is present in a field, it cannot feasibly be eradicated using known methods. Although soybean is the major economic crop attacked by SCN, SCN attacks some fifty hosts in total, including field crops, vegetables, ornamentals, and weeds.

Cotton root knot nematode (RKN) is a destructive nematode, which forms galls on the roots of cotton plants. The causative agent is *Meloidogyne incognita* (Kofoid and White) Chitwood, a nematode which can infest a variety of plant species. Nutrient and water uptake are decreased in infested plants, and plants may become susceptible to pathogens, especially Fusarium wilt. Consequently, yield is decreased in plants infested with RKN. In the US alone, an estimated 10.93% of cotton yield loss in 2004 was attributed to RKN (Blasingame and Patel, *Proceedings of the Beltwide Cotton Conferences* 1:259-262 (2005). RKN is widespread throughout the U.S. Cotton Belt. Methods to mitigate RKN damage include rotating cotton crops with non-susceptible crops and application of costly nematicides. However, the most effective way for cotton growers to reduce yield loss and crop damage due to RKN is to grow RKN resistant cotton cultivars.

Signs of nematode damage include stunting and yellowing of leaves, as well as wilting of the plants during hot periods. However, nematodes, including SCN, can cause significant yield loss without obvious above-ground symptoms. For example, an infestation of SCN to a plant can result in dwarfed or stunted roots, decrease the number of nitrogen-fixing nodules on the roots, and/or make the roots more susceptible to attack by other soil-borne plant pests or pathogens.

In contrast to many viral and bacterial pathogens, little is known about the molecular basis of the nematode-plant interaction, limiting the available approaches useful in controlling nematodes. Chemicals useful in controlling nematode plant pests include organophosphates and carbamates, the oldest extant class of nematicides, which target acetylcholinesterase. Imidazole derivatives such as benzimidazole exert their nematicidal effects by binding tubulin. Levamisole acts as an agonist on the nicotinic acetylcholine receptor, and avermectins act as irreversible agonists at glutamate-gated chloride channels. Unfortunately, there are certain debilitating nematode infestations which are difficult, if not impossible, to eradicate with existing control measures. In addition, the currently available

nematode control agents have drawbacks in terms of efficacy, expense and environmental safety. For example, methyl bromide, which is an effective pre-plant soil fumigant used to control nematodes in many high-input, high-value crops in the US, is being phased out due to environmental and human health concerns. However, because methyl bromide has provided a reliable return on investment for nematode control, many growers of high value crops may be negatively impacted if effective and economical alternatives are not identified. In addition, environmental concerns, primarily groundwater contamination, ozone depletion, and pesticide residues in food have prompted the removal of Aldicarb, DGBCP, and other toxic nematicides from the market by the US Environmental Protection Agency. Physical control measures (such as solarization and hot water treatment), biological control measures (e.g., crop rotation), and integrated approaches have been used to ameliorate the damage caused by plant nematode pests, but no single method or combination of measures is uniformly effective.

Nematode resistant germplasm and transgenic plants have also been considered as alternatives or complements to chemical control measures. For example, transgenic plants expressing a protease inhibitor shows some resistance to cyst and root-knot nematodes (Urwin et al. 1997. Plant J. 12:455-461). Use of such alternative control measures requires a greater knowledge of the nematode-plant interaction to achieve satisfactory results. Several studies have generated gene expression data suggesting that many host plant genes are up- or down-regulated in response to nematode invasion (Szakasits et al. 2009. *Plant J.* 57:771-784; Puthoff et al. 2003. *Plant J.* 33:911-921; Bethke et al. 2009. *Proc. Natl. Acad. Sci.* 106:8067-8072; Stepanova et al. 2007. *Plant Cell* 19:2169-2185 and Kilian et al. 2007. *Plant J.* 50:347-363). However, none of these studies aid the skilled person in predicting which, if any, such genes could be successfully utilized in controlling nematodes, particularly in chimeric gene constructs for deployment in a transgenic plant.

Accordingly, the invention overcomes the deficiencies in the art by providing compositions and methods comprising recombinant nucleic acid molecules and their encoded polypeptides for control of nematode pest infestations in plants.

SUMMARY OF THE INVENTION

The needs outlined above are met by the invention which, in various embodiments, provides new compositions and methods of controlling economically important nematode pests. In particular, transgenic plants and/or plant parts expressing at least one recombinant nucleic acid molecule of the invention which modulates expression of proteins of the

invention are found to reduce the ability of nematode pests to survive, grow and reproduce, or of limiting nematode-related damage or loss to the transgenic plants. The invention is also drawn to transgenic nematode-resistant plants which overexpress or have reduced expression of a protein of the invention in the transgenic plant and to methods of using the transgenic plants alone or in combination with other nematode control measures to confer maximal nematode control efficiency with reduced environmental impact. Transgenic plants and plant parts that have a protein of the invention overexpressed or inhibited (e.g., reduced amount and/or reduced activity, and the like, as compared to a control) are more tolerant or resistant to nematode pest infestation. For example, the economically important nematode pest, soybean cyst nematode (*Heterodera glycines*) can be controlled by transgenic soybean plants which over-express a protein of the invention or which comprise a nucleic acid molecule of the invention that reduces the expression of a protein of the invention.

In one aspect of the invention, a method of controlling a nematode plant pest is provided, the method comprising contacting the nematode pest with a transgenic plant, or part thereof, having incorporated into its genome a recombinant nucleic acid molecule that modulates the expression of one or more polypeptides having the amino acid sequence of **SEQ ID NOs:29-42, SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046,** or any combination thereof, thereby controlling the nematode plant pest. In another aspect of the invention, the recombinant nucleic acid molecule is capable of producing a double stranded RNA comprising an antisense strand and a sense strand, wherein the antisense strand is complementary to a portion of a nucleotide sequence encoding the one or more polypeptides, the portion comprising, consisting essentially of , consisting of about 18 to about 25 consecutive nucleotides having substantial identity to any one of the nucleotide sequences of **SEQ ID NOs:1-28, SEQ ID NOs:43-134, SEQ ID NOs:210-242, SEQ ID NOs:261-664,** or any combination thereof.

In yet another aspect of the invention, a recombinant nucleic acid molecule is provided, the nucleic acid molecule comprising a nucleotide sequence operatively linked to a promoter that functions in a plant or plant cell, wherein the nucleotide sequence is: (a) a nucleotide sequence of any of **SEQ ID NOs:1-28, SEQ ID NOs:43-134, SEQ ID NOs:210-242, SEQ ID NOs:261-664**; (b) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence of any of **SEQ ID NOs:29-42, SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046**; (c) a nucleotide sequence having at least 70% sequence identity to a nucleotide sequence of (a) and (b) above; (d) a nucleotide sequence which anneals under stringent hybridization conditions to the nucleotide sequence of (a), (b)

or (c); (e) a nucleotide sequence that differs from the nucleotide sequences of (a), (b), (c) or (d) above due to the degeneracy of the genetic code; or (f) any combination of the nucleotide sequences of (a)-(e).

In another aspect of the invention, a polypeptide is provided, the polypeptide comprising, consisting essentially of, or consisting of an amino acid sequence of any of **SEQ ID NOs:29-42, SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046,** or any combination thereof.

In a further aspect of the invention, a method of producing a transgenic plant cell, comprising introducing into a plant cell a recombinant nucleic acid molecule is provided, the recombinant nucleic acid molecule comprising a nucleotide sequence operatively linked to a promoter that functions in a plant or plant cell, wherein the nucleotide sequence is: (a) a nucleotide sequence of any of **SEQ ID NOs:1-28, SEQ ID NOs:43-134, SEQ ID NOs:210-242, SEQ ID NOs:261-644**; (b) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence of any one of the amino acid sequences of **SEQ ID NOs:29-42, SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046**; (c) a nucleotide sequence having at least 70% sequence identity to a nucleotide sequence of (a) and (b) above; (d) a nucleotide sequence which anneals under stringent hybridization conditions to the nucleotide sequence of (a), (b) or (c); (e) a nucleotide sequence that differs from the nucleotide sequences of (a), (b), (c) or (d) above due to the degeneracy of the genetic code; or (f) any combination of the nucleotide sequences of (a)-(e), thereby producing a transgenic plant cell that can regenerate a plant having increased resistance to a nematode plant pest.

A still further aspect of this invention provides a method of producing a soybean plant having increased resistance to infestation by a nematode plant pest, the method comprising the steps of (a) crossing the transgenic plant of the invention with itself or another plant to produce seed comprising the nucleic acid molecule of this invention, or the vector of the invention; (b) growing a progeny plant from said seed to produce a plant having increased resistance to infestation by nematode plant pests.

In additional aspects of the invention, transgenic plant cells, transgenic plants and parts thereof comprising a nucleic acid molecule that comprises one or more of the nucleotide sequences of the invention are provided and methods of using the same to control, suppress, and/or reduce infectivity of a nematode plant pest. Further provided are polypeptides of the invention and methods of using the same to control, suppress, and/or reduce the infectivity, infestation and/or cyst development of a nematode plant pest, comprising contacting a nematode plant pest with an effective amount of the polypeptide(s). In some embodiments,

contacting the nematode plant pest with an effective amount of a polypeptide comprises contacting the nematode plant pest with a transgenic plant comprising a nucleic acid molecule of the invention.

The invention additionally provides a crop comprising a plurality of the transgenic plants of the invention planted together in an agricultural field. In some aspects, the invention provides a method of improving the yield of a plant crop contacted with a nematode plant pest, the method comprising cultivating a plurality of plants comprising a nucleic acid molecule of the invention as the plant crop, wherein the plurality of plants of said plant crop have increased resistance to nematode infection, thereby improving the yield of said plant crop.

The invention further provides a method of improving yield in a crop contacted with a nematode plant pest, the method comprising contacting the nematode plant pest with an effective amount of the polypeptide of the invention or the nematicidal composition of the invention, wherein the yield of the crop is improved.

These and other aspects of the invention are set forth in more detail in the description of the invention below.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1 is a binary vector useful for transforming plants and/or plant cells with a recombinant nucleic acid molecule of the invention.

Figure 2 is an empty vector useful as a negative control in plant and/or plant cell transformation experiments.

Figure 3 is a binary vector useful for transforming plants and/or plant cells with a recombinant nucleic acid molecule of the invention.

Figure 4 is an empty vector useful as a negative control in plant and/or plant cell transformation experiments.

Figure 5 is a schematic illustration of the modified pGI binary plasmid containing the At6669 promoter and the GUSintron (pQYN 6669) that can be used for expressing the isolated polynucleotide sequences of the invention. RB - T-DNA right border; LB - T-DNA left border; MCS – Multiple cloning site; RE – any restriction enzyme; NOS pro = nopaline

synthase promoter; NPT-II = neomycin phosphotransferase gene; NOS ter = nopaline synthase terminator; Poly-A signal (polyadenylation signal); GUSintron – the GUS reporter gene (coding sequence and intron). In some embodiments, the isolated polynucleotide sequences of the invention were cloned into the vector while replacing the GUSintron reporter gene.

Figure 6 is a schematic illustration of the modified pGI binary plasmid containing the At6669 promoter (pQFN or pQFNc) used for expressing the isolated polynucleotide sequences of the invention. RB - T-DNA right border; LB - T-DNA left border; MCS – Multiple cloning site; RE – any restriction enzyme; NOS pro = nopaline synthase promoter; NPT-II = neomycin phosphotransferase gene; NOS ter = nopaline synthase terminator; Poly-A signal (polyadenylation signal); GUSintron – the GUS reporter gene (coding sequence and intron). In some embodiments, the isolated polynucleotide sequences of the invention were cloned into the MCS of the vector.

Figure 7 is a schematic illustration of pQXNc plasmid, which is a modified pGI binary plasmid used for expressing the isolated polynucleotide sequences of some embodiments of the invention. RB - T-DNA right border; LB - T-DNA left border; NOS pro = nopaline synthase promoter; NPT-II = neomycin phosphotransferase gene; NOS ter = nopaline synthase terminator; RE = any restriction enzyme; Poly-A signal (polyadenylation signal); 35S – the 35S promoter. In some embodiments, the isolated polynucleotide sequences were cloned into the MCS (Multiple cloning site) of the vector.

BRIEF DESCRIPTION OF THE SEQUENCES IN THE SEQUENCE LISTING

SEQ ID NOs:1-14 are nucleotide sequences of the invention comprising untranslated regions and coding regions.

SEQ ID NOs:15-28 are coding sequences of the invention encoding the amino acid sequences of **SEQ ID NOs:29-42**.

SEQ ID NOs:29-42 are amino acid sequences of proteins of the invention that when overexpressed or inhibited in transgenic plants confer tolerance or resistance to nematodes.

SEQ ID NOs:43-134 are nucleotide sequences that encode the amino acid sequences of **SEQ ID NOs:29-42, 135-209**.

SEQ ID NOs:135-209 are amino acid sequences of homologues of **SEQ ID NOs:29-42**.

SEQ ID NOs: 210-223 are nucleotide sequences of the invention comprising untranslated regions and coding regions.

SEQ ID NOs:224-242 are coding sequences of the invention encoding the amino acid sequences of **SEQ ID NOs:243-260**.

SEQ ID NOs: 243-260 are amino acid sequences of proteins of the invention that when overexpressed or reduced in amount or activity in transgenic plants confer tolerance or resistance to nematodes.

SEQ ID NOs:261-664 are nucleotide sequences of the invention encoding homologues of the **SEQ ID NOs:210-242**.

SEQ ID NOs:665-1046 are amino acid sequences of proteins of the invention that when overexpressed or reduced in amount or activity in transgenic plants confer tolerance or resistance to nematodes.

DETAILED DESCRIPTION OF THE INVENTION

This description is not intended to be a detailed catalog of all the different ways in which the invention may be implemented, or all the features that may be added to the instant invention. For example, features illustrated with respect to one embodiment may be incorporated into other embodiments, and features illustrated with respect to a particular embodiment may be deleted from that embodiment. Thus, the invention contemplates that in some embodiments of the invention, any feature or combination of features set forth herein can be excluded or omitted. In addition, numerous variations and additions to the various embodiments suggested herein will be apparent to those skilled in the art in light of the instant disclosure, which do not depart from the instant invention. Hence, the following descriptions are intended to illustrate some particular embodiments of the invention, and not to exhaustively specify all permutations, combinations and variations thereof.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. The terminology used in the description of the invention herein is for the purpose of describing particular embodiments only and is not intended to be limiting of the invention.

All publications and patent applications mentioned in this specification are indicative of the level of skill of those skilled in the art that this invention pertains. Further, publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety.

As used in the description of the embodiments of the invention and the appended claims, the singular forms "a," "an," and "the" are intended to include the plural forms as well, unless the context clearly indicates otherwise.

As used herein, "and/or" refers to and encompasses any and all possible combinations of one or more of the associated listed items.

The term "about," as used herein when referring to a measurable value such as an amount of a compound, dose, time, temperature, and the like, is meant to encompass variations of 20%, 10%, 5%, 1%, 0.5%, or even 0.1% of the specified amount.

The terms "comprise," "comprises" and/or "comprising," when used in this specification, specify the presence of stated features, integers, steps, operations, elements, and/or components, but do not preclude the presence or addition of one or more other features, integers, steps, operations, elements, components, and/or groups thereof.

As used herein, the transitional phrase "consisting essentially of" (and grammatical variants) means that the scope of a claim is to be interpreted to encompass the specified materials or steps recited in the claim and those that do not materially alter the basic and novel characteristic(s)" of the claimed invention. Thus, the term "consisting essentially of" when used in a claim of this invention is not intended to be interpreted to be equivalent to "comprising."

The invention is directed in part to the discovery that modulating expression by over expressing or reducing expression in a plant of at least one polypeptide described herein can result in the plant having increased resistance to nematode pests. The term "modulating" or "modulates" in the context of the invention means an alteration in the expression of a protein of the invention by over-expressing the protein or reducing the expression of the protein. Therefore, in one embodiment, the invention encompasses a method of controlling a nematode plant pest comprising contacting the nematode pest with a transgenic plant, or part thereof, having incorporated into its genome a recombinant nucleic acid molecule that modulates the expression of one or more polypeptides having any one of the amino acid sequences of **SEQ ID NOs:29-42, SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046,** or any combination thereof, thereby controlling the nematode plant pest. In another embodiment, the recombinant nucleic molecule comprises a nucleotide sequence operatively linked to a promoter that functions in a plant or plant cell, wherein the nucleotide sequence comprises, consists essentially of, or consists of: (a) a nucleotide sequence of any one of **SEQ ID NOs:1-28, SEQ ID NOs:43-134, SEQ ID NOs:210-242, SEQ ID NOs:261-644**; (b) a nucleotide sequence that encodes a polypeptide comprising an amino acid

sequence of any one of **SEQ ID NOs:29-42, SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046**; (c) a nucleotide sequence having at least 70% sequence identity to the nucleotide sequence of (a) or (b); (d) a nucleotide sequence which anneals under stringent hybridization conditions to the nucleotide sequence of (a), (b) or (c), or a complement thereof; (e) a nucleotide sequence that differs from the nucleotide sequences of (a), (b), (c) or (d) above due to the degeneracy of the genetic code; and (f) any combination of the nucleotide sequences of (a)-(e). In more particular embodiments, the nucleotide sequence can comprise, consist essentially of, or consist of: (a) a nucleotide sequence of any one of **SEQ ID NOs:15, 17, 20, 22, 23, 24, 26, 226, 227,228, 230, 232, 233**; (b) a nucleotide sequence that encodes a polypeptide comprising an amino acid sequence of any one of **SEQ ID NOs:29-38, 40-42, 52, 243, 244, 245, 246, 248-252, 254, 256-259**; (c) a nucleotide sequence having at least 70% sequence identity to the nucleotide sequence of (a) or (b); (d) a nucleotide sequence which anneals under stringent hybridization conditions to the nucleotide sequence of (a), (b) or (c), or a complement thereof; (e) a nucleotide sequence that differs from the nucleotide sequences of (a), (b), (c) or (d) above due to the degeneracy of the genetic code; and (f) any combination of the nucleotide sequences of (a)-(e). In further embodiments, the nucleotide sequence can comprise, consist essentially of, or consist of: (a) a nucleotide sequence of any one of **SEQ ID NOs: 56-63, 66-127, 389-401, 408-633, 637-642**; (b) a nucleotide sequence that encodes a polypeptide comprising an amino acid sequence of any one of **SEQ ID NOs: 56-63, 66-127, 389-401, 408-633, 637-642**; (c) a nucleotide sequence having at least 70% sequence identity to the nucleotide sequence of (a) or (b); (d) a nucleotide sequence which anneals under stringent hybridization conditions to the nucleotide sequence of (a), (b) or (c), or a complement thereof; (e) a nucleotide sequence that differs from the nucleotide sequences of (a), (b), (c) or (d) above due to the degeneracy of the genetic code; and (f) any combination of the nucleotide sequences of (a)-(e).

In yet another embodiment, the recombinant nucleic acid molecule is capable of producing a double stranded RNA comprising an antisense strand and a sense strand, wherein the antisense strand is complementary to a portion of a nucleotide sequence encoding the one or more polypeptides, the portion comprising, consisting essentially of, consisting of about 18 to about 25 consecutive nucleotides (e.g., about 18, 19, 20, 21, 22, 23, 24, or 25 consecutive nucleotides) having substantial identity to any one of the nucleotide sequences of **SEQ ID NOs:1-28, SEQ ID NOs:43-134, SEQ ID NOs:210-242, SEQ ID NOs:261-644,** or any combination thereof. In still another embodiment, the recombinant nucleic acid molecule modulates the expression of the one or more polypeptides of the invention (e.g., **SEQ ID**

NOs:29-42, SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046) by causing overexpression of the one or more polypeptides in the transgenic plant. In another embodiment, the recombinant nucleic acid molecule modulates the expression of the one or more polypeptides of the invention (e.g., **SEQ ID NOs:29-42, SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046**) by causing the reduction of or reducing the expression of the one or more polypeptides in the transgenic plant.

In another embodiment, the transgenic plant or plant part of the invention is a transgenic soybean plant, a transgenic sugar beet plant, a transgenic corn plant, a transgenic cotton plant, a transgenic canola plant, a transgenic wheat plant, a transgenic sugar cane plant, or a transgenic rice plant, or a part thereof.

In still another embodiment, the nematode pest is selected from the group consisting of: a cyst nematode (*Heterodera* spp.), a root knot nematode (*Meloidogyne* spp.), a lance nematode (*Hoplolaimus* spp.), a stunt nematode (*Tylenchorhynchus* spp.), a spiral nematode (*Helicotylenchus* spp.), a lesion nematode (*Pratylenchus* spp.), a sting nematode (*Belonoluimus* spp.), a reniform nematode (*Rotylenchulus reniformis*), a burrowing nematode (*Radopholus similis*), a ring nematode (*Criconema* spp.), and any combination thereof. In another embodiment, the nematode is a soybean cyst nematode or a sugar beet cyst nematode. Overexpression or reduced expression of a polypeptide described herein can result in the plant having increased resistance to nematode plant pests. Thus, in one aspect, the invention provides a recombinant nucleic acid molecule comprising one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, and the like) nucleotide sequences, each of which when expressed in a plant confer increased resistance to a nematode plant pest, wherein the one or more nucleotide sequences comprise, consist essentially of, or consist of: (a) a nucleotide sequence of any of **SEQ ID NOs:1-28, SEQ ID NOs:43-134, SEQ ID NOs:210-242, SEQ ID NOs:261-644**; (b) a nucleotide sequence that encodes a polypeptide comprising, consisting essentially of, or consisting of the amino acid sequence of any of **SEQ ID NOs:29-42, SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046**; (c) a nucleotide sequence having at least 70% sequence identity to a nucleotide sequence of (a) and (b) above; (d) a nucleotide sequence which anneals under stringent hybridization conditions to the nucleotide sequence of (a), (b) or (c); (e) a nucleotide sequence that differs from the nucleotide sequences of (a), (b), (c) or (d) above due to the degeneracy of the genetic code; or (f) any combination of the nucleotide sequences of (a)-(e). In more particular embodiments, the nucleotide sequences can comprise, consist essentially of, or consist of: (a) a nucleotide sequence of any of **SEQ ID NOs:15, 17, 20, 22, 23, 24, 26, 226, 227,228, 230, 232, 233**; (b)

a nucleotide sequence that encodes a polypeptide comprising, consisting essentially of, or consisting of the amino acid sequence of any of **SEQ ID NOs: 29, 31, 34, 36-38, 40, 244-246, 250, 251;** (c) a nucleotide sequence having at least 70% sequence identity to a nucleotide sequence of (a) and (b) above; (d) a nucleotide sequence which anneals under stringent hybridization conditions to the nucleotide sequence of (a), (b) or (c); (e) a nucleotide sequence that differs from the nucleotide sequences of (a), (b), (c) or (d) above due to the degeneracy of the genetic code; or (f) any combination of the nucleotide sequences of (a)-(e). In further embodiments, the nucleotide sequences can comprise, consist essentially of, or consist of: (a) a nucleotide sequence of any of **SEQ ID NOs: 56-63, 66-127, 389-401, 408-633, 637-642**; (b) a nucleotide sequence that encodes a polypeptide comprising, consisting essentially of, or consisting of the amino acid sequence of any of **SEQ ID NOs: 56-63, 66-127, 389-401, 408-633, 637-642**; (c) a nucleotide sequence having at least 70% sequence identity to a nucleotide sequence of (a) and (b) above; (d) a nucleotide sequence which anneals under stringent hybridization conditions to the nucleotide sequence of (a), (b) or (c); (e) a nucleotide sequence that differs from the nucleotide sequences of (a), (b), (c) or (d) above due to the degeneracy of the genetic code; or (f) any combination of the nucleotide sequences of (a)-(e).

In some embodiments, in addition to the nucleotide sequences described above, a nucleic acid molecule of the invention can comprise one or more nucleotide sequences that confer increased resistance to a nematode plant pest in a plant when expressed in the plant, the one or more nucleotide sequences comprising, consisting essentially of, or consisting of: a nucleotide sequence of any of **SEQ ID NOs:1-28, SEQ ID NOs:43-134, SEQ ID NOs:210-242, SEQ ID NOs:261-644**, or any combination thereof. In some particular embodiments, a nucleic acid molecule of the invention can comprise one or more nucleotide sequences that confer increased resistance to a nematode plant pest in a plant when expressed in the plant, the one or more nucleotide sequences comprising, consisting essentially of, or consisting of: a nucleotide sequence of any of **SEQ ID NOs: 15, 17, 20, 22, 23, 24, 26, 226, 227,228, 230, 232, 233**, or any combination thereof.

Thus, in some embodiments, the invention provides a recombinant nucleic acid molecule comprising one or more nucleotide sequences, wherein the one or more nucleotide sequences comprise, consist essentially of, or consist of: (a) a nucleotide sequence of any of **SEQ ID NOs:1-28, SEQ ID NOs:43-134, SEQ ID NOs:210-242, SEQ ID NOs:261-644**; (b) a nucleotide sequence that encodes a polypeptide comprising, consisting essentially of, or consisting of the amino acid sequence of any of **SEQ ID NOs:29-42, SEQ ID NOs:135-209,**

SEQ ID NOs:243-260, SEQ ID NOs:665-1046; (c) a nucleotide sequence having significant sequence identity to a nucleotide sequence of (a), (b) above; (d) a nucleotide sequence which anneals under stringent hybridization conditions to the nucleotide sequence of (a)-(c) above; (e) a nucleotide sequence that differs from the nucleotide sequences of (a)-(d) above due to the degeneracy of the genetic code; or (f) any combination of the nucleotide sequences of (a)-(e).

In some embodiments of the invention, nucleotide sequences having significant sequence identity to the nucleotide sequences of the invention are provided. "Significant sequence identity" or "significant sequence similarity" means at least about 70%, 75%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, and/or 100% identity or similarity with another nucleotide sequence. Thus, in additional embodiments, "significant sequence identity" or "significant sequence similarity" means a range of about 70% to about 100%, about 75% to about 100%, about 80% to about 100%, about 81% to about 100%, about 82% to about 100%, about 83% to about 100%, about 84% to about 100%, about 85% to about 100%, about 86% to about 100%, about 87% to about 100%, about 88% to about 100%, about 89% to about 100%, about 90% to about 100%, about 91% to about 100%, about 92% to about 100%, about 93% to about 100%, about 94% to about 100%, about 95% to about 100%, about 96% to about 100%, about 97% to about 100%, about 98% to about 100%, and/or about 99% to about 100% identity or similarity with another nucleotide sequence. Therefore, in some embodiments, a nucleotide sequence of the invention is a nucleotide sequence that has significant sequence identity to the nucleotide sequence of any of **SEQ ID NOs:1-28, SEQ ID NOs:43-134, SEQ ID NOs:210-242, SEQ ID NOs:261-644.** In some particular embodiments, a nucleotide sequence of the invention is a nucleotide sequence that has significant sequence identity to the nucleotide sequence of any of **SEQ ID NOs:15, 17, 20, 22, 23, 24, 26, 226, 227,228, 230, 232** and/or **233.**

In some embodiments of the invention, the nucleotide sequences and/or nucleic acid molecules of the invention can be expressed to produce polypeptides, each of which when produced in a plant result in increased resistance to a nematode plant pest. Thus, in other aspects of the invention, a polypeptide is provided, the polypeptide comprising, consisting essentially of, or consisting of an amino acid sequence of any of **SEQ ID NOs:29-42, SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046**, wherein production of said polypeptide in a plant results in increased resistance to a nematode plant pest in the plant.

A still further aspect of the invention is a nematicidal composition comprising one or more polypeptides of the invention. In some embodiments, the composition comprises a polypeptide comprising, consisting essentially of, or consisting of an amino acid sequence of any of **SEQ ID NOs:29-42, SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046**, or any combination thereof.

In some embodiments, a polypeptide of the invention comprises, consists essentially of, or consists of an amino acid sequence that is at least 70% identical, *e.g.*, at least 70%, 75%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, and/or 100% identical to an amino acid sequence of any of **SEQ ID NOs:29-42, SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046**.

The polypeptides of the invention can be produced in and collected from cells transformed with the nucleic acid molecules comprising the nucleotide sequences of the invention. Therefore, the polypeptides can be isolated and provided in a composition of the invention as a partially or fully purified full-length polypeptide, or as an active variant or fragment thereof, or the polypeptides can be provided as a cell extract or cell lysate from the cell or cells of an organism producing said polypeptide(s). Complete purification is not required in any case. The polypeptide, variant or fragment thereof can be at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% pure (w/w), or more.

In some embodiments, a polypeptide or nucleotide sequence of the invention can be a conservatively modified variant. As used herein, "conservatively modified variant" refer to polypeptide and nucleotide sequences containing individual substitutions, deletions or additions that alter, add or delete a single amino acid or nucleotide or a small percentage of amino acids or nucleotides in the sequence, where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art.

As used herein, a conservatively modified variant of a polypeptide is biologically active and therefore possesses the desired activity of the reference polypeptide (e.g., conferring increased resistance to a nematode plant pest, reducing the growth of a nematode plant pest, reducing nematode cyst development) as described herein. The variant can result from, for example, a genetic polymorphism or human manipulation. A biologically active variant of the reference polypeptide can have at least about 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more sequence identity or similarity (e.g., about 40% to about 99% or more sequence identity or

similarity and any range therein) to the amino acid sequence for the reference polypeptide as determined by sequence alignment programs and parameters described elsewhere herein. An active variant can differ from the reference polypeptide sequence by as few as 1-15 amino acid residues, as few as 1-10, such as 6-10, as few as 5, as few as 4, 3, 2, or even 1 amino acid residue.

Naturally occurring variants may exist within a population. Such variants can be identified by using well-known molecular biology techniques, such as the polymerase chain reaction (PCR), and hybridization as described below. Synthetically derived nucleotide sequences, for example, sequences generated by site-directed mutagenesis or PCR-mediated mutagenesis which still encode a polypeptide of the invention, are also included as variants. One or more nucleotide or amino acid substitutions, additions, or deletions can be introduced into a nucleotide or amino acid sequence disclosed herein, such that the substitutions, additions, or deletions are introduced into the encoded protein. The additions (insertions) or deletions (truncations) may be made at the N-terminal or C-terminal end of the native protein, or at one or more sites in the native protein. Similarly, a substitution of one or more nucleotides or amino acids may be made at one or more sites in the native protein.

For example, conservative amino acid substitutions may be made at one or more predicted, preferably nonessential amino acid residues. A "nonessential" amino acid residue is a residue that can be altered from the wild-type sequence of a protein without altering the biological activity, whereas an "essential" amino acid is required for biological activity. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue with a similar side chain. Families of amino acid residues having similar side chains are known in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Such substitutions would not be made for conserved amino acid residues, or for amino acid residues residing within a conserved motif, where such residues are essential for protein activity.

For example, amino acid sequence variants of the reference polypeptide can be prepared by mutating the nucleotide sequence encoding the enzyme. The resulting mutants can be expressed recombinantly in plants, and screened for those that retain biological

activity by assaying for activity against nematodes and plants using standard assay techniques as described herein. Methods for mutagenesis and nucleotide sequence alterations are known in the art. *See, e.g.*, Kunkel (1985) *Proc. Natl. Acad. Sci. USA* 82:488-492; Kunkel *et al.* (1987) *Methods in Enzymol.* 154:367-382; and *Techniques in Molecular Biology* (Walker & Gaastra eds., MacMillan Publishing Co. 1983) and the references cited therein; as well as US Patent No. 4,873,192. Clearly, the mutations made in the DNA encoding the variant must not disrupt the reading frame and preferably will not create complimentary regions that could produce secondary mRNA structure. See, EP Patent Application Publication No. 75,444. Guidance as to appropriate amino acid substitutions that do not affect biological activity of the protein of interest may be found in the model of Dayhoff *et al.* (1978) *Atlas of Protein Sequence and Structure* (National Biomedical Research Foundation, Washington, D.C.), herein incorporated by reference.

The deletions, insertions and substitutions in the polypeptides described herein are not expected to produce radical changes in the characteristics of the polypeptide (*e.g.*, the activity of the polypeptide). However, when it is difficult to predict the exact effect of the substitution, deletion or insertion in advance of doing so, one of skill in the art will appreciate that the effect can be evaluated by routine screening assays that can screen for the particular polypeptide activities of interest (e.g., conferring increased resistance to a nematode plant pest, reducing the growth of a nematode plant pest, reducing nematode cyst development).

In some embodiments, the compositions of the invention can comprise active fragments of the polypeptide. As used herein, "fragment" means a portion of the reference polypeptide that retains the polypeptide activity of conferring increased resistance to a nematode plant pest, reducing the growth of a nematode plant pest, reducing cyst development. A fragment also means a portion of a nucleic acid molecule encoding the reference polypeptide. An active fragment of the polypeptide can be prepared, for example, by isolating a portion of a polypeptide-encoding nucleic acid molecule that expresses the encoded fragment of the polypeptide (*e.g.*, by recombinant expression *in vitro*), and assessing the activity of the fragment. Nucleic acid molecules encoding such fragments can be at least about 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 800, 900, 1,000, 1,100, 1,200, 1,300, 1,400, 1,500, 1,600, 1,700, 1,800, 1,900, or 2000 contiguous nucleotides, or up to the number of nucleotides present in a full-length polypeptide-encoding nucleic acid molecule. As such, polypeptide fragments can be at least about 50, 60, 70, 80, 90, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, 525, 550, 525,

550, 600, 625, 650, 675, or 700 contiguous amino acid residues, or up to the total number of amino acid residues present in the full-length polypeptide.

Thus, in some embodiments, a variant or functional fragment of a polypeptide of this invention or a variant or functional fragment having substantial identity to a polypeptide sequence of this invention (e.g., **SEQ ID NOs:29-42, SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046**) when produced in a transgenic plant reduces the ability of nematode pests to survive, grow and reproduce in/on or around the transgenic plant, or reduces nematode-related damage or loss to the transgenic plants producing said polypeptides.

In some embodiments, the nematicidal composition further comprises an agriculturally acceptable carrier. As used herein an "agriculturally-acceptable carrier" can include natural, synthetic, organic and/or inorganic material which is combined with the active component to facilitate its application to the plant, or part thereof. An agriculturally-acceptable carrier includes, but is not limited to, inert components, dispersants, surfactants, adjuvants, tackifiers, stickers, binders, or combinations thereof, that can be used in agricultural formulations. In other embodiments, as agriculturally acceptable carrier can be a transgenic plant or plant part.

In some embodiments, the nematicidal composition can further comprise one or more additional nematicidal and/or insecticidal compounds. Such nematicidal compounds include, without limitation, chloropicrin, metam sodium, metam potassium, dazomet, iodomethane, dimethyl disulfide (DMDS), sulfryl fluoride, oxamyl and fosthiazate.

In other embodiments, the nematicidal composition can further comprise polypeptides having insecticidal activity. Such insecticidal polypeptides include, without limitation, crystal (Cry) endotoxins from *Bacillus thuringiensis* and vegetative insecticidal proteins (VIPs) from *Bacillus* sp.

The polypeptides and compositions thereof of the invention can be applied to the surface of a plant or plant part, including but not limited to, seed, leaves, flowers, stems, tubers, roots, and the like. In some embodiments, the polypeptides and compositions of the invention are delivered orally to a nematode, wherein the nematode ingests one or more parts of a plant to which a composition comprising the polypeptides of the invention has been applied. Applying the compositions of the invention to a plant can be done using any method known to those of skill in the art for applying compounds, compositions, formulations and the like to plant surfaces. Some non-limiting examples of applying include spraying, dusting, sprinkling, scattering, misting, atomizing, broadcasting, soaking, soil injection, soil

incorporation, drenching (e.g., root, soil treatment), dipping, pouring, coating, leaf or stem infiltration, side dressing or seed treatment, and the like, and combinations thereof. These and other procedures for applying a compound(s), composition(s) or formulation(s) to a plant or part thereof are well-known to those of skill in the art. In some embodiments, the polypeptides are delivered orally to a nematode in the form of a transgenic plant comprising one or more nucleotide sequences encoding one or more polypeptides of the invention.

As used herein, the terms "express," "expresses," "expressed" or "expression," and the like, with respect to a nucleic acid molecule and/or a nucleotide sequence (*e.g.*, RNA or DNA) indicates that the nucleic acid molecule and/or a nucleotide sequence is transcribed and, optionally, translated. Thus, a nucleic acid molecule and/or a nucleotide sequence may express a polypeptide of interest or a functional untranslated RNA.

A "heterologous" nucleotide sequence is a nucleotide sequence not naturally associated with a host cell into which it is introduced, including non- naturally occurring multiple copies of a naturally occurring nucleotide sequence.

A "native" or "wild type" nucleic acid, nucleotide sequence, polypeptide or amino acid sequence refers to a naturally occurring or endogenous nucleic acid, nucleotide sequence, polypeptide or amino acid sequence. Thus, for example, a "wild type mRNA" is an mRNA that is naturally occurring in or endogenous to the organism. A "homologous" nucleic acid sequence is a nucleotide sequence naturally associated with a host cell into which it is introduced.

Also as used herein, the terms "nucleic acid," "nucleic acid molecule," "nucleotide sequence" and "polynucleotide" can be used interchangeably and encompass both RNA and DNA, including cDNA, genomic DNA, mRNA, synthetic (*e.g.*, chemically synthesized) DNA or RNA and chimeras of RNA and DNA. The term polynucleotide, nucleotide sequence, or nucleic acid refers to a chain of nucleotides without regard to length of the chain. The nucleic acid can be double-stranded or single-stranded. Where single-stranded, the nucleic acid can be a sense strand or an antisense strand. The nucleic acid can be synthesized using oligonucleotide analogs or derivatives (*e.g.*, inosine or phosphorothioate nucleotides). Such oligonucleotides can be used, for example, to prepare nucleic acids that have altered base-pairing abilities or increased resistance to nucleases. The present invention further provides a nucleic acid that is the complement (which can be either a full complement or a partial complement) of a nucleic acid, nucleotide sequence, or polynucleotide of this invention. Nucleic acid molecules and/or nucleotide sequences provided herein are presented herein in the 5' to 3' direction, from left to right and are represented using the standard code

for representing the nucleotide characters as set forth in the U.S. sequence rules, 37 CFR §§1.821 - 1.825 and the World Intellectual Property Organization (WIPO) Standard ST.25.

The term "antisense nucleotide sequence" or "antisense oligonucleotide" as used herein, refers to a nucleotide sequence that is complementary to a specified DNA or RNA sequence. Antisense oligonucleotides and nucleic acids that express the same can be made in accordance with conventional techniques. *See, e.g.*, U.S. Patent No. 5,023,243 to Tullis; U.S. Patent No. 5,149,797 to Pederson *et al.* The antisense nucleotide sequence can be complementary to the entire nucleotide sequence encoding the polypeptide or a portion thereof of at least 10, 20, 40, 50, 75, 100, 150, 200, 300, or 500 contiguous bases and will reduce the level of polypeptide production.

Those skilled in the art will appreciate that it is not necessary that the antisense nucleotide sequence be fully complementary to the target sequence as long as the degree of sequence similarity is sufficient for the antisense nucleotide sequence to hybridize to its target and reduce production of the polypeptide or transcript. As is known in the art, a higher degree of sequence similarity is generally required for short antisense nucleotide sequences, whereas a greater degree of mismatched bases will be tolerated by longer antisense nucleotide sequences.

For example, hybridization of such nucleotide sequences can be carried out under conditions of reduced stringency, medium stringency or even stringent conditions (*e.g.*, conditions represented by a wash stringency of 35-40% formamide with 5x Denhardt's solution, 0.5% SDS and 1x SSPE at 37°C; conditions represented by a wash stringency of 40-45% formamide with 5x Denhardt's solution, 0.5% SDS, and 1x SSPE at 42°C; and/or conditions represented by a wash stringency of 50% formamide with 5x Denhardt's solution, 0.5% SDS and 1x SSPE at 42°C, respectively) to the nucleotide sequences specifically disclosed herein. *See, e.g.*, Sambrook *et al.*, Molecular Cloning: A Laboratory Manual 2nd Ed. (Cold Spring Harbor, NY, 1989).

In other embodiments, antisense nucleotide sequences of the invention have at least about 70%, 80%, 90%, 95%, 97%, 98% or higher sequence similarity with the complement of the coding sequences specifically disclosed herein and will reduce the level of polypeptide production.

In other embodiments, the antisense nucleotide sequence can be directed against any coding sequence, the silencing of which results in a modulation of a polypeptide of this invention (e.g., **SEQ ID NOs:29-42, 135-209, 243-260**, and/or **665-1046**).

The length of the antisense nucleotide sequence (*i.e.*, the number of nucleotides therein) is not critical as long as it binds selectively to the intended location and reduces transcription and/or translation of the target sequence, and can be determined in accordance with routine procedures. In general, the antisense nucleotide sequence will be from about eight, ten or twelve nucleotides in length to about 20, 30, 50, 75, 100, 200, 300, 400 nucleotides, or longer, in length.

An antisense nucleotide sequence can be constructed using chemical synthesis and enzymatic ligation reactions by procedures known in the art. For example, an antisense nucleotide sequence can be chemically synthesized using naturally occurring nucleotides or various modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleotide sequences, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which can be used to generate the antisense nucleotide sequence include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomet- hyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopenten- yladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleotide sequence can be produced using an expression vector into which a nucleic acid has been cloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest).

The antisense nucleotide sequences of the invention further include nucleotide sequences wherein at least one, or all, of the internucleotide bridging phosphate residues are modified phosphates, such as methyl phosphonates, methyl phosphonothioates, phosphoromorpholidates, phosphoropiperazidates and phosphoramidates. For example, every other one of the internucleotide bridging phosphate residues can be modified as described. In another non-limiting example, the antisense nucleotide sequence is a nucleotide

sequence in which one, or all, of the nucleotides contain a 2' lower alkyl moiety (*e.g.*, C_1-C_4, linear or branched, saturated or unsaturated alkyl, such as methyl, ethyl, ethenyl, propyl, 1-propenyl, 2-propenyl, and isopropyl). For example, every other one of the nucleotides can be modified as described. *See also*, Furdon *et al.*, *Nucleic Acids Res. 17*:9193 (1989); Agrawal *et al.*, *Proc. Natl. Acad. Sci. USA 87*:1401 (1990); Baker *et al.*, *Nucleic Acids Res.* 18:3537 (1990); Sproat *et al.*, *Nucleic Acids Res. 17*:3373 (1989); Walder and Walder, *Proc. Natl. Acad. Sci. USA 85*:5011 (1988); incorporated by reference herein for their teaching of methods of making antisense molecules, including those containing modified nucleotide bases).

Triple helix base-pairing methods can also be employed to inhibit production of polypeptides of this invention (e.g., SEQ ID NOs:29-42, 135-209, 243-260, and/or 665-1046).. Triple helix pairing is believed to work by inhibiting the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors, or regulatory molecules. Recent therapeutic advances using triplex DNA have been described in the literature (*e.g.*, Gee *et al.*, (1994) In: Huber *et al.*, Molecular and Immunologic Approaches, Futura Publishing Co., Mt. Kisco, NY).

Different nucleic acids or proteins having homology are referred to herein as "homologues." The term homologue includes homologous sequences from the same and other species and orthologous sequences from the same and other species. "Homology" refers to the level of similarity between two or more nucleic acid and/or amino acid sequences in terms of percent of positional identity (*i.e.*, sequence similarity or identity). Homology also refers to the concept of similar functional properties among different nucleic acids or proteins. Thus, the compositions and methods of the invention further comprise homologues to the nucleotide sequences and polypeptide sequences of this invention. "Orthologous," as used herein, refers to homologous nucleotide sequences and/ or amino acid sequences in different species that arose from a common ancestral gene during speciation. A homologue of this invention has a significant sequence identity (e.g., 70%, 75%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, and/or 100%) to the nucleotide sequences of the invention.

A homologue as described herein can be utilized with any composition or method of the invention, alone or in combination with one another and/or with one or more nucleotide sequences or polypeptide sequences of the invention. Thus, in one embodiment, the invention provides a nucleic acid molecule comprising, consisting essentially of, or consisting of one or more nucleotide sequences of the invention and/or one or more

homologues of any nucleotide sequence of the invention. In a further embodiment, the invention provides polypeptide compositions comprising, consisting essentially of, or consisting of one or more of the polypeptides of this invention and/or a homologue thereof.

As used herein "sequence identity" refers to the extent to which two optimally aligned polynucleotide or peptide sequences are invariant throughout a window of alignment of components, *e.g.*, nucleotides or amino acids. "Identity" can be readily calculated by known methods including, but not limited to, those described in: *Computational Molecular Biology* (Lesk, A. M., ed.) Oxford University Press, New York (1988); *Biocomputing: Informatics and Genome Projects* (Smith, D. W., ed.) Academic Press, New York (1993); *Computer Analysis of Sequence Data, Part I* (Griffin, A. M., and Griffin, H. G., eds.) Humana Press, New Jersey (1994); *Sequence Analysis in Molecular Biology* (von Heinje, G., ed.) Academic Press (1987); and *Sequence Analysis Primer* (Gribskov, M. and Devereux, J., eds.) Stockton Press, New York (1991).

As used herein, the term "percent sequence identity" or "percent identity" refers to the percentage of identical nucleotides in a linear polynucleotide sequence of a reference ("query") polynucleotide molecule (or its complementary strand) as compared to a test ("subject") polynucleotide molecule (or its complementary strand) when the two sequences are optimally aligned. In some embodiments, "percent identity" can refer to the percentage of identical amino acids in an amino acid sequence.

As used herein, the phrase "substantially identical," in the context of two nucleic acid molecules, nucleotide sequences or protein sequences, refers to two or more sequences or subsequences that have at least about 70%, at least about 75%, at least about 80%, at least about 81%, at least about 82%, at least about 83%, at least about 84%, at least about 85%, at least about 86%, at least about 87%, at least about 88%, at least about 89%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% nucleotide or amino acid residue identity, when compared and aligned for maximum correspondence, as measured using one of the following sequence comparison algorithms or by visual inspection. In some embodiments of the invention, the substantial identity exists over a region of the sequences that is at least about 50 residues to about 150 residues in length. Thus, in some embodiments of the invention, the substantial identity exists over a region of the sequences that is at least about 50, about 60, about 70, about 80, about 90, about 100, about 110, about 120, about 130, about 140, about 150, or more residues in length. In some particular embodiments, the sequences are substantially identical over at least about 150 residues. In a further embodiment, the sequences are substantially identical

over the entire length of the coding regions. Furthermore, in representative embodiments, substantially identical nucleotide or protein sequences perform substantially the same function (e.g., conferring increased resistance to a nematode plant pest, reducing the growth of a nematode plant pest, reducing nematode cyst development).

For sequence comparison, typically one sequence acts as a reference sequence to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated if necessary, and sequence algorithm program parameters are designated. The sequence comparison algorithm then calculates the percent sequence identity for the test sequence(s) relative to the reference sequence, based on the designated program parameters.

Optimal alignment of sequences for aligning a comparison window are well known to those skilled in the art and may be conducted by tools such as the local homology algorithm of Smith and Waterman, the homology alignment algorithm of Needleman and Wunsch, the search for similarity method of Pearson and Lipman, and optionally by computerized implementations of these algorithms such as GAP, BESTFIT, FASTA, and TFASTA available as part of the GCG® Wisconsin Package® (Accelrys Inc., San Diego, CA). An "identity fraction" for aligned segments of a test sequence and a reference sequence is the number of identical components which are shared by the two aligned sequences divided by the total number of components in the reference sequence segment, *i.e.*, the entire reference sequence or a smaller defined part of the reference sequence. Percent sequence identity is represented as the identity fraction multiplied by 100. The comparison of one or more polynucleotide sequences may be to a full-length polynucleotide sequence or a portion thereof, or to a longer polynucleotide sequence. For purposes of this invention "percent identity" may also be determined using BLASTX version 2.0 for translated nucleotide sequences and BLASTN version 2.0 for polynucleotide sequences.

Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, 1990). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters

M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when the cumulative alignment score falls off by the quantity X from its maximum achieved value, the cumulative score goes to zero or below due to the accumulation of one or more negative-scoring residue alignments, or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix *(see* Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89: 10915 (1989)).

In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences *(see, e.g.,* Karlin & Altschul, *Proc. Nat'l. Acad. Sci. USA* 90: 5873-5787 (1993)). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a test nucleic acid sequence is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleotide sequence to the reference nucleotide sequence is less than about 0.1 to less than about 0.001. Thus, in some embodiments of the invention, the smallest sum probability in a comparison of the test nucleotide sequence to the reference nucleotide sequence is less than about 0.001.

Two nucleotide sequences can also be considered to be substantially identical when the two sequences hybridize to each other under stringent conditions. In some representative embodiments, two nucleotide sequences considered to be substantially identical hybridize to each other under highly stringent conditions.

"Stringent hybridization conditions" and "stringent hybridization wash conditions" in the context of nucleic acid hybridization experiments such as Southern and Northern hybridizations are sequence dependent, and are different under different environmental parameters. An extensive guide to the hybridization of nucleic acids is found in Tijssen *Laboratory Techniques in Biochemistry and Molecular Biology-Hybridization with Nucleic Acid Probes* part I chapter 2 "Overview of principles of hybridization and the strategy of nucleic acid probe assays" Elsevier, New York (1993). Generally, highly stringent

hybridization and wash conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH.

The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Very stringent conditions are selected to be equal to the T_m for a particular probe. An example of stringent hybridization conditions for hybridization of complementary nucleotide sequences which have more than 100 complementary residues on a filter in a Southern or northern blot is 50% formamide with 1 mg of heparin at 42°C, with the hybridization being carried out overnight. An example of highly stringent wash conditions is 0.1 5M NaCl at 72°C for about 15 minutes. An example of stringent wash conditions is a 0.2x SSC wash at 65°C for 15 minutes (*see,* Sambrook, *infra*, for a description of SSC buffer). Often, a high stringency wash is preceded by a low stringency wash to remove background probe signal. An example of a medium stringency wash for a duplex of, e.g., more than 100 nucleotides, is 1x SSC at 45°C for 15 minutes. An example of a low stringency wash for a duplex of, *e.g.,* more than 100 nucleotides, is 4-6x SSC at 40°C for 15 minutes. For short probes (*e.g.,* about 10 to 50 nucleotides), stringent conditions typically involve salt concentrations of less than about 1.0 M Na ion, typically about 0.01 to 1.0 M Na ion concentration (or other salts) at pH 7.0 to 8.3, and the temperature is typically at least about 30°C. Stringent conditions can also be achieved with the addition of destabilizing agents such as formamide. In general, a signal to noise ratio of 2x (or higher) than that observed for an unrelated probe in the particular hybridization assay indicates detection of a specific hybridization. Nucleotide sequences that do not hybridize to each other under stringent conditions are still substantially identical if the proteins that they encode are substantially identical. This can occur, for example, when a copy of a nucleotide sequence is created using the maximum codon degeneracy permitted by the genetic code.

The following are examples of sets of hybridization/wash conditions that may be used to clone homologous nucleotide sequences that are substantially identical to reference nucleotide sequences of the invention. In one embodiment, a reference nucleotide sequence hybridizes to the "test" nucleotide sequence in 7% sodium dodecyl sulfate (SDS), 0.5 M $NaPO_4$, 1 mM EDTA at 50°C with washing in 2X SSC, 0.1% SDS at 50°C. In another embodiment, the reference nucleotide sequence hybridizes to the "test" nucleotide sequence in 7% sodium dodecyl sulfate (SDS), 0.5 M $NaPO_4$, 1 mM EDTA at 50°C with washing in 1X SSC, 0.1% SDS at 50°C or in 7% sodium dodecyl sulfate (SDS), 0.5 M $NaPO_4$, 1 mM EDTA at 50°C with washing in 0.5X SSC, 0.1% SDS at 50°C. In still further embodiments, the reference nucleotide sequence hybridizes to the "test" nucleotide sequence in 7% sodium

dodecyl sulfate (SDS), 0.5 M $NaPO_4$, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 50°C, or in 7% sodium dodecyl sulfate (SDS), 0.5 M $NaPO_4$, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 65°C.

In particular embodiments, a further indication that two nucleotide sequences or two polypeptide sequences are substantially identical can be that the protein encoded by the first nucleic acid is immunologically cross reactive with, or specifically binds to, the protein encoded by the second nucleic acid. Thus, in some embodiments, a polypeptide can be substantially identical to a second polypeptide, for example, where the two polypeptides differ only by conservative substitutions.

In some embodiments, the recombinant nucleic acids molecules, nucleotide sequences and polypeptides of the invention are "isolated." An "isolated" nucleic acid molecule, an "isolated" nucleotide sequence or an "isolated" polypeptide is a nucleic acid molecule, nucleotide sequence or polypeptide that, by the hand of man, exists apart from its native environment and is therefore not a product of nature. An isolated nucleic acid molecule, nucleotide sequence or polypeptide may exist in a purified form that is at least partially separated from at least some of the other components of the naturally occurring organism or virus, for example, the cell or viral structural components or other polypeptides or nucleic acids commonly found associated with the polynucleotide. In representative embodiments, the isolated nucleic acid molecule, the isolated nucleotide sequence and/or the isolated polypeptide is at least about 1%, 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, or more pure.

In other embodiments, an isolated nucleic acid molecule, nucleotide sequence or polypeptide may exist in a non-native environment such as, for example, a recombinant host cell. Thus, for example, with respect to nucleotide sequences, the term "isolated" means that it is separated from the chromosome and/or cell in which it naturally occurs. A polynucleotide is also isolated if it is separated from the chromosome and/or cell in which it naturally occurs in and is then inserted into a genetic context, a chromosome and/or a cell in which it does not naturally occur (e.g., a different host cell, different regulatory sequences, and/or different position in the genome than as found in nature). Accordingly, the recombinant nucleic acid molecules, nucleotide sequences and their encoded polypeptides are "isolated" in that, by the hand of man, they exist apart from their native environment and therefore are not products of nature, however, in some embodiments, they can be introduced into and exist in a recombinant host cell.

In some embodiments, the nucleotide sequences and/or nucleic acid molecules of the invention can be operatively associated with a variety of promoters for expression in host cells (e.g., plant cells). Thus, in some embodiments, the invention provides transformed host cells and transformed organisms comprising the transformed host cells, wherein the host cells and organisms are transformed with one or more nucleic acid molecules/nucleotide sequences of the invention. As used herein, "operatively associated with," when referring to a first nucleic acid sequence that is operatively linked to a second nucleic acid sequence, means a situation when the first nucleic acid sequence is placed in a functional relationship with the second nucleic acid sequence. For instance, a promoter is operatively associated with a coding sequence if the promoter effects the transcription or expression of the coding sequence.

A DNA "promoter" is an untranslated DNA sequence upstream of a coding region that contains the binding site for RNA polymerase and initiates transcription of the DNA. A "promoter region" can also include other elements that act as regulators of gene expression. Promoters can include, for example, constitutive, inducible, temporally regulated, developmentally regulated, chemically regulated, tissue-preferred and tissue-specific promoters for use in the preparation of recombinant nucleic acid molecules, i.e., chimeric genes. In particular aspects, a "promoter" useful with the invention is a promoter capable of initiating transcription of a nucleotide sequence in a cell of a plant.

A "chimeric gene" is a recombinant nucleic acid molecule in which a promoter or other regulatory nucleotide sequence is operatively associated with a nucleotide sequence that codes for an mRNA or which is expressed as a protein, such that the regulatory nucleotide sequence is able to regulate transcription or expression of the associated nucleotide sequence. The regulatory nucleotide sequence of the chimeric gene is not normally operatively linked to the associated nucleotide sequence as found in nature.

The choice of promoter will vary depending on the temporal and spatial requirements for expression, and also depending on the host cell to be transformed. Thus, for example, expression of the nucleotide sequences of the invention can be in any plant and/or plant part, (e.g., in leaves, in stalks or stems, in ears, in inflorescences (e.g. spikes, panicles, cobs, etc.), in roots, seeds and/or seedlings, and the like). In many cases, however, protection against more than one type of pest is sought, and thus expression in multiple tissues is desirable. Although many promoters from dicotyledons have been shown to be operational in monocotyledons and vice versa, ideally dicotyledonous promoters are selected for expression in dicotyledons, and monocotyledonous promoters for expression in monocotyledons.

However, there is no restriction to the provenance of selected promoters; it is sufficient that they are operational in driving the expression of the nucleotide sequences in the desired cell.

Promoters useful with the invention include, but are not limited to, those that drive expression of a nucleotide sequence constitutively, those that drive expression when induced, and those that drive expression in a tissue- or developmentally-specific manner. These various types of promoters are known in the art.

Examples of constitutive promoters include, but are not limited to, cestrum virus promoter (cmp) (U.S. Patent No. 7,166,770), the rice actin 1 promoter (Wang *et al.* (1992) *Mol. Cell. Biol.* 12:3399-3406; as well as US Patent No. 5,641,876), CaMV 35S promoter (Odell *et al.* (1985) *Nature* 313:810-812), CaMV 19S promoter (Lawton *et al.* (1987) *Plant Mol. Biol.* 9:315-324), nos promoter (Ebert *et al.* (1987) *Proc. Natl. Acad. Sci USA* 84:5745-5749), Adh promoter (Walker *et al.* (1987) *Proc. Natl. Acad. Sci. USA* 84:6624-6629), sucrose synthase promoter (Yang & Russell (1990) *Proc. Natl. Acad. Sci. USA* 87:4144-4148), and the ubiquitin promoter. The constitutive promoter derived from ubiquitin accumulates in many cell types. Ubiquitin promoters have been cloned from several plant species for use in transgenic plants, for example, sunflower (Binet *et al.*, 1991. *Plant Science* 79: 87-94), maize (Christensen *et al.*, 1989. *Plant Molec. Biol.* 12: 619-632), and arabidopsis (Norris et al. 1993. *Plant Molec. Biol.* 21:895-906). The maize ubiquitin promoter (*UbiP*) has been developed in transgenic monocot systems and its sequence and vectors constructed for monocot transformation are disclosed in the patent publication EP 0 342 926. The ubiquitin promoter is suitable for the expression of the nucleotide sequences of the invention in transgenic plants, especially monocotyledons. Further, the promoter expression cassettes described by McElroy *et al.* (*Mol. Gen. Genet.* 231: 150-160 (1991)) can be easily modified for the expression of the nucleotide sequences of the invention and are particularly suitable for use in monocotyledonous hosts.

In some embodiments, tissue specific/tissue preferred promoters can be used. Tissue specific or preferred expression patterns include, but are not limited to, green tissue specific or preferred, root specific or preferred, stem specific or preferred, and flower specific or preferred. Promoters suitable for expression in green tissue include many that regulate genes involved in photosynthesis and many of these have been cloned from both monocotyledons and dicotyledons. In one embodiment, a promoter useful with the invention is the maize PEPC promoter from the phosphoenol carboxylase gene (Hudspeth & Grula, *Plant Molec. Biol.* 12:579-589 (1989)). Non-limiting examples of tissue-specific promoters include those associated with genes encoding the seed storage proteins (such as β-conglycinin, cruciferin,

napin and phaseolin), zein or oil body proteins (such as oleosin), or proteins involved in fatty acid biosynthesis (including acyl carrier protein, stearoyl-ACP desaturase and fatty acid desaturases (fad 2-1)), and other nucleic acids expressed during embryo development (such as Bce4, *see, e.g.*, Kridl *et al.* (1991) *Seed Sci. Res.* 1:209-219; as well as EP Patent No. 255378). Tissue-specific or tissue-preferential promoters useful for the expression of the nucleotide sequences of the invention in plants, particularly maize, include but are not limited to those that direct expression in root, pith, leaf or pollen. Such promoters are disclosed, for example, in WO 93/07278, herein incorporated by reference in its entirety. Other non-limiting examples of tissue specific or tissue preferred promoters useful with the invention the cotton rubisco promoter disclosed in US Patent 6,040,504; the rice sucrose synthase promoter disclosed in US Patent 5,604,121; the root specific promoter described by de Framond (FEBS 290:103-106 (1991); EP 0 452 269 to Ciba- Geigy); the stem specific promoter described in U.S. Patent 5,625,136 (to Ciba-Geigy) and which drives expression of the maize trpA gene; and the cestrum yellow leaf curling virus promoter disclosed in WO 01/73087, all incorporated by reference

Additional examples of tissue-specific/tissue preferred promoters include, but are not limited to, the root-specific promoters *RCc3* (Jeong et al. *Plant Physiol.* 153:185-197 (2010)) and RB7 (U.S. Patent No. 5459252), the lectin promoter (Lindstrom *et al.* (1990) *Der. Genet.* 11:160-167; and Vodkin (1983) *Prog. Clin. Biol. Res.* 138:87-98), corn alcohol dehydrogenase 1 promoter (Dennis *et al.* (1984) *Nucleic Acids Res.* 12:3983-4000), S-adenosyl-L-methionine synthetase (SAMS) (Vander Mijnsbrugge et al. (1996) *Plant and Cell Physiology*, 37(8):1108-1115), corn light harvesting complex promoter (Bansal *et al.* (1992) *Proc. Natl. Acad. Sci. USA* 89:3654-3658), corn heat shock protein promoter (O'Dell *et al.* (1985) *EMBO J.* 5:451-458; and Rochester *et al.* (1986) *EMBO J.* 5:451-458), pea small subunit RuBP carboxylase promoter (Cashmore, "Nuclear genes encoding the small subunit of ribulose-l,5-bisphosphate carboxylase" pp. 29-39 In: *Genetic Engineering of Plants* (Hollaender ed., Plenum Press 1983; and Poulsen *et al.* (1986) *Mol. Gen. Genet.* 205:193-200), Ti plasmid mannopine synthase promoter (Langridge *et al.* (1989) *Proc. Natl. Acad. Sci. USA* 86:3219-3223), Ti plasmid nopaline synthase promoter (Langridge *et al.* (1989), *supra*), petunia chalcone isomerase promoter (van Tunen *et al.* (1988) *EMBO J.* 7:1257-1263), bean glycine rich protein 1 promoter (Keller *et al.* (1989) *Genes Dev.* 3:1639-1646), truncated CaMV 35S promoter (O'Dell *et al.* (1985) *Nature* 313:810-812), potato patatin promoter (Wenzler *et al.* (1989) *Plant Mol. Biol.* 13:347-354), root cell promoter (Yamamoto *et al.* (1990) *Nucleic Acids Res.* 18:7449), maize zein promoter (Kriz *et al.* (1987) *Mol. Gen.*

Genet. 207:90-98; Langridge *et al.* (1983) *Cell* 34:1015-1022; Reina *et al.* (1990) *Nucleic Acids Res.* 18:6425; Reina *et al.* (1990) *Nucleic Acids Res.* 18:7449; and Wandelt *et al.* (1989) *Nucleic Acids Res.* 17:2354), globulin-1 promoter (Belanger *et al.* (1991) *Genetics* 129:863-872), α-tubulin cab promoter (Sullivan *et al.* (1989) *Mol. Gen. Genet.* 215:431-440), PEPCase promoter (Hudspeth & Grula (1989) *Plant Mol. Biol.* 12:579-589), R gene complex-associated promoters (Chandler *et al.* (1989) *Plant Cell* 1:1175-1183), and chalcone synthase promoters (Franken *et al.* (1991) *EMBO J.* 10:2605-2612). In some particular embodiments, the nucleotide sequences of the invention are operatively associated with a root-preferred promoter.

Particularly useful for seed-specific expression is the pea vicilin promoter (Czako *et al.* (1992) *Mol. Gen. Genet.* 235:33-40; as well as the seed-specific promoters disclosed in U.S. Patent No. 5,625,136. Useful promoters for expression in mature leaves are those that are switched on at the onset of senescence, such as the SAG promoter from *Arabidopsis* (Gan *et al.* (1995) *Science* 270:1986-1988).

In addition, promoters functional in plastids can be used. Non-limiting examples of such promoters include the bacteriophage T3 gene 9 5' UTR and other promoters disclosed in U.S. Patent No. 7,579,516. Other promoters useful with the invention include but are not limited to the S-E9 small subunit RuBP carboxylase promoter and the Kunitz trypsin inhibitor gene promoter (Kti3).

In some embodiments of the invention, inducible promoters can be used. Thus, for example, chemical-regulated promoters can be used to modulate the expression of a gene in a plant through the application of an exogenous chemical regulator. Regulation of the expression of nucleotide sequences of the invention via promoters that are chemically regulated enables the polypeptides of the invention to be synthesized only when the crop plants are treated with the inducing chemicals. Depending upon the objective, the promoter may be a chemical-inducible promoter, where application of a chemical induces gene expression, or a chemical-repressible promoter, where application of the chemical represses gene expression.

Chemical inducible promoters are known in the art and include, but are not limited to, the maize *In2*-2 promoter, which is activated by benzenesulfonamide herbicide safeners, the maize GST promoter, which is activated by hydrophobic electrophilic compounds that are used as pre-emergent herbicides, and the tobacco *PR-1* a promoter, which is activated by salicylic acid (*e.g.*, the PR1a system), steroid steroid-responsive promoters (*see, e.g.*, the glucocorticoid-inducible promoter in Schena et al. (1991) *Proc. Natl. Acad. Sci. USA* 88,

10421-10425 and McNellis et al. (1998) *Plant J.* 14, 247-257) and tetracycline-inducible and tetracycline-repressible promoters (*see, e.g.*, Gatz et al. (1991) *Mol. Gen. Genet.* 227, 229-237, and U.S. Patent Numbers 5,814,618 and 5,789,156, Lac repressor system promoters, copper-inducible system promoters, salicylate-inducible system promoters (*e.g.*, the PR1a system), glucocorticoid-inducible promoters (Aoyama *et al.* (1997) *Plant J.* 11:605-612), and ecdysone-inducible system promoters.

Other non-limiting examples of inducible promoters include ABA- and turgor-inducible promoters, the auxin-binding protein gene promoter (Schwob *et al.* (1993) *Plant J.* 4:423-432), the UDP glucose flavonoid glycosyl-transferase promoter (Ralston *et al.* (1988) *Genetics* 119:185-197), the MPI proteinase inhibitor promoter (Cordero *et al.* (1994) *Plant J.* 6:141-150), and the glyceraldehyde-3-phosphate dehydrogenase promoter (Kohler *et al.* (1995) *Plant Mol. Biol.* 29:1293-1298; Martinez *et al.* (1989) *J. Mol. Biol.* 208:551-565; and Quigley *et al.* (1989) *J. Mol. Evol.* 29:412-421). Also included are the benzene sulphonamide-inducible (US Patent No. 5,364,780) and alcohol-inducible (Int'l Patent Application Publication Nos. WO 97/06269 and WO 97/06268) systems and glutathione S-transferase promoters. Likewise, one can use any of the inducible promoters described in Gatz (1996) *Current Opinion Biotechnol.* 7:168-172 and Gatz (1997) *Annu. Rev. Plant Physiol. Plant Mol. Biol.* 48:89-108. Other chemically inducible promoters useful for directing the expression of the nucleotide sequences of this invention in plants are disclosed in US Patent 5,614,395 herein incorporated by reference in its entirety. Chemical induction of gene expression is also detailed in the published application EP 0 332 104 (to Ciba- Geigy) and U.S. Patent 5,614,395. In some embodiments, a promoter for chemical induction can be the tobacco PR-1a promoter.

In further aspects, the nucleotide sequences of the invention can be operatively associated with a promoter that is wound inducible or inducible by pest or pathogen infection (e.g., a nematode plant pest). Numerous promoters have been described which are expressed at wound sites and/or at the sites of pest attack (e.g., insect/nematode feeding) or phytopathogen infection. Ideally, such a promoter should be active only locally at or adjacent to the sites of attack, and in this way expression of the nucleotide sequences of the invention will be focused in the cells that are being invaded. Such promoters include, but are not limited to, those described by Stanford et al., *Mol. Gen. Genet.* 215:200-208 (1989), Xu *et al. Plant Molec. Biol.* 22:573-588 (1993), Logemann *et al. Plant Cell* 1:151-158 (1989), Rohrmeier and Lehle, *Plant Molec. Biol.* 22:783-792 (1993), Firek *et al. Plant Molec. Biol.* 22:129-142 (1993), Warner *et al. Plant J.* 3:191-201 (1993), U.S. Patent No. 5,750,386, U.S.

Patent No. 5,955, 646, U.S. Patent No. 6,262,344, U.S. Patent No. 6,395,963, U.S. Patent No. 6,703,541, U.S. Patent No. 7,078,589, U.S. Patent No. 7,196,247, U.S. Patent No. 7,223,901, and U.S. Patent Application Publication 2010043102.

As used herein, "expression cassette" means a nucleic acid molecule comprising a nucleotide sequence of interest (e.g., the nucleotide sequences of the invention), wherein said nucleotide sequence is operatively associated with at least a control sequence (e.g., a promoter). Thus, some embodiments of the invention provide expression cassettes designed to express the nucleotides sequences of the invention. In this manner, for example, one or more plant promoters operatively associated with one or more nucleotide sequences of the invention (e.g., **SEQ ID NOs:1-28, SEQ ID NOs:43-134, SEQ ID NOs:210-242, SEQ ID NOs:261-644**) are provided in expression cassettes for expression in an organism or cell thereof (e.g., a plant, plant part and/or plant cell).

An expression cassette comprising a nucleotide sequence of interest may be chimeric, meaning that at least one of its components is heterologous with respect to at least one of its other components. An expression cassette may also be one that is naturally occurring but has been obtained in a recombinant form useful for heterologous expression. Typically, however, the expression cassette is heterologous with respect to the host, i.e., the particular nucleic acid sequence of the expression cassette does not occur naturally in the host cell and must have been introduced into the host cell or an ancestor of the host cell by a transformation event.

In addition to the promoters operatively linked to the nucleotide sequences of the invention, an expression cassette of the invention can also include other regulatory sequences. As used herein, "regulatory sequences" means nucleotide sequences located upstream (5' non-coding sequences), within or downstream (3' non-coding sequences) of a coding sequence, and which influence the transcription, RNA processing or stability, or translation of the associated coding sequence. Regulatory sequences include, but are not limited to, promoters, enhancers, introns, translation leader sequences, termination signals, and polyadenylation signal sequences.

For purposes of the invention, the regulatory sequences or regions can be native/analogous to the plant, plant part and/or plant cell and/or the regulatory sequences can be native/analogous to the other regulatory sequences. Alternatively, the regulatory sequences may be heterologous to the plant (and/or plant part and/or plant cell) and/or to each other (i.e., the regulatory sequences). Thus, for example, a promoter can be heterologous when it is operatively linked to a polynucleotide from a species different from the species from which the polynucleotide was derived. Alternatively, a promoter can also be

heterologous to a selected nucleotide sequence if the promoter is from the same/analogous species from which the polynucleotide is derived, but one or both (i.e., promoter and/or polynucleotide) are substantially modified from their original form and/or genomic locus, and/or the promoter is not the native promoter for the operably linked polynucleotide.

A number of non-translated leader sequences derived from viruses are known to enhance gene expression. Specifically, leader sequences from Tobacco Mosaic Virus (TMV, the "ω-sequence"), Maize Chlorotic Mottle Virus (MCMV) and Alfalfa Mosaic Virus (AMV) have been shown to be effective in enhancing expression (Gallie *et al.* (1987) *Nucleic Acids Res.* 15:8693-8711; and Skuzeski *et al.* (1990) *Plant Mol. Biol.* 15:65-79). Other leader sequences known in the art include, but are not limited to, picornavirus leaders such as an encephalomyocarditis (EMCV) 5' noncoding region leader (Elroy-Stein *et al.* (1989) *Proc. Natl. Acad. Sci. USA* 86:6126-6130); potyvirus leaders such as a Tobacco Etch Virus (TEV) leader (Allison *et al.* (1986) *Virology* 154:9-20); Maize Dwarf Mosaic Virus (MDMV) leader (Allison *et al.* (1986), *supra*); human immunoglobulin heavy-chain binding protein (BiP) leader (Macejak & Samow (1991) *Nature* 353:90-94); untranslated leader from the coat protein mRNA of AMV (AMV RNA 4; Jobling & Gehrke (1987) *Nature* 325:622-625); tobacco mosaic TMV leader (Gallie *et al.* (1989) *Molecular Biology of RNA* 237-256); and MCMV leader (Lommel *et al.* (1991) *Virology* 81:382-385). *See also*, Della-Cioppa *et al.* (1987) *Plant Physiol.* 84:965-968.

An expression cassette also can optionally include a transcriptional and/or translational termination region (*i.e.*, termination region) that is functional in plants. A variety of transcriptional terminators are available for use in expression cassettes and are responsible for the termination of transcription beyond the heterologous nucleotide sequence of interest and correct mRNA polyadenylation. The termination region may be native to the transcriptional initiation region, may be native to the operably linked nucleotide sequence of interest, may be native to the plant host, or may be derived from another source (*i.e.*, foreign or heterologous to the promoter, the nucleotide sequence of interest, the plant host, or any combination thereof). Appropriate transcriptional terminators include, but are not limited to, the CAMV 35S terminator, the tml terminator, the nopaline synthase terminator and/or the pea rbcs E9 terminator. These can be used in both monocotyledons and dicotyledons. In addition, a coding sequence's native transcription terminator can be used.

An expression cassette of the invention also can include a nucleotide sequence for a selectable marker, which can be used to select a transformed plant, plant part and/or plant cell. As used herein, "selectable marker" means a nucleotide sequence that when expressed

imparts a distinct phenotype to the plant, plant part and/or plant cell expressing the marker and thus allows such transformed plants, plant parts and/or plant cells to be distinguished from those that do not have the marker. Such a nucleotide sequence may encode either a selectable or screenable marker, depending on whether the marker confers a trait that can be selected for by chemical means, such as by using a selective agent (*e.g.*, an antibiotic, herbicide, or the like), or on whether the marker is simply a trait that one can identify through observation or testing, such as by screening (*e.g.*, the R-locus trait). Of course, many examples of suitable selectable markers are known in the art and can be used in the expression cassettes described herein.

Examples of selectable markers include, but are not limited to, a nucleotide sequence encoding *neo* or *nptII*, which confers resistance to kanamycin, G418, and the like (Potrykus *et al.* (1985) *Mol. Gen. Genet.* 199:183-188); a nucleotide sequence encoding *bar,* which confers resistance to phosphinothricin; a nucleotide sequence encoding an altered 5-enolpyruvylshikimate-3-phosphate (EPSP) synthase, which confers resistance to glyphosate (Hinchee *et al.* (1988) *Biotech.* 6:915-922); a nucleotide sequence encoding a nitrilase such as *bxn* from *Klebsiella ozaenae* that confers resistance to bromoxynil (Stalker *et al.* (1988) *Science* 242:419-423); a nucleotide sequence encoding an altered acetolactate synthase (ALS) that confers resistance to imidazolinone, sulfonylurea or other ALS-inhibiting chemicals (EP Patent Application No. 154204); a nucleotide sequence encoding a methotrexate-resistant dihydrofolate reductase (DHFR) (Thillet *et al.* (1988) *J. Biol. Chem.* 263:12500-12508); a nucleotide sequence encoding a dalapon dehalogenase that confers resistance to dalapon; a nucleotide sequence encoding a mannose-6-phosphate isomerase (also referred to as phosphomannose isomerase (PMI)) that confers an ability to metabolize mannose (US Patent Nos. 5,767,378 and 5,994,629); a nucleotide sequence encoding an altered anthranilate synthase that confers resistance to 5-methyl tryptophan; and/or a nucleotide sequence encoding *hph* that confers resistance to hygromycin. One of skill in the art is capable of choosing a suitable selectable marker for use in an expression cassette of the invention.

Additional selectable markers include, but are not limited to, a nucleotide sequence encoding β-glucuronidase or *uidA* (GUS) that encodes an enzyme for which various chromogenic substrates are known; an R-locus nucleotide sequence that encodes a product that regulates the production of anthocyanin pigments (red color) in plant tissues (Dellaporta *et al.*, "Molecular cloning of the maize R-nj allele by transposon-tagging with Ac," pp. 263-282 In: *Chromosome Structure and Function: Impact of New Concepts*, 18th Stadler Genetics Symposium (Gustafson & Appels eds., Plenum Press 1988)); a nucleotide sequence

encoding β-lactamase, an enzyme for which various chromogenic substrates are known (*e.g.*, PADAC, a chromogenic cephalosporin) (Sutcliffe (1978) *Proc. Natl. Acad. Sci. USA* 75:3737-3741); a nucleotide sequence encoding *xylE* that encodes a catechol dioxygenase (Zukowsky *et al.* (1983) *Proc. Natl. Acad. Sci. USA* 80:1101-1105); a nucleotide sequence encoding tyrosinase, an enzyme capable of oxidizing tyrosine to DOPA and dopaquinone, which in turn condenses to form melanin (Katz *et al.* (1983) *J. Gen. Microbiol.* 129:2703-2714); a nucleotide sequence encoding β-galactosidase, an enzyme for which there are chromogenic substrates; a nucleotide sequence encoding luciferase (lux) that allows for bioluminescence detection (Ow *et al.* (1986) *Science* 234:856-859); a nucleotide sequence encoding aequorin, which may be employed in calcium-sensitive bioluminescence detection (Prasher *et al.* (1985) *Biochem. Biophys. Res. Comm.* 126:1259-1268); or a nucleotide sequence encoding green fluorescent protein (Niedz *et al.* (1995) *Plant Cell Reports* 14:403-406). One of skill in the art is capable of choosing a suitable selectable marker for use in an expression cassette of the invention.

An expression cassette of the invention also can include nucleotide sequences that encode other desired traits. Such desired traits can be other nucleotide sequences which confer nematode resistance, insect resistance, or which confer other agriculturally desirable traits. Such nucleotide sequences can be stacked with any combination of nucleotide sequences to create plants, plant parts or plant cells having the desired phenotype. Stacked combinations can be created by any method including, but not limited to, cross breeding plants by any conventional methodology, or by genetic transformation. If stacked by genetically transforming the plants, nucleotide sequences encoding additional desired traits can be combined at any time and in any order. For example, a transgenic plant comprising one or more desired traits can be used as the target to introduce further traits by subsequent transformation. The additional nucleotide sequences can be introduced simultaneously in a co-transformation protocol with a nucleotide sequence, nucleic acid molecule, nucleic acid construct, and/or composition of the invention, provided by any combination of expression cassettes. For example, if two nucleotide sequences will be introduced, they can be incorporated in separate cassettes (*trans*) or can be incorporated on the same cassette (*cis*). Expression of the nucleotide sequences can be driven by the same promoter or by different promoters. It is further recognized that nucleotide sequences can be stacked at a desired genomic location using a site-specific recombination system. *See, e.g.*, Int'l Patent Application Publication Nos. WO 99/25821; WO 99/25854; WO 99/25840; WO 99/25855 and WO 99/25853.

Thus, an expression cassette can include a coding sequence for one or more polypeptides for agronomic traits that primarily are of benefit to a seed company, grower or grain processor. A polypeptide of interest can be any polypeptide encoded by a nucleotide sequence of interest. Non-limiting examples of polypeptides of interest that are suitable for production in plants include those resulting in agronomically important traits such as herbicide resistance (also sometimes referred to as "herbicide tolerance"), virus resistance, bacterial pathogen resistance, insect resistance, nematode resistance, and/or fungal resistance. *See*, e.g., U.S. Patent Nos. 5,569,823; 5,304,730; 5,495,071; 6,329,504; and 6,337,431. Thus, in some embodiments, the expression cassette or expression vector of the invention can comprise one or more nucleotide sequences that confer insect resistance and/or additional nematode resistance.

In other embodiments, a polypeptide of interest also can be one that increases plant vigor or yield (including traits that allow a plant to grow at different temperatures, soil conditions and levels of sunlight and precipitation), or one that allows identification of a plant exhibiting a trait of interest (*e.g.*, a selectable marker, seed coat color, *etc.*). Various polypeptides of interest, as well as methods for introducing these polypeptides into a plant, are described, for example, in US Patent Nos. 4,761,373; 4,769,061; 4,810,648; 4,940,835; 4,975,374; 5,013,659; 5,162,602; 5,276,268; 5,304,730; 5,495,071; 5,554,798; 5,561,236; 5,569,823; 5,767,366; 5,879,903, 5,928,937; 6,084,155; 6,329,504 and 6,337,431; as well as US Patent Publication No. 2001/0016956. *See also*, on the World Wide Web at lifesci.sussex.ac.uk/home/Neil_Crickmore/Bt/.

In some particular embodiments of the invention, a nucleotide sequence of interest includes, but is not limited to, RNAi (siRNA, antisense RNA) and/or miRNA known to be associated with nematode resistance, and/or nucleotide sequences coding for insect resistance including, but not limited to, nucleotide sequences coding for *Bacillus thuringiensis* (Bt) toxins, for example, the various delta-endotoxin genes such as *Cry1Aa*, *Cry1Ab*, *Cry1Ac*, *Cry1B*, *Cry1C*, *Cry1D*, *Cry1Ea*, *Cry1Fa*, *Cry3A*, *Cry9A*, *Cry9C* and *Cry9B*; as well as genes encoding vegetative insecticidal proteins such as *Vip1*, *Vip2* and *Vip3*). An extensive list of Bt toxins can be found on the worldwide web at *Bacillus thuringiensis* Toxin Nomenclature Database maintained by the University of Sussex (*see also*, Crickmore *et al.* (1998) *Microbiol. Mol. Biol. Rev.* 62:807-813).

In addition to expression cassettes, the nucleic acid molecules and nucleotide sequences described herein can be used in connection with vectors. The term "vector" refers to a composition for transferring, delivering or introducing a nucleic acid (or nucleic acids)

into a cell. A vector comprises a nucleic acid molecule comprising the nucleotide sequence(s) to be transferred, delivered or introduced. Vectors for use in transformation of plants and other organisms are well known in the art. Non-limiting examples of general classes of vectors include a viral vector including but not limited to an adenovirus vector, a retroviral vector, an adeno-associated viral vector, a plasmid vector, a phage vector, a phagemid vector, a cosmid, a fosmid, a bacteriophage, or an artificial chromosome,. The selection of a vector will depend upon the preferred transformation technique and the target species for transformation. Accordingly, in further embodiments, a recombinant nucleic acid molecule of the invention can be comprised within a recombinant vector. The size of a vector can vary considerably depending on whether the vector comprises one or multiple expression cassettes (e.g., for molecular stacking). Thus, a vector size can range from about 3 kb to about 30 kb. Thus, in some embodiments, a vector is about 3 kb, 4kb, 5 kb, 6 kb, 7 kb, 8 kb, 9 kb, 10 kb, 11 kb, 12 kb, 13 kb, 14kb, 15 kb, 16 kb, 17 kb, 18 kb, 19 kb, 20 kb, 21 kb, 22 kb, 23 kb, 24kb, 25 kb, 26 kb, 27 kb, 28 kb, 29 kb, 30 kb, or any range therein, in size. In some particular embodiments, a vector can be about 3 kb to about 10 kb in size.

In additional embodiments of the invention, a method of producing a transgenic plant cell is provided, said method comprising introducing into a plant cell a recombinant nucleic acid molecule/nucleotide sequence of the invention, thereby producing a transgenic plant cell that can regenerate a transgenic plant having increased resistance to a nematode plant pest as compared to a plant regenerated from a plant cell that does not comprise said nucleic acid molecule. In some embodiments, the transgenic plant cell comprises more than one (e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10, etc.) nucleic acid molecule/nucleotide sequence of the invention. Thus, in some aspects of the invention, the transgenic plants, or parts thereof, comprise and express one or more nucleic acid molecule/nucleotide sequences of the invention, thereby producing one or more polypeptides of the invention.

In representative embodiments, a method of producing a transgenic plant cell is provided, said method comprising introducing into a plant cell a recombinant nucleic acid molecule of the invention, said recombinant nucleic acid molecule comprising a nucleotide sequence operatively linked to a promoter, which when expressed in a plant confer increased resistance to a nematode plant pest, the nucleotide sequence comprising, consisting essentially of, or consisting of: (a) a nucleotide sequence of **SEQ ID NOs:1-28, SEQ ID NOs:43-134, SEQ ID NOs:210-242, SEQ ID NOs:261-644**; (b) a nucleotide sequence that encodes a polypeptide comprising, consisting essentially of, or consisting of the amino acid sequence of any one of **SEQ ID NOs:29-42, SEQ ID NOs:135-209, SEQ ID NOs:243-260,**

SEQ ID NOs:665-1046; (c) a nucleotide sequence having significant sequence identity to nucleotide sequence of (a) and (b) above; (d) a nucleotide sequence which anneals under stringent hybridization conditions to the nucleotide sequence of (a), (b) or (c); (e) a nucleotide sequence that differs from the nucleotide sequences of (a), (b), (c) or (d) above due to the degeneracy of the genetic code; or (f) any combination of the nucleotide sequences of (a)-(e), thereby producing a transgenic plant cell that can regenerate a plant having increased resistance to a nematode plant pest as compared to a plant regenerated from a plant cell that does not comprise said recombinant nucleic acid molecule. In further embodiments, a method of producing a transgenic plant cell is provided, said method comprising introducing into a plant cell a recombinant nucleic acid molecule of the invention, said recombinant nucleic acid molecule comprising a nucleotide sequence operatively linked to a promoter, which when expressed in a plant confer increased resistance to a nematode plant pest, the nucleotide sequence comprising, consisting essentially of, or consisting of: (a) a nucleotide sequence of **SEQ ID NOs: 15, 17, 20, 22, 23, 24, 26, 226, 227,228, 230, 232 and/or 233**; (b) a nucleotide sequence that encodes a polypeptide comprising, consisting essentially of, or consisting of the amino acid sequence of any one of **SEQ ID NOs: 29, 31, 34, 36-38, 40, 244-246, 250, 251**; (c) a nucleotide sequence having significant sequence identity to nucleotide sequence of (a) and (b) above; (d) a nucleotide sequence which anneals under stringent hybridization conditions to the nucleotide sequence of (a), (b) or (c); (e) a nucleotide sequence that differs from the nucleotide sequences of (a), (b), (c) or (d) above due to the degeneracy of the genetic code; or (f) any combination of the nucleotide sequences of (a)-(e), thereby producing a transgenic plant cell that can regenerate a plant having increased resistance to a nematode plant pest as compared to a plant regenerated from a plant cell that does not comprise said recombinant nucleic acid molecule.

Thus, in some embodiments, the invention provides a transgenic plant or part thereof that is regenerated from the transgenic plant cell of the invention, wherein the transgenic plant or plant part has increased resistance to a nematode plant pest as compared to a control plant or plant part that is regenerated from a plant cell that does not comprise said recombinant nucleic acid molecule.

The terms "increase," "increasing," "increased," "enhance," "enhanced," "enhancing," and "enhancement" (and grammatical variations thereof), as used herein, describe an increase in the resistance of a plant to a nematode plant pest (e.g., a soybean plant having increased resistance to the soybean cyst nematode) by the introduction of a recombinant nucleic acid molecule of the invention into the plant, thereby producing a transgenic plant having

increased resistance to the pest. This increase in resistance can be observed by comparing the resistance of the plant transformed with the recombinant nucleic acid molecule of the invention to the resistance of a plant lacking (i.e., not transformed with) the recombinant nucleic acid molecule of the invention (i.e., a control).

As used herein, the terms "reduce," "reduced," "reducing," "reduction," "diminish," "suppress," and "decrease" (and grammatical variations thereof), describe, for example, a decrease in the growth of a nematode plant pest, a decrease in the ability of the nematode to survive, grow, feed, and/or reproduce, a decrease in the infectivity of a nematode plant pest, a decrease in the infestation of a plant by a nematode plant pest, and/or a decrease in nematode cyst development by a nematode plant pest on roots of a plant as compared to a control as described herein.

A further aspect of the invention provides transformed non-human host cells and transformed non-human organisms comprising the transformed non-human cells, wherein the transformed cells and transformed organisms comprise nucleic acid molecules comprising one or more nucleotide sequences of the invention. In some embodiments, the transformed non-human host cell includes but is not limited to a transformed bacterial cell, and/or a transformed plant cell. Thus, in some embodiments, the transformed non-human organism comprising the transformed non-human host cell includes, but is not limited to, a transformed bacterium, and/or a transformed plant.

In some particular embodiments, the invention provides a transgenic plant cell comprising a nucleic acid molecule of the invention and/or a transgenic plant regenerated from said transgenic plant cell. Accordingly, in some embodiments of the invention, a transgenic plant having increased resistance to a nematode plant pest is provided, said transgenic plant regenerated from a transgenic plant cell comprising at least one recombinant nucleic acid molecule/nucleotide sequence of the invention.

Additional aspects of the invention include a harvested product produced from the transgenic plants and/or parts thereof of the invention, as well as a processed product produced from said harvested product. A harvested product can be a whole plant or any plant part, as described herein, wherein said harvested product comprises a recombinant nucleic acid molecule/nucleotide sequence of the invention. Thus, in some embodiments, non-limiting examples of a harvested product include a seed, a fruit, a flower or part thereof (e.g., an anther, a stigma, and the like), a leaf, a stem, and the like. In other embodiments, a processed product includes, but is not limited to, a flour, meal, oil, starch, cereal, and the like

produced from a harvested seed of the invention, wherein said seed comprises a recombinant nucleic acid molecule/nucleotide sequence of the invention.

Non-limiting examples of plants can include vegetable crops, including artichokes, kohlrabi, arugula, leeks, asparagus, lettuce (*e.g.*, head, leaf, romaine), bok choy, malanga, melons (*e.g.*, muskmelon, watermelon, crenshaw, honeydew, cantaloupe), cole crops (e.g., brussels sprouts, cabbage, cauliflower, broccoli, collards, kale, chinese cabbage, bok choy) cardoni, carrots, napa, okra, onions, celery, parsley, chick peas, parsnips, chicory, peppers, potatoes, cucurbits (e.g., marrow, cucumber, zucchini, squash, pumpkin), radishes, dry bulb onions, rutabaga, eggplant (also called brinjal), salsify, escarole, shallots, endive, garlic, spinach, green onions, squash, greens, beet (sugar beet and fodder beet), sweet potatoes, swiss chard, horseradish, tomatoes, turnips, and spices; a fruit and/or vine crop such as apples, apricots, cherries, nectarines, peaches, pears, plums, prunes, cherry, quince, almonds, chestnuts, filberts, pecans, pistachios, walnuts, citrus, blueberries, boysenberries, cranberries, currants, loganberries, raspberries, strawberries, blackberries, grapes, avocados, bananas, kiwi, persimmons, pomegranate, pineapple, tropical fruits, pomes, melon, mango, papaya, and lychee; a field crop plant such as clover, alfalfa, evening primrose, meadow foam, corn/maize (field, sweet, popcorn), hops, jojoba, peanuts, rice, safflower, small grains (barley, oats, rye, wheat, etc.), sorghum, tobacco, kapok, a leguminous plant (beans, lentils, peas, soybeans), an oil plant (rape, mustard, poppy, olive, sunflower, coconut, castor oil plant, cocoa bean, groundnut), *Arabidopsis*, a fibre plant (cotton, flax, hemp, jute), lauraceae (cinnamon, camphor), or a plant such as coffee, sugar cane, tea, and natural rubber plants; and/or a bedding plant such as a flowering plant, a cactus, a succulent and/or an ornamental plant, as well as trees such as forest (broad-leaved trees and evergreens, such as conifers), fruit, ornamental, and nut-bearing trees, as well as shrubs and other nursery stock.

In some embodiments, a plant can be any plant species or plant varieties susceptible to soybean cyst nematode infection including, but not limited to, China pinks, edible beans, lespedeza, vetch (common, hairy or winter), lupine, clover (crimson, scarlet or alsike), sweetclover, birdsfoot trefoil, crownvetch, garden pea, cowpea, black-eyed pea, soybeans (wild and cultivated), black locust, honey locust, portulaca, Bells of Ireland, common chickweed, mousear chickweed, mullein, sicklepod, *Digitalis penstemon*, pokeweed, purslane, bittercress, Rocky Mountain beeplant, spotted geranium, toadflax, winged pigweed, *Psoralea spp., Cleome serrulata,* vetch (American, Carolina or wood), burclover (*Medicago minima*), chick-weed (*Cerastium vulgatum*), dalea, Canadian milkvetch, hemp sesbania, borage, canary bird flower, cup flower, caraway, Chinese lantern plant, blue gem viscaria,

coralbell, Margaret double carnation, *Rosa multiflora*, pink queen, geranium (*Geranium maculatum*), cup-flower, delphinium, foxglove, geum, common horehound, poppy, sage, snapdragon, beard-tongue (*Penstemon digitalis*), *Desmodium nudifolorum, D. marilandicum, D. viridiflorum,* corn cockle, sweet basil, sweetpea, verbena, henbit (*Lamium amplexicaule*), purple deadnettle (*Lamium purpureum*), (field pennycress (*Thlaspi arvense*), shepherd's-purse (*Capsella bursa-pastoris*), hop clovers, beggars weed, tick clover, corn cockle, hogpeanut, milkpea, and wildbean (*Strophostyles helvola*).

In some particular embodiments, a transgenic plant of the invention includes, but is not limited to, a transgenic soybean plant, a transgenic sugar beet plant, a transgenic corn plant, a transgenic cotton plant, a transgenic canola plant, a transgenic wheat plant, or a transgenic rice plant. In other embodiments, a transgenic plant cell of the invention includes, but is not limited to, a transgenic soybean cell, a transgenic sugar beet cell, a transgenic corn cell, a transgenic cotton cell, a transgenic canola cell, a transgenic sugar cane cell, a transgenic wheat cell, or a transgenic rice cell.

As used herein, the term "plant part" includes but is not limited to embryos, pollen, ovules, seeds, leaves, flowers, branches, fruit, kernels, ears, cobs, husks, stalks, roots, root tips, anthers, plant cells including plant cells that are intact in plants and/or parts of plants, plant protoplasts, plant tissues, plant cell tissue cultures, plant calli, plant clumps, and the like. Further, as used herein, "plant cell" refers to a structural and physiological unit of the plant, which comprises a cell wall and also may refer to a protoplast. A plant cell of the invention can be in the form of an isolated single cell or can be a cultured cell or can be a part of a higher-organized unit such as, for example, a plant tissue or a plant organ. A "protoplast" is an isolated plant cell without a cell wall or with only parts of the cell wall. Thus, in some embodiments of the invention, a transgenic cell comprising a nucleic acid molecule and/or nucleotide sequence of the invention is a cell of any plant or plant part including, but not limited to, a root cell, a leaf cell, a tissue culture cell, a seed cell, a flower cell, a fruit cell, a pollen cell, and the like.

In some particular embodiments, the invention provides a transgenic seed produced from a transgenic plant of the invention, wherein the transgenic seed comprises a nucleic acid molecule/nucleotide sequence of the invention.

"Plant cell culture" means cultures of plant units such as, for example, protoplasts, cell culture cells, cells in plant tissues, pollen, pollen tubes, ovules, embryo sacs, zygotes and embryos at various stages of development. In some embodiments of the invention, a

transgenic tissue culture or transgenic plant cell culture is provided, wherein the transgenic tissue or cell culture comprises a nucleic acid molecule/nucleotide sequence of the invention.

As used herein, a "plant organ" is a distinct and visibly structured and differentiated part of a plant such as a root, stem, leaf, flower bud, or embryo.

"Plant tissue" as used herein means a group of plant cells organized into a structural and functional unit. Any tissue of a plant *in planta* or in culture is included. This term includes, but is not limited to, whole plants, plant organs, plant seeds, tissue culture and any groups of plant cells organized into structural and/or functional units. The use of this term in conjunction with, or in the absence of, any specific type of plant tissue as listed above or otherwise embraced by this definition is not intended to be exclusive of any other type of plant tissue.

The term "nematode plant pest" as used herein includes any nematode species that is a pest on a plant. Non-limiting examples of nematode pests include cyst nematodes (*Heterodera* spp.), especially the soybean cyst nematode (*Heterodera glycines*), root knot nematodes (*Meloidogyne* spp.), lance nematodes (*Hoplolaimus* spp.), stunt nematodes (*Tylenchorhynchus* spp.), spiral nematodes (*Helicotylenchus* spp.), lesion nematodes (*Pratylenchus* spp.), sting nematodes (*Belonoluimus* spp.), reniform nematodes (*Rotylenchulus reniformis*), burrowing nematodes (*Radopholus similis*), Citrus nematode (*Tylenchulus semipenetrans*), and ring nematodes (*Criconema* spp.).

"Introducing," in the context of a nucleotide sequence of interest (e.g., the nucleotide sequences and nucleic acid molecules of the invention), means presenting the nucleotide sequence of interest to the plant, plant part, and/or plant cell in such a manner that the nucleotide sequence gains access to the interior of a cell. Where more than one nucleotide sequence is to be introduced these nucleotide sequences can be assembled as part of a single polynucleotide or nucleic acid construct, or as separate polynucleotide or nucleic acid constructs, and can be located on the same or different transformation vectors. Accordingly, these polynucleotides can be introduced into plant cells in a single transformation event, in separate transformation events, or, e.g., as part of a breeding protocol. Thus, the term "transformation" as used herein refers to the introduction of a heterologous nucleic acid into a cell. Transformation of a cell may be stable or transient. Thus, in some embodiments, a plant cell of the invention is stably transformed with a nucleic acid molecule of the invention. In other embodiments, a plant of the invention is transiently transformed with a nucleic acid molecule of the invention.

"Transient transformation" in the context of a polynucleotide means that a polynucleotide is introduced into the cell and does not integrate into the genome of the cell.

By "stably introducing" or "stably introduced" in the context of a polynucleotide introduced into a cell is intended the introduced polynucleotide is stably incorporated into the genome of the cell, and thus the cell is stably transformed with the polynucleotide.

"Stable transformation" or "stably transformed" as used herein means that a nucleic acid is introduced into a cell and integrates into the genome of the cell. As such, the integrated nucleic acid is capable of being inherited by the progeny thereof, more particularly, by the progeny of multiple successive generations. "Genome" as used herein also includes the nuclear and the plastid genome, and therefore includes integration of the nucleic acid into, for example, the chloroplast genome. Stable transformation as used herein can also refer to a transgene that is maintained extrachromasomally, for example, as a minichromosome.

Transient transformation may be detected by, for example, an enzyme-linked immunosorbent assay (ELISA) or Western blot, which can detect the presence of a peptide or polypeptide encoded by one or more transgene introduced into an organism. Stable transformation of a cell can be detected by, for example, a Southern blot hybridization assay of genomic DNA of the cell with nucleic acid sequences which specifically hybridize with a nucleotide sequence of a transgene introduced into an organism (e.g., a plant). Stable transformation of a cell can be detected by, for example, a Northern blot hybridization assay of RNA of the cell with nucleic acid sequences which specifically hybridize with a nucleotide sequence of a transgene introduced into a plant or other organism. Stable transformation of a cell can also be detected by, *e.g.*, a polymerase chain reaction (PCR) or other amplification reactions as are well known in the art, employing specific primer sequences that hybridize with target sequence(s) of a transgene, resulting in amplification of the transgene sequence, which can be detected according to standard methods Transformation can also be detected by direct sequencing and/or hybridization protocols well known in the art.

A nucleic acid of the invention (e.g., one or more of the nucleotide sequences of **SEQ ID NOs:1-28, SEQ ID NOs:43-134, SEQ ID NOs:210-242, SEQ ID NOs:261-644**, or a nucleotide sequence encoding one or more polypeptides having the amino acid sequence of any one of **SEQ ID NOs:29-42, SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046**) can be introduced into a cell by any method known to those of skill in the art.

In some embodiments of the invention, transformation of a cell comprises nuclear transformation. In other embodiments, transformation of a cell comprises plastid

transformation (e.g., chloroplast transformation).

Procedures for transforming plants are well known and routine in the art and are described throughout the literature. Non-limiting examples of methods for transformation of plants include transformation via bacterial-mediated nucleic acid delivery (*e.g.*, via *Agrobacteria*), viral-mediated nucleic acid delivery, silicon carbide or nucleic acid whisker-mediated nucleic acid delivery, liposome mediated nucleic acid delivery, microinjection, microparticle bombardment, calcium-phosphate-mediated transformation, cyclodextrin-mediated transformation, electroporation, nanoparticle-mediated transformation,, sonication, infiltration, PEG-mediated nucleic acid uptake, as well as any other electrical, chemical, physical (mechanical) and/or biological mechanism that results in the introduction of nucleic acid into the plant cell, including any combination thereof. General guides to various plant transformation methods known in the art include Miki *et al.* ("Procedures for Introducing Foreign DNA into Plants" in *Methods in Plant Molecular Biology and Biotechnology*, Glick, B. R. and Thompson, J. E., Eds. (CRC Press, Inc., Boca Raton, 1993), pages 67-88) and Rakowoczy-Trojanowska (*Cell. Mol. Biol. Lett.* 7:849-858 (2002)).

Agrobacterium-mediated transformation is a commonly used method for transforming plants, in particular, dicot plants, because of its high efficiency of transformation and because of its broad utility with many different species. *Agrobacterium*-mediated transformation typically involves transfer of the binary vector carrying the foreign DNA of interest to an appropriate *Agrobacterium* strain that may depend on the complement of *vir* genes carried by the host *Agrobacterium* strain either on a co-resident Ti plasmid or chromosomally (Uknes *et al.* (1993) *Plant Cell* 5:159-169). The transfer of the recombinant binary vector to *Agrobacterium* can be accomplished by a triparental mating procedure using *Escherichia coli* carrying the recombinant binary vector, a helper *E. coli* strain that carries a plasmid that is able to mobilize the recombinant binary vector to the target *Agrobacterium* strain. Alternatively, the recombinant binary vector can be transferred to *Agrobacterium* by nucleic acid transformation (Höfgen & Willmitzer (1988) *Nucleic Acids Res.* 16:9877).

Transformation of a plant by recombinant *Agrobacterium* usually involves co-cultivation of the *Agrobacterium* with explants from the plant and follows methods well known in the art. Transformed tissue is regenerated on selection medium carrying an antibiotic or herbicide resistance marker between the binary plasmid T-DNA borders.

Another method for transforming plants, plant parts and/or plant cells involves propelling inert or biologically active particles at plant tissues and cells. *See, e.g.*, US Patent Nos. 4,945,050; 5,036,006 and 5,100,792. Generally, this method involves propelling inert

or biologically active particles at the plant cells under conditions effective to penetrate the outer surface of the cell and afford incorporation within the interior thereof. When inert particles are utilized, the vector can be introduced into the cell by coating the particles with the vector containing the nucleic acid of interest. Alternatively, a cell or cells can be surrounded by the vector so that the vector is carried into the cell by the wake of the particle. Biologically active particles (*e.g.*, dried yeast cells, dried bacterium or a bacteriophage, each containing one or more nucleic acids sought to be introduced) also can be propelled into plant tissue.

Thus, in particular embodiments of the invention, a plant cell can be transformed by any method known in the art and as described herein and intact plants can be regenerated from these transformed cells using any of a variety of known techniques. Plant regeneration from plant cells, plant tissue culture and/or cultured protoplasts is described, for example, in Evans *et al.* (*Handbook of Plant Cell Cultures,* Vol. 1, MacMilan Publishing Co. New York (1983)); and Vasil I. R. (ed.) (*Cell Culture and Somatic Cell Genetics of Plants,* Acad. Press, Orlando, Vol. I (1984), and Vol. II (1986)). Methods of selecting for transformed transgenic plants, plant cells and/or plant tissue culture are routine in the art and can be employed in the methods of the invention provided herein.

Likewise, the genetic properties engineered into the transgenic seeds and plants, plant parts, and/or plant cells of the invention described above can be passed on by sexual reproduction or vegetative growth and therefore can be maintained and propagated in progeny plants. Generally, maintenance and propagation make use of known agricultural methods developed to fit specific purposes such as harvesting, sowing or tilling.

A nucleotide sequence therefore can be introduced into the plant, plant part and/or plant cell in any number of ways that are well known in the art. The methods of the invention do not depend on a particular method for introducing one or more nucleotide sequences into a plant, only that they gain access to the interior of at least one cell of the plant. Where more than one nucleotide sequence is to be introduced, they can be assembled as part of a single nucleic acid construct, or as separate nucleic acid constructs, and can be located on the same or different nucleic acid constructs. Accordingly, the nucleotide sequences can be introduced into the cell of interest in a single transformation event, in separate transformation events, or, for example, in plants, as part of a breeding protocol.

Thus, in additional embodiments, the invention provides a method of producing a plant having increased resistance to infestation by a nematode plant pest, the method comprising the steps of (a) crossing a transgenic plant of the invention with itself or another

plant to produce seed comprising a recombinant nucleic acid molecule or vector of the invention; and (b) growing a progeny plant from said seed to produce a plant having increased resistance to infestation by nematode plant pests. In some embodiments, the method further comprises (c) crossing the progeny plant of (b) with itself or another plant and (d) repeating steps (b) and (c) for an additional 0-7 (e.g., 0, 1, 2, 3, 4, 5, 6, 7) generations to produce a plant having increased resistance to infestation by nematode plant pests.

In further embodiments, a method of producing a soybean plant having increased resistance to infestation by a nematode plant pest is provided, the method comprising the steps of (a) crossing a transgenic soybean plant of the invention with itself or another soybean plant to produce soybean seed comprising a recombinant nucleic acid molecule or vector of the invention; and (b) growing a progeny soybean plant from said seed to produce a soybean plant having increased resistance to infestation by nematode plant pests. In some embodiments, the method further comprises (c) crossing the progeny soybean plant of (b) with itself or another soybean plant and (d) repeating steps (b) and (c) for an additional 0-7 (e.g., 0, 1, 2, 3, 4, 5, 6, 7) generations to produce a soybean plant having increased resistance to infestation by nematode plant pests.

The invention further provides a plant crop comprising a plurality of transgenic plants of the invention planted together in an agricultural field.

In addition, a method of improving the yield of a plant crop when said plant crop is contacted with a nematode plant pest is provided, the method comprising cultivating a plurality of plants comprising a recombinant nucleic acid molecule of the invention as the plant crop, wherein the plurality of plants of said plant crop have increased resistance to nematode infection, thereby improving the yield of said plant crop as compared to a control plant crop contacted with said nematode plant pest, wherein the control plant crop is produced from a plurality of plants lacking said nucleic acid molecule. In some particular embodiments of the invention, the crop is a soybean crop.

In some embodiments, a method of improving the yield of a crop when said crop is contacted with a nematode plant pest is provided, the method comprising contacting the nematode plant pest with an effective amount of a polypeptide of the invention or a nematicidal composition of the invention, wherein the yield of the crop is improved as compared to a plant crop contacted with a nematode plant pest that has not been contacted with said polypeptide and/or nematicidal composition. In some particular embodiments of the invention, the crop is a soybean crop.

In still other embodiments, the invention further provides methods for controlling a nematode plant pest, methods of reducing the infectivity of a nematode plant pest toward a plant, methods of reducing infestation of a plant by a nematode plant pest, methods of reducing nematode cyst development, and methods of reducing the growth of a nematode plant pest comprising contacting the nematode plant pest with a composition of the invention, wherein said composition comprises a recombinant nucleic acid molecule, a nucleotide sequence, and/or a polypeptide of this invention. In some particular embodiments, the composition of the invention is a transgenic plant cell, transgenic plant or transgenic plant part comprising and expressing a recombinant nucleic acid molecule/nucleotide sequence of the invention.

Accordingly, in one embodiment, the invention provides a method of controlling a nematode plant pest, comprising contacting the nematode plant pest with an effective amount of a polypeptide of the invention or composition thereof, thereby controlling the nematode plant pest as compared to the control of a nematode plant pest which has not been contacted with said polypeptide or composition thereof.

Thus, in a further embodiment, the invention provides a method of controlling a nematode plant pest, comprising contacting the nematode plant pest with a transgenic plant and/or a part thereof comprising a recombinant nucleic acid molecule of the invention, thereby controlling the nematode plant pest as compared to the control of a nematode plant pest contacted with a control plant or plant part, said control plant lacking said recombinant nucleic acid molecule.

To "contact" a nematode plant pest with a polypeptide of the invention and/or composition thereof or to "deliver" to a nematode plant pest a polypeptide of the invention and/or composition thereof means that the nematode plant pest comes into contact with, is exposed to, the polypeptides of this invention and/or compositions thereof, resulting in a toxic effect on and control of the nematode (e.g., control, reduced infectivity, reduced infestation, reduced cyst formation, reduced growth, and the like). A nematode plant pest can be contacted with a polypeptide of the invention or nematicidal composition of the invention using any art known method. For example, contacting includes but is not limited to, (1) providing the polypeptide(s) of the invention in a transgenic plant, wherein the nematode eats (ingests) one or more parts of the transgenic plant, (2) in a protein composition(s) that can be applied to the surface of a plant or plant part, for example, sprayed onto the plant surface , applied as a soil drench near the plant roots, or as a dip for a whole plant or parts thereof (e.g., roots) or (3) any other art-recognized delivery system.

"Effective amount" refers to that concentration or amount of a polypeptide or nematicidal composition that inhibits or reduces the ability of a nematode plant pest to survive, grow, feed and/or reproduce, or that limits nematode-related damage or loss in crop plants. Thus, in some embodiments of the invention, an "effective amount" can mean killing the nematode. In other embodiments, an "effective amount" does not mean killing the nematode.

The term "control" in the context of an effect on an organism (e.g., nematode plant pest) means to inhibit or reduce, through a toxic effect, the ability of the organism to survive, grow, feed, and/or reproduce, or to limit damage or loss in crop plants that is related to the activity of the organism. To "control" an organism may or may not mean killing the organism, although in some embodiments "control" means killing the organism.

Thus, in particular embodiments, the overexpression of a nucleic acid molecule of the invention in a plant results in the production of the encoded polypeptide, thereby conferring on a plant resistance to a nematode plant pest. While not wishing to be bound by any particular theory, the polypeptides of this invention may have a "direct toxic" effect on the nematodes or instead may be triggers for the production of other proteins or metabolites or for one or more different pathways any of which may exert a toxic effect on nematode plant pests.

In other embodiments of the invention, a method of reducing the infectivity of a nematode plant pest to a plant is provided, the method comprising contacting the nematode plant pest with an effective amount of a polypeptide of the invention, thereby reducing the infectivity of the nematode plant pest to the plant as compared to the infectivity of a nematode plant pest to which said polypeptide has not been delivered.

As used herein, "infect," and "infectivity" means the ability of the nematode plant pest to infect, infest or parasitize a plant host. "Infest" and "infestation" refers to a pest nematode inhabiting or overrunning a plant in numbers or quantities that are large enough to be harmful to the plant.

In some embodiments of the invention, a method of reducing the infectivity of a nematode plant pest to a plant is provided, the method comprising contacting the nematode plant pest with a transgenic plant comprising a recombinant nucleic acid molecule of the invention, thereby reducing the infectivity of the nematode plant pest as compared to a nematode plant pest contacted with a control plant or plant part, wherein said control plant lacks said recombinant nucleic acid molecule.

In other embodiments, the invention provides a method of reducing nematode cyst development by a nematode plant pest on the roots of a plant, comprising contacting a nematode plant pest with an effective amount of the polypeptide of the invention, wherein nematode cyst development by the nematode plant pest on the roots of said plant is reduced as compared to cyst development on the roots of a plant by a nematode plant pest not contacted with said polypeptide.

In additional embodiments, a method of reducing nematode cyst development by a nematode plant pest on roots of a plant is provided, the method comprising contacting a nematode plant pest with the roots of a transgenic plant comprising a recombinant nucleic acid molecule of the invention, wherein cyst development by the nematode plant pest on the roots of the transgenic plant is reduced as compared cyst development on the roots of a control plant lacking said recombinant nucleic acid molecule.

In other embodiments of the invention, a method of reducing the growth of a nematode plant pest population is provided, the method comprising contacting the nematode plant pest population with an effective amount of a polypeptide of the invention, wherein the growth of a nematode plant pest population is reduced as compared to the growth of a control nematode plant pest population not contacted with the polypeptide.

In still other embodiments, a method of reducing the growth of a nematode plant pest population is provided, the method comprising contacting the nematode plant pest population with a transgenic plant comprising a recombinant nucleic acid molecule of the invention, wherein the growth of a nematode plant pest population is reduced as compared to the growth of a nematode plant pest population contacted with a control plant or plant part, said control plant or plant part lacking the recombinant nucleic acid molecule.

Thus, when a transgenic plant comprising a recombinant nucleic acid molecule of the invention, or a part thereof, is exposed to or brought into contact with a nematode plant pest such that the nematode feeds on or otherwise contacts the transgenic plant or part thereof, the ability of the nematode plant pest to survive, grow, feed, and/or reproduce in association with a plant is inhibited or reduced, thereby controlling the nematode/nematode population and/or reducing the ability of the nematode plant pest to infect or infest a plant or produce cysts on a plant. Additionally, one or more polypeptides of the invention or compositions comprising one or more polypeptides of the invention can be used directly to control or reduce the growth of a nematode plant pest, thereby reducing the ability of the nematode plant pest to infect or infest a plant or produce cysts on a plant.

The invention will now be described with reference to the following examples. It should be appreciated that these examples are not intended to limit the scope of the claims to the invention, but are rather intended to be exemplary of certain embodiments. Any variations in the exemplified methods that occur to the skilled artisan are intended to fall within the scope of the invention.

EXAMPLES

Example 1: Construction of Expression Cassettes for Hairy Root Transformation

At least one nucleic acid of the invention comprising a nucleotide sequence of any one of the nucleotide sequences of **SEQ ID NOs:1-28**, **SEQ ID NOs:43-134**, **SEQ ID NOs:210-242**, **SEQ ID NOs:261-644**, or a nucleotide sequence encoding any one of the polypeptides having the amino acid sequences of **SEQ ID NOs:29-42**, **SEQ ID NOs:135-209**, **SEQ ID NOs:243-260**, **SEQ ID NOs:665-1046**, is cloned into an expression cassette having the basic structure from 5' to 3' of: 5'-promoter-nucleic acid of the invention-terminator-3'. Expression cassettes may also comprise enhancers, introns, leader sequences and the like. One such expression cassette has the structure: prActin2(including Act2 intron):cEVO18010081 (**SEQ ID NO:24**):tNOS or prActin2(including Act2 intron):cEVO18010044 (**SEQ ID NO:224**):tNOS. Other nucleic acids of the invention can be substituted for the cEVO18010081 or EVO18010044 coding sequence to create different expression cassettes. The expression cassette is then cloned into a binary expression vector to create a hairy root (HR) transformation vector. A cEVO18010081 (**SEQ ID NO:24**) or cEVO18010044 (**SEQ ID NO: 224**) HR transformation vector was created by cloning the cEVO18010081 (**SEQ ID NO:24**) or cEVO18010044 (**SEQ ID NO: 224**) expression cassette, respectively, and a second expression cassette encoding a scorable marker into a binary vector. As an example, the resulting HR transformation vector 20844 comprising cEVO18010081 (**SEQ ID NO:24**) is shown in **Figure 1**.

Example 2: Expression in Transgenic Soybean Roots

The binary expression vector described in Example 1 containing a nucleic acid of the invention and an empty vector (without a nucleic acid of the invention) shown in Figure 2 was transformed into soybean roots to test the binary vector's ability to express a protein that is capable of reducing soybean cyst nematode (SCN) cysts. Soybean cultivar Williams 82 was used as the germplasm for the hairy root transformation. Soybean seeds were germinated on 1% agar containing 0.5% sucrose in Petri dishes at approximately 27 °C for 5 days. The cotyledons were then cut off the seedlings, and the wounded surface was inoculated with cultures of an *Agrobacterium rhizogenes* strain (e.g., K599) carrying the binary expression vector or empty vector. The cotyledons were placed on 1% agar for about 6 days and then transferred onto selection media. In about two weeks, independent transgenic hairy root events induced from the cotyledons were harvested and transferred onto

culture media, and cultured in the darkness at about 27 °C. Narayanan *et al.* (*Crop Science* 39, 1680-1686 (1999)) indicates that SCN resistance phenotypes in a whole soybean plant are preserved in transgenic hairy roots, therefore the transgenic hairy root system is useful for evaluating candidate SCN resistance genes and predicting activity in whole soybean plants.

Approximately two weeks after transfer onto the culture plates, the transformed hairy roots were inoculated with surface-sterilized J2 stage soybean cyst nematodes (SCN J2) and the roots were grown in darkness at about 27 °C, which allows cyst formation on the hairy root events. One month after nematode inoculation, the number of cysts were determined for the roots expressing the polynucleotides of **SEQ ID NOs:15-28, 31, 35, 225, 227, 228, 230-234,** or **238-240** (i.e., producing the polypeptides of **SEQ ID NOs: 29-38, 40-42, 52, 243, 244, 246, 248-252, 25,** or **256-259)** or for roots expressing the polynucleotides of **SEQ ID NOs:1047-1062** and for roots expressing the empty vector (as a negative control). The experiments were repeated at least one time.

The results of the experiments are shown in **Tables 1-25** below.

Table 1.

Plasmid_ID	Nucleotide sequence	Average cyst number (Avg)	Number of hairy root events (n)	Standard error (SE)
SCNBHR10	SEQ ID NO:15	22.1	17	2.5
SCNBHR25	SEQ ID NO:21	24	3	5.6
SCNBHR52	SEQ ID NO:23	12. 2	11	3.4
SCNBHR81	SEQ ID NO:24	33.6	14	4
SCNBHRCK	Empty Vector	21.2	11	3

Table 2

Plasmid_ID	Nucleotide sequence	Avg	n	SE
SCNBHR18	SEQ ID NO:18	10.8	16	2.4
SCNBHR21	SEQ ID NO:20	6.4	18	1.2
SCNBHR25	SEQ ID NO:21	10.5	13	1.1
SCNBHR36	SEQ ID NO:22	12	8	1.7
SCNBHR52	SEQ ID NO:23	2	1	
SCNBHR84	SEQ ID NO:27	14.1	20	1.4
SCNBHRCK	Empty Vector	13.3	9	1.7

Table 3

Plasmid_ID	Nucleotide sequence	Avg	n	SE
SCNBHR15	SEQ ID NO:17	15	9	3.6
SCNBHR82	SEQ ID NO:25	16.9	15	2.5
SCNBHRCK	Empty Vector	10.4	12	1.6

Table 4

Plasmid_ID	Nucleotide sequence	Avg	n	SE
SCNBHR10	SEQ ID NO:15	15	2	2
SCNBHR15	SEQ ID NO:17	12.3	7	2.4
SCNBHR36	SEQ ID NO:22	14.5	10	2.6
SCNBHR52	SEQ ID NO:23	6	1	
SCNBHR81	SEQ ID NO:24	5	3	0
SCNBHR82	SEQ ID NO:25	8	1	
SCNBHRCK	Empty Vector	20.5	2	2.5

Table 5

Plasmid_ID	Nucleotide sequence	Avg	n	SE
SCNBHR11	SEQ ID NO:16	27.6	16	2.3
SCNBHR19	SEQ ID NO:19	24.1	16	3
SCNBHR83	SEQ ID NO:26	17.8	14	2.2
SCNBHR88	SEQ ID NO:28	21.6	13	2.7
SCNBHRCK	Empty Vector	18.5	10	2.5

Table 6

Plasmid_ID	Nucleotide sequence	Avg	n	SE
SCNBHR10	SEQ ID NO:15	43	1	
SCNBHR15	SEQ ID NO:17	41.3	3	12.4
SCNBHR21	SEQ ID NO:20	27.9	7	2.9
SCNBHR36	SEQ ID NO:22	32	3	11.9
SCNBHR52	SEQ ID NO:23	42.7	7	4.2
SCNBHR81	SEQ ID NO:24	19	1	
SCNBHR83	SEQ ID NO:26	31.5	2	1.5
SCNBHRCK	Empty Vector	60.8	5	4

Table 7

Plasmid_ID	Nucleotide sequence	Avg	n	SE
SCNBHR40	SEQ ID NO:1047	34.5	12	6
SCNBHR44	SEQ ID NO:225	29.6	12	3.5
SCNBHR47	SEQ ID NO:227	29.1	13	3.5
SCNBHR50	SEQ ID NO:1048	31.1	13	3.2
SCNBHR55	SEQ ID NO:1049	36.5	15	3.8
SCNBHR57	SEQ ID NO:1050	40.1	14	3.2
SCNBHR60	SEQ ID NO:232	20.7	11	3.2
SCNBHR65	SEQ ID NO:1051	33.8	11	5.9
SCNBHRCK	Empty Vector	39.9	11	4.3

Table 8.

Plasmid_ID	Nucleotide sequence	Avg	n	SE
SCNBHR43	SEQ ID NO:1052	70.9	7	4.8
SCNBHR48	SEQ ID NO:228	23.3	7	9.7
SCNBHR52	SEQ ID NO:23	24.8	4	6.2
SCNBHR71	SEQ ID NO:1053	66.6	8	11.1
SCNBHR72	SEQ ID NO:1054	71.6	9	5.2
SCNBHR79	SEQ ID NO:1055	108.8	4	32.6
SCNBHR91	SEQ ID NO:1056	48	4	12.2
SCNBHRCK	Empty Vector	72.7	3	22.3

Table 9.

Plasmid_ID	Nucleotide sequence	Avg	n	SE
SCNBHR58	SEQ ID NO:1057	43.6	8	6
SCNBHR59	SEQ ID NO:231	97	13	8.1
SCNBHR86	SEQ ID NO:1058	58.4	7	15.2
SCNBHR89	SEQ ID NO:1059	45.5	6	7
SCNBHRCK	Empty Vector	62.9	10	9.4

Table 10.

Plasmid_ID	Nucleotide sequence	Avg	n	SE
SCNBHR43	SEQ ID NO:1052	44.9	10	5.1
SCNBHR79	SEQ ID NO:1055	44.7	12	4.2
SCNBHR91	SEQ ID NO:1056	30.7	3	9.8
SCNBHRCK	Empty Vector	46.8	10	5.8

Table 11.

Plasmid_ID	Nucleotide sequence	Avg	n	SE
SCNBHR71	SEQ ID NO:1053	65	7	11
SCNBHR72	SEQ ID NO:1054	53.7	8	8.9
SCNBHR91	SEQ ID NO:1056	46	3	7.6
SCNBHRCK	Empty Vector	65.4	8	7.4

Table 12.

Plasmid_ID	Nucleotide sequence	Avg	n	SE
SCNBHR48	SEQ ID NO:228	34.6	8	7.4
SCNBHR61	SEQ ID NO:233	53.2	6	5.9
SCNBHR73	SEQ ID NO:238	44	7	8
SCNBHR77	SEQ ID NO:239	34.8	6	6.4
SCNBHRCK	Empty Vector	78	9	10.6

Table 13.

Plasmid_ID	Nucleotide sequence	Avg	n	SE
SCNBHR68	SEQ ID NO:1060	46.2	6	10.7
SCNBHR70	SEQ ID NO:1061	53.7	3	12.8
SCNBHR80	SEQ ID NO:240	34.5	2	7.5
SCNBHR85	SEQ ID NO:1062	45	2	5
SCNBHRCK	Empty Vector	55.2	6	6.3

Table 14.

Plasmid_ID	Nucleotide sequence	Avg	n	SE
SCNBHR15	SEQ ID NO:17	45.8	12	3.6
SCNBHR21	SEQ ID NO:20	51.1	14	4.1
SCNBHR36	SEQ ID NO:22	50.4	5	4.9
SCNBHR52	SEQ ID NO:23	45.5	13	4.1
SCNBHR66	SEQ ID NO:236	62	7	11.7
SCNBHR77	SEQ ID NO:239	57.2	12	6
SCNBHR81	SEQ ID NO:24	30.2	12	2.6
SCNBHRCK	Empty Vector	65.7	17	5.8

Table 15.

Plasmid_ID	Nucleotide sequence	Avg	n	SE
SCNBHR10	SEQ ID NO:15	63	11	3.9
SCNBHRCK	Empty Vector	97.4	14	8.3

Table 16.

Plasmid_ID	Nucleotide sequence	Avg	n	SE
SCNBHR59	SEQ ID NO:231	398.1	19	17.15435
SCNBHRCK	Empty Vector	312.4	11	29.17074

Table 17.

Plasmid_ID	Nucleotide sequence	Avg	n	SE
SCNBHR43	SEQ ID NO:1052	84.5	14	6.8
SCNBHR58	SEQ ID NO:1057	85.4	9	5.9
SCNBHRCK	Empty Vector	89.8	11	4.2

Table 18.

Plasmid_ID	Nucleotide sequence	Avg	n	SE
SCNBHR54	SEQ ID NO:230	69.9	13	4.9
SCNBHR61	SEQ ID NO:233	66.3	13	5.1
SCNBHR73	SEQ ID NO:238	96.5	13	11.6
SCNBHRCK	Empty Vector	103.2	13	9.6

Table 19.

Plasmid_ID	Nucleotide sequence	Avg	n	SE
SCNBHR60	SEQ ID NO:232	82.6	9	5.8
SCNBHRCK	Empty Vector	145.8	10	17.8

Table 20.

Plasmid_ID	Nucleotide sequence	Avg	n	SE
SCNBHR80	SEQ ID NO:240	65.3	19	4.6
SCNBHRCK	Empty Vector	61	14	5.4

Table 21.

Plasmid_ID	Nucleotide sequence	Avg	n	SE
SCNBHR47	SEQ ID NO:227	57.5	13	3.7
SCNBHR53	SEQ ID NO:229	61.9	16	3.4
SCNBHR92	SEQ ID NO:242	85.3	15	5.6
SCNBHRCK	Empty Vector	81.5	16	5

Table 22.

Plasmid_ID	Nucleotide sequence	Avg	n	SE
SCNBHR83	SEQ ID NO:26	75.7	15	5.9
SCNBHRCK	Empty Vector	104.7	14	8.

Table 23.

Plasmid_ID	Nucleotide sequence	Avg	n	SE
SCNBHR44	SEQ ID NO:225	97.9	20	5
SCNBHR60	SEQ ID NO:232	72.3	12	5.8
SCNBHR63	SEQ ID NO:234	102.5	19	5.7
SCNBHR82	SEQ ID NO:25	109.8	17	3.9
SCNBHRCK	Empty Vector	109.6	16	4.8

Table 24.

Plasmid_ID	Nucleotide sequence	Cysts	n	SE
SCNBHR77	SEQ ID NO:239	63	18	3.3
SCNBHRCK	Empty Vector	71	13	4.4

Table 25.

Vector	Nucleotide sequence	Cysts	n	SE
SCNBHR54	SEQ ID NO:230	36	19	2.3
SCNBHR73	SEQ ID NO:238	40	11	1.5
SCNBHRCK	Empty Vector	33	19	2.3

The results of these experiments show that the number of cysts formed on soybean roots expressing at least a polynucleotide sequence having the nucleotide sequence of **SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:230, SEQ ID NO:232** and/or **SEQ ID NO:233** was significantly lower than on transgenic soybean roots comprising the empty vector control. Those skilled in the art would understand that the genomic sequences and/or mRNA plus UTR and ORF sequences corresponding to the above

SEQ ID NOs as provided herein could also be used to reduce nematode parasitism (e.g., **SEQ ID NOs:1, 3, 6, 8, 9, 10, 12, 43, 45, 48, 50, 51, 53, 211, 212, 214, 216, 217**).

Polynucleotides having substantial sequence identity (e.g., at least 80% identity) to the polynucleotides shown above as reducing the number of cysts on soybean roots may also be useful for reducing nematode infestation, cyst number, and the like, in plants. Non-limiting examples of polynucleotides having substantial identity to the nucleotide sequence of **SEQ ID NO:15** include the nucleotide sequences of **SEQ ID NOs: 56-60**; to the nucleotide sequence of **SEQ ID NO:17** includes the nucleotide sequence of **SEQ ID NO:63**; to the nucleotide sequence of **SEQ ID NO:20** includes the nucleotide sequences of **SEQ ID NO:66** and/or **SEQ ID NO:67**; to the nucleotide sequence of **SEQ ID NO:22** includes the nucleotide sequences of **SEQ ID NOs:68-112**; to the nucleotide sequence of **SEQ ID NO:23** includes the nucleotide sequences of **SEQ ID NOs:113-118**; to the nucleotide sequence of **SEQ ID NO:24** includes the nucleotide sequence of **SEQ ID NO:119**; to the nucleotide sequence of SEQ ID NO:26 includes the nucleotide sequences of **SEQ ID NOs:120-124**; to the nucleotide sequence of **SEQ ID NO:227** includes the nucleotide sequences of **SEQ ID NOs:226, 389-398**; to the nucleotide sequence of **SEQ ID NO:228** includes the nucleotide sequences of **SEQ ID NOs:399-401**; to the nucleotide sequence of **SEQ ID NO:230** includes the nucleotide sequences of **SEQ ID NOs:408-633**; and/or to the nucleotide sequence of **SEQ ID NO:232** includes the nucleotide sequences of **SEQ ID NOs:637-642**.

Example 3: Construction of Expression Cassettes and Vectors for Soybean Transformation

The expression cassettes described in Example 1 are used in soybean transformation experiments or different expression cassettes are constructed. At least one nucleic acid comprising a nucleotide sequence selected from the nucleotide sequences of any one of **SEQ ID NOs:1-28, 43-134, 210-242, 261-664** or nucleotide sequences encoding the polypeptide having the amino acid sequence of any one of **SEQ ID NOs:29-42, 135-209, 243-260, 665-1046**, is cloned into an expression cassette and the expression cassette cloned into a binary vector for the generation of transgenic soybean plants. The genetic material to be transferred to the soybean plant is cloned between the left border and the right border of the binary vector. One such expression cassette has the structure: eFMV:e35S:prAct2(including Act2 intron): cEVO18010081 (**SEQ ID NO:24**):tNOS. The cEVO18010081 (**SEQ ID NO:24**) expression cassette and a second expression cassette encoding a selectable marker are cloned into a binary vector to create 20944 EVO shown in **Figure 3**. Another exemplary expression

cassette has the structure: eFMV:e35S:prAct2(including Act2 intron): cEVO18010044 (**SEQ ID NO:224**):tNOS.

The binary vector comprising an expression cassette described above is introduced into an *Agrobacterium tumefaciens* strain (e.g., EHA101), using electroporation. Single bacterial colonies containing the binary vector are selected to confirm the presence of intact vector and used for further experiments.

Example 4: Production of Transgenic Soybean

Transformation of soybean to produce transgenic soybean plants was accomplished using targets prepared from germinated seeds of variety Williams 82 via Agrobacterium tumefaciens-mediated transformation as described here. Mature soybean seeds were harvested, dried and sterilized with chlorine gas. Sterilized seeds were placed in laminar flow hoods for 2 weeks before germination. Seeds were placed on germinated media for 15 to 40 hours for germination. Explants were prepared as described in Khan (US patent application 20040034889) using germinated seeds by removing hypocotyls, one cotyledon and primary leaf primordial. The explants were then wounded by gentle wounding at the cotyledonary nodal region and also apical regions. Explants were then infected with Agrobacterium strain EHA101 containing appropriate binary vector. Infected explants were co-cultured in co-cultivation media as described in Hwang et al 2008 (WO08112044). Excess A. tumefaciens suspension was then removed by aspiration and explants were moved to plates containing a non-selective co-culture medium. Explants were co-cultured with the remaining A. tumefaciens at 23°C for 4 days in the dark. Explants were then transferred to recovery medium supplemented with an antibiotics mixture consisting of ticarcillin (75 mg/L), cefotaxime (75 mg/L) and vancomycin (75 mg/l) and incubated in the dark for seven days as described in Hwang et al 2008 (WO08112044). Explants were then transferred to regeneration medium containing glyphosate (75 to 100 uM) and a mixture of antibiotics consisting of ticarcillin (75 mg/L), cefotaxime (75 mg/L) and vancomycin (75 mg/l) to inhibit and kill *A. tumefaciens*. Shoot elongation was carried out in elongation media containing glyphosate (50 uM). The EPSPS gene was used as a selectable marker during the transformation process. Regenerated plantlets were transplanted to soil as described in Que et al (WO08112267) and tested for the presence of both EPSPS marker gene and spectinomycin resistance (Spec) sequences by TaqMan PCR analysis (Ingham et al., 2001). This screen allows for the selection of transgenic events that carry the T-DNA and are free of vector backbone DNA. Plants positive for EPSPS gene sequences and negative for the Spec gene

were transferred to the greenhouse for analysis of miRNA expression seed setting. Using this method, genetic elements within the left and right border regions of the transformation plasmid are efficiently transferred and integrated into the genome of the plant cell, while genetic elements outside these border regions are generally not transferred.

When the roots are about 2–3 inches, they are transplanted into 1-gallon pots using Fafard #3 soil and 30 grams of incorporated Osmocote Plus 15–9–12. They are watered in thoroughly and placed in the cubicle under florescent lighting set to a 16-hour day. The temperatures are about 85 °F (29.4 °C) during the day and about 70 °F (21 °C) at night. Plants are watered at least once daily.

The plants remain in the cubicle until secondary Taqman sampling has been performed, typically 1–2 weeks. The plants are then placed on an automatic drip watering system and watered twice daily. A cage is placed over the plant, and it may be pruned very lightly if needed. The lighting is a combination of Metal Halide and Sodium Vapor fixtures with 400- and 1000-watt bulbs with a 10-hour day period. The outside wall is darkened to keep out light that would extend the day length. Temperatures are set at about 79 °F (26 °C) during the day and about 70 °F (21 °C) at night. The humidity is ambient.

The plants are maintained in this manner until pods reach maturity, approximately 100 days based on the date of the Taqman selection. The pods are then harvested, placed in a paper bag, air-dried for about 2-days, and then machine dried at about 80 °F (27 °C) for 2-additional days. The pods are shelled and the T1 seeds are harvested and stored at about 4 °C until further testing.

Wild type Williams 82 or null segregants of the T1 generation are used as a control in the SCN assay. Alternatively, a control in the SCN assay can be a plant transformed with an empty vector such as shown in Figure 4 (i.e., an identical expression cassette but without a nucleotide sequence of **SEQ ID NOs:1-28**, **SEQ ID NOs: 43-134**, **SEQ ID NOs:210-242,** or **SEQ ID NOs:261-644**, and/or a nucleotide sequence encoding one or more polypeptides having the amino acid sequence of **SEQ ID NOs: 29-42, SEQ ID NOs:135-209, SEQ ID NOs:243-260,** or **SEQ ID NOs:665-1046**.

Example 5: Evaluation of cyst formation in the transformed soybean plants

Soybean plants transformed with the expression cassette harboring at least one nucleotide sequence of any one of the nucleotide sequences of **SEQ ID NOs:1-28**, **SEQ ID NOs: 43-134**, **SEQ ID NOs:210-242, SEQ ID NOs:261-644**, or a nucleotide sequence encoding any one of the polypeptides having the amino acid sequence of any one of **SEQ ID**

NOs: 29-42, SEQ ID NOs:135-209, SEQ ID NOs:243-260, or **SEQ ID NOs:665-1046** are inoculated with J2 stage soybean cyst nematodes (SCN J2). 3-week old transgenic T1 generation soybean seedlings grown in germination pouches individually are inoculated with SCN J2 suspension at the level of 500 J2 per plant. The soybean plants were cultured at 27 °C in a growth chamber with 16 hours per day of light period.

One month after nematode inoculation, the number of cysts is determined for both the transgenic soybean plants comprising the at least one nucleotide sequence as set forth above and for the null segregants (plants not having a nucleic acid of the invention) from the same T0 parents.

Example 6. Evaluation of the role of selected recombinant nucleic acids in resistance and/or tolerance to nematodes.

To validate the role of selected polynucleotides of the invention in plant resistance and or tolerance to nematodes the selected polynucleotides were over-expressed in plants, as follows.

Cloning strategy Selected polynucleotides having a nucleotide sequence of **SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:228,** or **SEQ ID NO:1047** were cloned into binary vectors for the generation of transgenic plants.

For cloning, the full-length open reading frame (ORF) was first identified. In case of ORF-EST clusters and in some cases already published mRNA sequences were analyzed to identify the entire open reading frame by comparing the results of several translation algorithms to known proteins from other plant species. To clone the full-length cDNAs, reverse transcription (RT) followed by polymerase chain reaction (PCR; RT-PCR) was performed on total RNA extracted from roots, leaves, flowers, siliques or other plant tissues, growing under normal and different treated conditions. Total RNA was extracted using methods well known in the art. Production of cDNA and PCR amplification was performed using standard protocols, which are well known to those skilled in the art (*See,* e.g., Sambrook J., E.F. Fritsch, and T. Maniatis. 1989. *Molecular cloning: a laboratory manual,* 2nd Ed. Cold Spring Harbor Laboratory Press, New York). PCR products were purified using PCR purification kit (Qiagen). In those instances where the entire coding sequence was not identified, RACE kit from Invitrogen (RACE = Rapid Amplification of cDNA Ends) was used to access the full cDNA transcript of the gene from the RNA samples described above.

RACE products were cloned into high copy vector followed by sequencing or directly sequenced. The information from the RACE procedure was used for cloning of the full length ORF of the corresponding genes.

When genomic DNA was cloned, the genes were amplified by direct PCR on genomic DNA extracted from leaf tissue using the DNAeasy kit (Qiagen Cat. No. 69104). Typically, 2 sets of primers were synthesized for the amplification of each gene from a cDNA or a genomic sequence; an external set of primers and an internal set (nested PCR primers). When needed, an additional primer (or two) of the nested PCR primers was used.

To facilitate the cloning of the cDNAs/ genomic sequences, an 8-12 bp extension was added to the 5' of each primer. The primer extension includes an endonuclease restriction site. The restriction sites were selected using two parameters: (a) the site does not exist in the cDNA sequence, and (b) the restriction sites in the forward and reverse primers are designed such that the digested cDNA is inserted in the sense formation into the binary vector that is utilized for transformation.

Each digested PCR product was inserted into a high copy vector pUC19 (New England BioLabs Inc) or into plasmids originating from this vector. In some cases, the undigested PCR product can be inserted into pCR-Blunt II-TOPO (Invitrogen).

Sequencing of the amplified PCR products was performed, using ABI 377 sequencer (Amersham Biosciences Inc). In some cases, after confirming the sequences of the cloned genes, the cloned cDNA was introduced into a modified pGI binary vector containing the At6669 promoter (**SEQ ID NO:1063)** via digestion with appropriate restriction endonucleases. The insert is then followed by single copy of the NOS terminator (Vancanneyt et al. *Molecular Genetics and Genomics* 220, 245-50, 1990). The digested products and the linearized plasmid vector were ligated using T4 DNA ligase enzyme (Roche, Switzerland). High copy plasmids containing the cloned genes were digested with the restriction endonucleases (New England BioLabs Inc) according to the sites designed in the primers and cloned into binary vectors.

Several DNA sequences of the selected genes were synthesized by a commercial supplier GeneArt (www.geneart.com). Synthetic DNA was designed *in silico*. Suitable restriction enzymes sites were added to the cloned sequences at the 5' end and at the 3' end to enable later cloning into the pQFNc binary vector downstream of the At6669 promoter

Binary vectors used for cloning: The plasmid pPI was constructed by inserting a synthetic poly-(A) signal sequence, originating from pGL3 basic plasmid vector (Promega, Acc No U47295; bp 4658-4811) into the *Hind*III restriction site of the binary vector pBI101.3

(Clontech, Acc. No. U12640). pGI (pBXYN) is similar to pPI, but the original gene in the backbone, the GUS gene, was replaced by the GUS-Intron gene followed by the NOS terminator. pGI was used in the past to clone the polynucleotide sequences, initially under the control of 35S promoter (Odell et al. *Nature* 313, 810 - 812 (28 February 1985)).

The modified pGI vectors (pQXNc (**Fig. 7**); or pQFN (**Fig. 6**), pQFNc (**Fig. 6**) or pQYN 6669 (**Fig. 5**) are modified versions of the pGI vector in which the cassette was inverted between the left and right borders so the gene and its corresponding promoter are close to the right border and the NPTII gene is close to the left border.

At6669, the *Arabidopsis thaliana* promoter sequence (**SEQ ID NO:1063**) was inserted in the modified pGI binary vector, upstream to the cloned genes, followed by DNA ligation and binary plasmid extraction from positive *E. coli* colonies, as described above.

Colonies were analyzed by PCR using the primers covering the insert which were designed to span the introduced promoter and gene. Positive plasmids were identified, isolated and sequenced.

For cloning of each gene at least 2 primers were used, forward and reverse. In some cases, four primers were used: external forward, external reverse, nested forward or nested reverse. The genes were cloned from the indicated organism, except for the genes that were synthetically produced by GeneArt.

Example 7. Producing transgenic Arabidopsis plants expressing selected polynucleotides.

Production of Agrobacterium tumefaciens cells harboring the binary vectors according to some embodiments of the invention. Each of the binary vectors described in Example 6 above was used to transform Agrobacterium cells. An additional binary construct, having only the At6669 promoter was used as negative control. The binary vectors were introduced to *Agrobacterium tumefaciens* GV301, or LB4404 competent cells (about 10^9 cells/mL) by electroporation. The electroporation was performed using a MicroPulser electroporator (Biorad), 0.2 cm cuvettes (Biorad) and EC-2 electroporation program (Biorad). The treated cells were cultured in LB liquid medium at 28 °C for 3 hours, then plated over LB agar supplemented with gentamycin (50 mg/L; for *Agrobacterium* strains GV301) or streptomycin (300 mg/L; for *Agrobacterium* strain LB4404) and kanamycin (50 mg/L) at 28 °C for 48 hours. Agrobacterium colonies, which were developed on the selective media, were further analyzed by PCR using the primers designed to span the inserted sequence in the pPI plasmid. The resulting PCR products were isolated and sequenced to verify that the correct

polynucleotide sequences of the invention were properly introduced to the Agrobacterium cells.

Preparation of Arabidopsis plants for transformation - *Arabidopsis thaliana* var Columbia (T_0 plants) were transformed according to the floral dip procedure (Clough et al. (1998) *Plant J.* 16(6): 735-43; and Desfeux et al. (2000) *Plant Physiol.* 123(3): 895-904) with minor modifications. Briefly, *Arabidopsis thaliana* Columbia (Col0) T_0 plants were sown in 250 ml pots filled with wet peat-based growth mix. The pots were covered with aluminum foil and a plastic dome, kept at 4 °C for 3–4 days, then uncovered and incubated in a growth chamber at 18–24 °C under 16/8 hours light/dark cycles. The T_0 plants were ready for transformation six days before anthesis.

Preparation of the Agrobacterium carrying the binary vectors to transformation into Arabidopsis plants - Single colonies of Agrobacterium carrying the binary vectors harboring the genes of some embodiments of the invention were cultured in LB medium supplemented with kanamycin (50 mg/L) and gentamycin (50 mg/L). The cultures were incubated at 28 °C for 48 hours under vigorous shaking and centrifuged at 4000 rpm for 5 minutes. The pellets comprising Agrobacterium cells were resuspended in a transformation medium which contains half-strength (2.15 g/L) Murashige-Skoog (Duchefa); 0.044 μM benzylamino purine (Sigma); 112 μg/L B5 Gambourg vitamins (Sigma); 5 % sucrose; and 0.2 ml/L Silwet L-77 (OSI Specialists, CT) in double-distilled water, at pH of 5.7.

Transformation of Arabidopsis plants with the Agrobacterium - Transformation of T_0 plants was performed by inverting each plant into an Agrobacterium suspension such that the above ground plant tissue is submerged for 3-5 seconds. Each inoculated T_0 plant was immediately placed in a plastic tray, then covered with clear plastic dome to maintain humidity and was kept in the dark at room temperature for 18 hours to facilitate infection and transformation. Transformed (transgenic) plants were then uncovered and transferred to a greenhouse for recovery and maturation. The transgenic T_0 plants were grown in the greenhouse for 3-5 weeks until siliques are brown and dry, then seeds were harvested from plants and kept at room temperature until sowing.

Generation of T1 and T2 transgenic plants - For generating T_1 and T_2 transgenic plants harboring the genes, seeds collected from transgenic T_0 plants were surface-sterilized by soaking in 70 % ethanol for 1 minute, followed by soaking in 5 % sodium hypochlorite and 0.05 % triton for 5 minutes. The surface-sterilized seeds were thoroughly washed in sterile distilled water then placed on culture plates containing half-strength Murashig-Skoog

(Duchefa); 2 % sucrose; 0.8 % plant agar; 50 mM kanamycin; and 200 mM carbenicylin (Duchefa). The culture plates were incubated at 4 °C for 48 hours then transferred to a growth room at 25 °C for an additional week of incubation. Vital T_1 Arabidopsis plants were transferred to a fresh culture plates for another week of incubation. Following incubation the T_1 plants were removed from culture plates and planted in growth mix contained in 250 ml pots. The transgenic plants were allowed to grow in a greenhouse to maturity. Seeds harvested from T_1 plants were cultured and grown to maturity as T_2 plants under the same conditions as used for culturing and growing the T_1 plants.

Example 8. Evaluation of transgenic Arabidopsis for reduced infection by nematodes.

The binary expression vector described above, pQFN or pQFNc including the At6669 promoter containing at least one nucleic acid of the invention or an empty vector (without a nucleic acid of the invention) were transformed into Arabidopsis to test the ability of the binary vector to express a protein that is capable of reducing sugar beet cyst nematode (BCN) cysts. Arabidopsis cultivar Columbia-0 was used as the germplasm for transformation. Arabidopsis seeds were germinated on 3% phytagel containing 0.5% sucrose in 1.5ml tubes at approximately 25 °C for 10 days. Individual plants, 5 to 10 plants per event and 3 to 7 events per SEQ ID, were then transferred to 0.25 liter pots containing sand and grown for additional 10 days in the green house. The pots were then inoculated with J2 stage sugar beet cyst nematodes (BCN J2) and plants were grown in green house at about 25 °C, which allows cyst formation on the root of the plants. One month after nematode inoculation, the number of cysts was determined for both the roots expressing at least one of the polynucleotides of **SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:228**, or **SEQ ID NO:1047** and the roots expressing the empty vector (as a negative control). The experiment was repeated at least one time.

Table 26. Genes showing reduced plant infection to nematodes.

		Nematode female cysts per plant			
SEQ ID NO	Event #	Mean	SE (±)	p-Value	% of control
Empty vector control	Mix135	9.89	1.20	1.00	-
SEQ ID NO:1047	61990.12	2.90	0.75	<.0001	29
SEQ ID NO:1047	61991.13	7.10	1.67	0.34	72
SEQ ID NO:1047	61995.2	6.10	0.74	0.08	62
SEQ ID NO:228	60025.11	1.00	0.52	<.0001	10

SEQ ID NO:228	62025.7	6.50	0.79	0.15	66
SEQ ID NO:228	62026.11	6.67	1.81	0.22	67
SEQ ID NO:16	62118.11	3.09	0.59	<.0001	31
SEQ ID NO:16	62118.12	3.10	0.66	0.00	31
SEQ ID NO:16	62121.6	3.30	0.60	0.00	33
SEQ ID NO:16	62122.4	3.80	1.28	0.00	38
SEQ ID NO:16	62392.4	2.50	0.91	<.0001	25

Table 27. Genes showing reduced plant infection to nematodes.

		Nematode female cysts per plant			
SEQ ID NO	Event #	Mean	SE (±)	p-Value	% of control
Empty vector control	mix138-b	11.5	0.63	1	-
SEQ ID NO:18	61888.3	5.5556	1.11	0.012	48
SEQ ID NO:18	61888.4	2.8889	0.66	<.0001	25
SEQ ID NO:18	61889.1	4.8889	1.18	0.0033	43
SEQ ID NO:18	61890.4	5.8889	1.55	0.0219	51
SEQ ID NO:18	61891.2	7.1111	1.46	0.1417	62
SEQ ID NO:24	61895.1	4	1.02	0.0013	35
SEQ ID NO:24	61896.1	4.75	0.68	0.0036	41
SEQ ID NO:24	61896.3	6.4	1.3182	0.0418	56
SEQ ID NO:24	61896.5	4.9	0.836	0.0024	43
SEQ ID NO:24	61896.6	3.5	0.85	<.0001	30
SEQ ID NO:24	61897.1	5.2	1.96	0.033	45
SEQ ID NO:24	61897.3	3.8	1	0.0002	33
SEQ ID NO:24	61898.1	3.2857	0.81	0.0003	29
SEQ ID NO:17	62236.3	5.2	1.27	0.0045	45
SEQ ID NO:17	62237.2	2	0.67	<.0001	17
SEQ ID NO:17	62237.3	3.1111	0.93	<.0001	27
SEQ ID NO:17	62239.2	3.4	1.63	0.0018	30
SEQ ID NO:17	62240.4	6.1	1.83	0.0251	53

Table 28. Genes showing reduced plant infection to nematodes.

		Nematode female cysts per plant			
SEQ ID NO	Event #	Mean	SE (±)	p-Value	% of control
Empty vector control	Mix136	5.33	0.62	1	-
SEQ ID NO:15	61433.2	1.17	0.31	0.0241	22
SEQ ID NO:15	61454.2	1.83	0.75	0.1045	34
SEQ ID NO:15	61455.4	2.67	1.59	0.4177	50
SEQ ID NO:15	61457.2	2.5	0.85	0.3301	47
SEQ ID NO:19	61535.5	2.33	0.56	0.2553	44
SEQ ID NO:19	61536.5	2.17	0.6	0.1934	41
SEQ ID NO:19	61536.6	3.67	0.72	0.9621	69

SEQ ID NO:26	62570.3	1.33	0.49	0.0358	25
SEQ ID NO:26	62570.4	0.83	0.31	0.0104	16
SEQ ID NO:26	62570.5	0.75	0.75	0.0284	14
SEQ ID NO:26	62571.1	0.83	0.54	0.0104	16
SEQ ID NO:26	62573.5	0.17	0.17	0.0016	3
SEQ ID NO:26	62573.6	1.5	0.67	0.0522	28
SEQ ID NO:26	62873.3	0.67	0.33	0.0066	13
SEQ ID NO:26	62576.4	0.2	0.2	0.0035	4
SEQ ID NO:27	62578.1	0.83333	0.4	0.0104	16
SEQ ID NO:27	62578.3	0.8	0.8	0.0164	15
SEQ ID NO:27	62578.4	0.5	0.34	0.0042	9
SEQ ID NO:27	62579.1	1.16667	0.48	0.0241	22
SEQ ID NO:27	62579.2	0.66667	0.33	0.0066	13

Table 29. Genes showing reduced plant infection to nematodes.

		Nematode female cysts per plant			
Gene name (SEQ ID NO)	Event #	Mean	SE (±)	p-Value	% of control
Empty vector control	Mix135	8.75	2.25	1	-
SEQ ID NO:23	61448.2	2.86	1	0.0003	33
SEQ ID NO:23	61448.3	1.43	0.65	<.0001	16
SEQ ID NO:23	61449.1	2.14	1.16	<.0001	24
SEQ ID NO:23	61449.3	2.14	0.8	<.0001	24
SEQ ID NO:23	61450.1	1.67	0.49	<.0001	19
SEQ ID NO:23	61450.2	0	0	<.0001	0
SEQ ID NO:23	61450.4	0.5	0.27	<.0001	6
SEQ ID NO:23	61452.4	1.75	0.85	0.0001	20
SEQ ID NO:20	61724.1	0	0	<.0001	0
SEQ ID NO:20	61724.4	0.71	0.57	<.0001	8
SEQ ID NO:20	61725.2	3	1.2	0.0004	34
SEQ ID NO:20	61725.3	0	0	<.0001	0
SEQ ID NO:20	61725.6	0	0	<.0001	0
SEQ ID NO:20	61726.2	2.3	0.7	<.0001	26
SEQ ID NO:20	61727.3	1.4	0.75	<.0001	16
SEQ ID NO:22	62124.3	3.5	2.22	0.0081	40
SEQ ID NO:22	62125.1	0.43	0.2	<.0001	5
SEQ ID NO:22	62125.3	0	0	<.0001	0
SEQ ID NO:22	62126.1	1.57	0.69	<.0001	18
SEQ ID NO:22	62126.3	4.33	1.67	0.0731	50
SEQ ID NO:22	62129.2	1	0.41	<.0001	11

Results of these experiments (**Tables 26-29**) indicate that the number of cysts formed on Arabidopsis roots expressing, for example, at least one polynucleotide having the

nucleotide sequence of **SEQ ID NOs:16, 20, 22, 23, 24, 26, 27, 228** and/or **1047** was significantly lower than on transgenic soybean roots comprising the empty vector control.

Similar to the polynucleotides identified as reducing nematode cyst development on soybean hairy root, polynucleotides having substantial sequence identity (e.g., at least 80% identity) to the polynucleotides shown above as reducing the number of cysts on Arabidopsis roots may also be useful for reducing nematode infestation, cyst number and the like, in plants. Non-limiting examples of polynucleotides having substantial identity to the nucleotide sequence of **SEQ ID NO:16** include **SEQ ID NO:61** and/or **SEQ ID NO:62**; to the nucleotide sequence of **SEQ ID NO:20** includes the nucleotide sequences of **SEQ ID NO:66** and/or **SEQ ID NO:67**; to the nucleotide sequence of **SEQ ID NO:22** includes the nucleotide sequences of **SEQ ID NOs:68-112**; to the nucleotide sequence of **SEQ ID NO:23** includes the nucleotide sequences of **SEQ ID NOs:113-118**; to the nucleotide sequence of **SEQ ID NO:24** includes **SEQ ID NO:119**; to the nucleotide sequence of **SEQ ID NO:26** includes the nucleotide sequences of **SEQ ID NOs:120-124**; to the nucleotide sequence of **SEQ ID NO:27** includes the nucleotide sequences of **SEQ ID NOs:125-127**; and/or to the nucleotide sequence of **SEQ ID NO:228** includes the nucleotide sequences of **SEQ ID NOs:399-401**.

Altogether, the results from **Tables 1-29** show that the polynucleotides/polypeptides of the invention can be useful for increasing resistance and or tolerance to plant nematodes.

The foregoing is illustrative of the invention, and is not to be construed as limiting thereof. The invention is defined by the following claims, with equivalents of the claims to be included therein.

AS CLAIMED HEREIN:

1. A method of controlling a nematode plant pest, comprising contacting the nematode plant pest with a transgenic plant, or part thereof, having incorporated into its genome a recombinant nucleic acid molecule that modulates the expression of one or more polypeptides selected from the group consisting of **SEQ ID NOs:29-42, SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046,** and any combination thereof, thereby controlling the nematode plant pest.

2. The method of claim 1,wherein the recombinant nucleic molecule comprises a nucleotide sequence operatively linked to a promoter functional in a plant or plant cell, and wherein the nucleotide sequence is selected from the group consisting of:

(a) a nucleotide sequence of any one of **SEQ ID NOs:1-28, SEQ ID NOs: 43-134, SEQ ID NOs:210-242, SEQ ID NOs:261-644**;

(b) a nucleotide sequence that encodes a polypeptide comprising an amino acid sequence of any one of **SEQ ID NOs:29-42, SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046**;

(c) a nucleotide sequence having at least 70% sequence identity to the nucleotide sequence of (a) or (b);

(d) a nucleotide sequence which anneals under stringent hybridization conditions to the nucleotide sequence of (a), (b) or (c), or a complement thereof;

(e) a nucleotide sequence that differs from the nucleotide sequences of (a), (b), (c) or (d) above due to the degeneracy of the genetic code; and

(f) any combination of the nucleotide sequences of (a)-(e).

3. The method of claim 1, wherein the recombinant nucleic acid molecule is capable of producing a double stranded RNA comprising an antisense strand and a sense strand, wherein the antisense strand is complementary to a portion of a nucleotide sequence encoding the one or more polypeptides, the portion comprising about 18 to about 25 consecutive nucleotides having substantial sequence identity to any one of **SEQ ID NOs:1-28, SEQ ID NOs: 43-134, SEQ ID NOs:210-242, SEQ ID NOs:261-644,** or any combination thereof.

4. The method of claim 1 or claim 2, wherein the recombinant nucleic acid molecule modulates the expression by causing overexpression of the one or more polypeptides in the transgenic plant.

5. The method of claim 1 or claim 3, wherein the recombinant nucleic acid molecule modulates the expression by causing the reduction of or reducing the expression of the one or more polypeptides in the transgenic plant.

6. The method of any one of claim 1 to 5, wherein the transgenic plant or plant part is a transgenic soybean plant, a transgenic sugar beet plant, a transgenic corn plant, a transgenic cotton plant, a transgenic canola plant, a transgenic wheat plant, or a transgenic rice plant, or a part thereof.

7. The method of any one of claims 1 to 6, wherein the nematode pest is selected from the group consisting of: a cyst nematode (*Heterodera* spp.), a root knot nematode (*Meloidogyne* spp.), a lance nematode (*Hoplolaimus* spp.), a stunt nematode (*Tylenchorhynchus* spp.), a spiral nematode (*Helicotylenchus* spp.), a lesion nematode (*Pratylenchus* spp.), a sting nematode (*Belonoluimus* spp.), a reniform nematode (*Rotylenchulus reniformis*), a burrowing nematode (*Radopholus similis*), a ring nematode (*Criconema* spp.), and any combination thereof.

8. The method of claim 7, wherein the nematode is a soybean cyst nematode or a sugar beet cyst nematode.

9. A transgenic plant, or part thereof, having incorporated into its genome a recombinant nucleic acid molecule that modulates the expression of one or more polypeptides selected from the group consisting of **SEQ ID NOs:29-42, SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046,** and any combination thereof, wherein the transgenic plant is resistant to a nematode pest.

10. A seed from the transgenic plant of claim 9.

11. A recombinant nucleic acid molecule comprising a nucleotide sequence operatively linked to a promoter functional in a plant, wherein the nucleotide sequence is selected from the group consisting of:

(a) a nucleotide sequence of any one of **SEQ ID NOs:1-28, SEQ ID NOs: 43-134, SEQ ID NOs:210-242, SEQ ID NOs:261-644**;

(b) a nucleotide sequence that encodes a polypeptide comprising an amino acid sequence of any one of **SEQ ID NOs:29-42, SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046**;

(c) a nucleotide sequence having at least 70% sequence identity to the nucleotide sequence of (a) or (b);

(d) a nucleotide sequence which anneals under stringent hybridization conditions to the nucleotide sequence of (a), (b) or (c), or a complement thereof;

(e) a nucleotide sequence that differs from the nucleotide sequences of (a), (b), (c) or (d) above due to the degeneracy of the genetic code; and

(f) any combination of the nucleotide sequences of (a)-(e).

12. A recombinant nucleic acid molecule capable of producing a double stranded RNA comprising an antisense strand and a sense strand, wherein the antisense strand is complementary to a portion of a nucleotide sequence encoding a polypeptide comprising an amino acid sequence of any of **SEQ ID NOs:29-42, SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046**, or any combination thereof, the portion consisting essentially of about 18 to about 25 consecutive nucleotides of any one of **SEQ ID NOs:1-28, SEQ ID NOs: 43-134, SEQ ID NOs:210-242, SEQ ID NOs:261-644**, or any combination thereof.

13. A vector comprising the recombinant nucleic acid molecule of claim 11 or claim 12.

14. A transgenic cell comprising the recombinant nucleic acid molecule of claim 11 or claim 12.

15. The transgenic cell of claim 14 that is a transgenic plant cell.

16. The transgenic plant cell of claim 15, wherein the plant cell is a transgenic soybean plant cell, a transgenic sugar beet plant cell, a transgenic corn plant cell, a transgenic cotton

plant cell, a transgenic canola plant cell, a transgenic sugar cane plant, a transgenic wheat plant cell, or a transgenic rice plant cell.

17. A transgenic plant comprising the transgenic plant cell of claim 15 or claim 16.

18. A seed from the transgenic plant of claim 17, wherein the seed comprises the recombinant nucleic acid molecule.

19. A nematicidal composition comprising a heterologous polypeptide comprising an amino acid sequence of any one of **SEQ ID NOs:29-42, SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046,** or any combination thereof, in an agriculturally acceptable carrier.

20. The nematicidal composition of claim 19, further comprising additional nematicidal or insecticidal compounds.

21. The nematicidal composition of claim 20, wherein the additional nematicidal compound is selected from the group consisting of chloropicrin, metam sodium, metam potassium, dazomet, iodomethane, dimethyl disulfide (DMDS), sulfryl fluoride, oxamyl and fosthiazate.

22. Anematicidal composition comprising the vector of claim 13.

23. A method of producing a transgenic plant, the method comprising introducing into a plant a recombinant nucleic acid molecule of claim 11 or claim 12, thereby producing a transgenic plant having increased resistance to a nematode plant pest.

24. The method of claim 23, wherein the introducing is done by transforming a plant cell and regenerating a transgenic plant or by breeding.

25. The method of claim 23 or claim 24, wherein the nematode plant pest is selected from the group consisting of: a cyst nematode (*Heterodera* spp.), a root knot nematode (*Meloidogyne* spp.), a lance nematode (*Hoplolaimus* spp.), a stunt nematode (*Tylenchorhynchus* spp.), a spiral nematode (*Helicotylenchus* spp.), a lesion nematode (*Pratylenchus* spp.), a sting nematode (*Belonoluimus* spp.), a reniform nematode

(*Rotylenchulus reniformis*), a burrowing nematode (*Radopholus similis*), a ring nematode (*Criconema* spp.), and any combination thereof.

26. A transgenic plant produced by the method of any one of claims 23-25.

27. A transgenic plant having increased resistance to a nematode plant pest produced by the method of any one of claims 23-25.

28. The transgenic plant of any one of claims 23-27, wherein the transgenic plant is a transgenic soybean plant, a transgenic sugar beet plant, a transgenic corn plant, a transgenic cotton plant, a transgenic canola plant, a transgenic wheat plant, or a transgenic rice plant.

29. A method of reducing the infectivity of a nematode plant pest to a plant, comprising contacting the nematode plant pest with the transgenic plant of claim 9 or the nematicidal composition of claim 19, thereby reducing the infectivity of the nematode plant pest to the plant.

30. A method of reducing nematode cyst development by a nematode plant pest, comprising contacting the nematode plant pest with the transgenic plant of claim 9 or the nematicidal composition of claim 19, wherein nematode cyst development by the nematode plant pest on the roots of the plant is reduced.

31. A method of reducing the growth of a nematode plant pest population, comprising contacting the nematode plant pest population with the transgenic plant of claim 9 or the nematicidal composition of claim 19, wherein the growth of a nematode plant pest population is reduced.

32. A method of producing a soybean plant having increased resistance to infestation by a nematode plant pest, the method comprising the steps of (a) crossing the transgenic plant of any one of claims 9, 17 or 26-28 with itself or another plant to produce seed comprising the nucleic acid molecule of claim11 or claim 12, or the vector of claim 13; (b) growing a progeny plant from said seed to produce a plant having increased resistance to infestation by nematode plant pests.

33. The method of claim 32, further comprising (c) crossing the progeny plant with itself or another plant and (d) repeating steps (b) and (c) for an additional 0-7 generations to produce a plant having increased resistance to infestation by nematode plant pests.

34. A crop comprising a plurality of the transgenic plants of any one of claims 9, 17 or 26-28 planted together in an agricultural field.

35. A method of improving yield of a plant crop, comprising: cultivating a plurality of the plants of any one of claims 9, 17 or 26-28 as a plant crop, wherein the plurality of plants of said plant crop have increased resistance to nematode infection, thereby improving the yield of said plant crop.

36. A post-harvest product derived from the plant of any one of claims 26-28.

37. The product of claim 36, wherein the product is seed meal, seed flour, seed oil, sugar or cereals manufactured in whole or in part to contain plant by-products.

FIG. 1

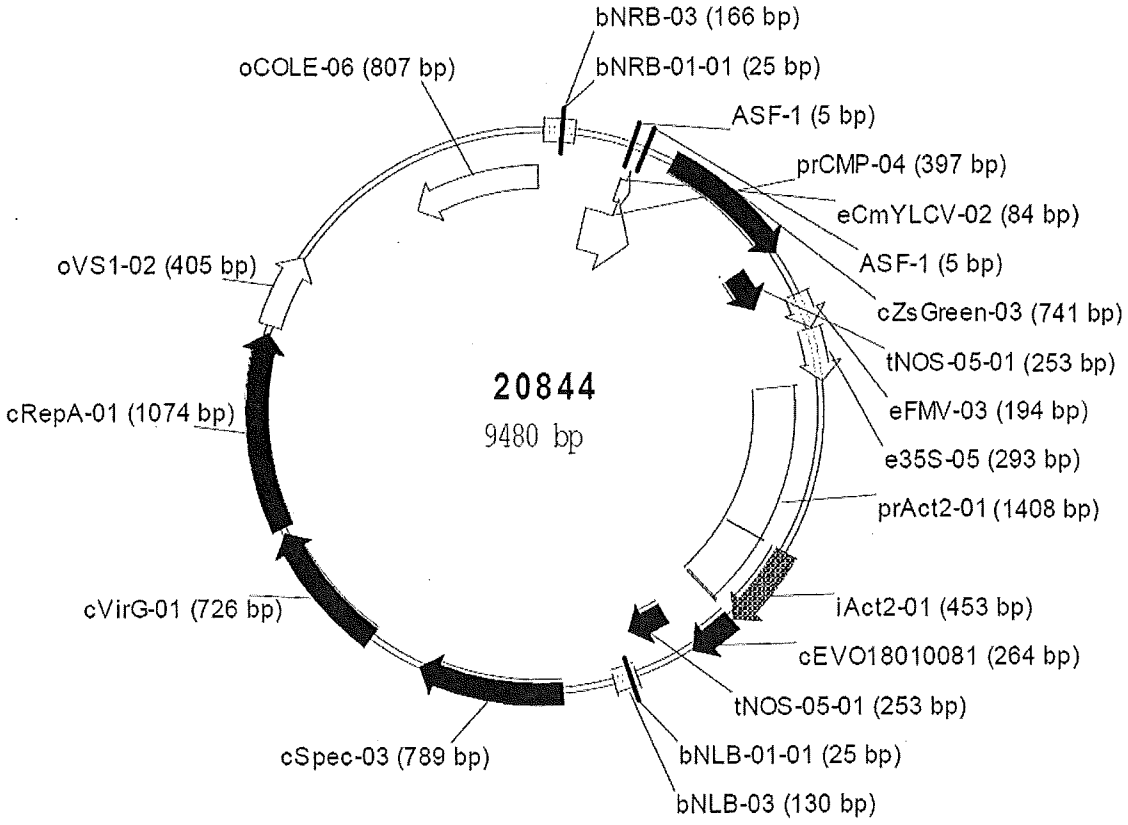

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ASF-1 (5 bp)
prCMP-04 (397 bp)
eCmYLCV-02 (84 bp)
ASF-1 (5 bp)
oVS1-02 (405 bp)
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9480 bp
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prAct2-01 (1408 bp)
iAct2-01 (453 bp)
cVirG-01 (726 bp)
cEVO18010081 (264 bp)
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FIG. 2

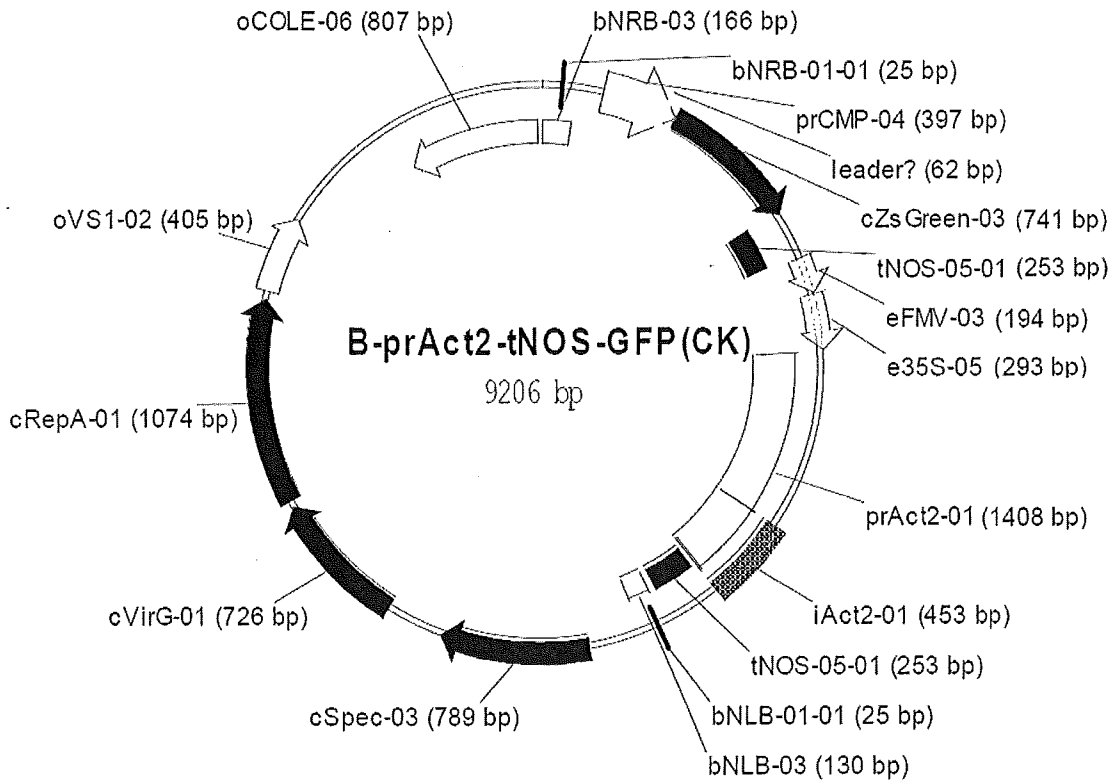

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leader? (62 bp)
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tNOS-05-01 (253 bp)
bNLB-01-01 (25 bp)
bNLB-03 (130 bp)
cSpec-03 (789 bp)
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9206 bp

FIG. 3

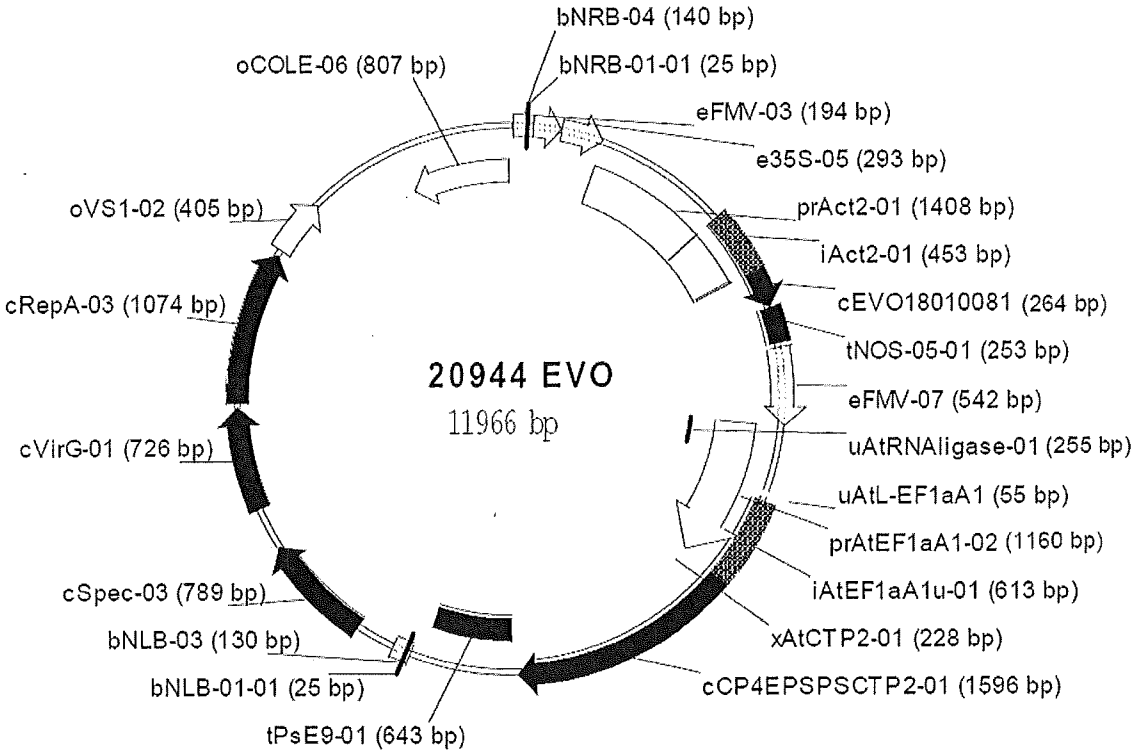
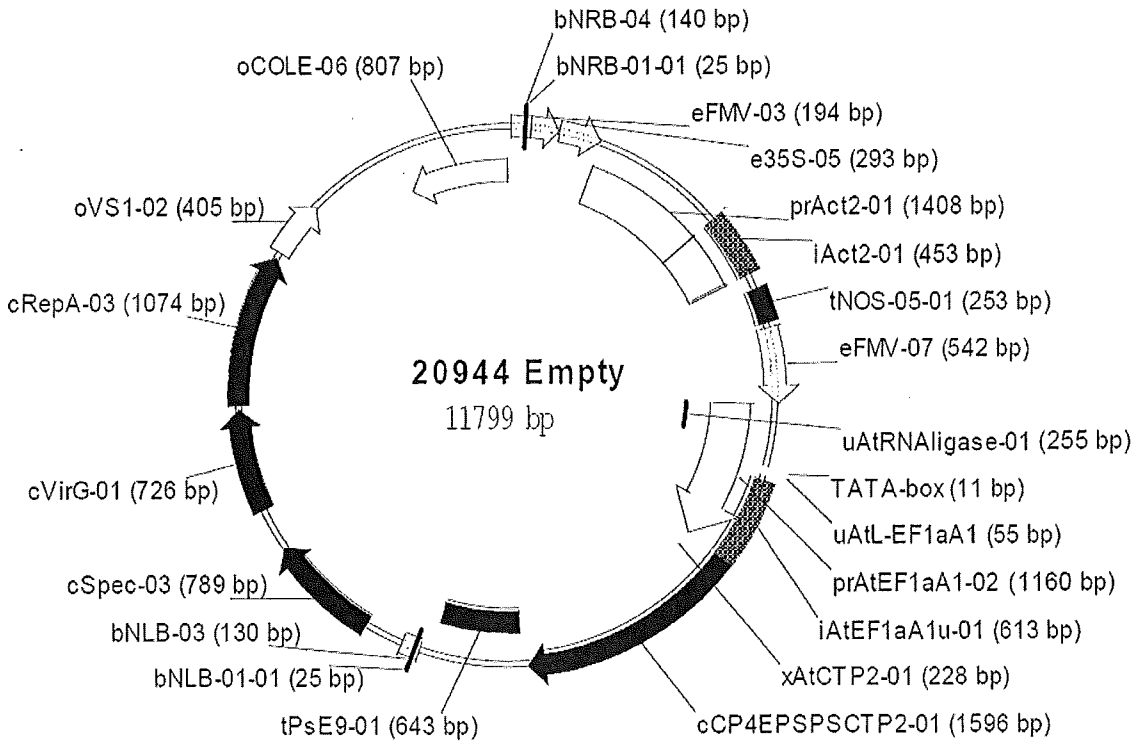
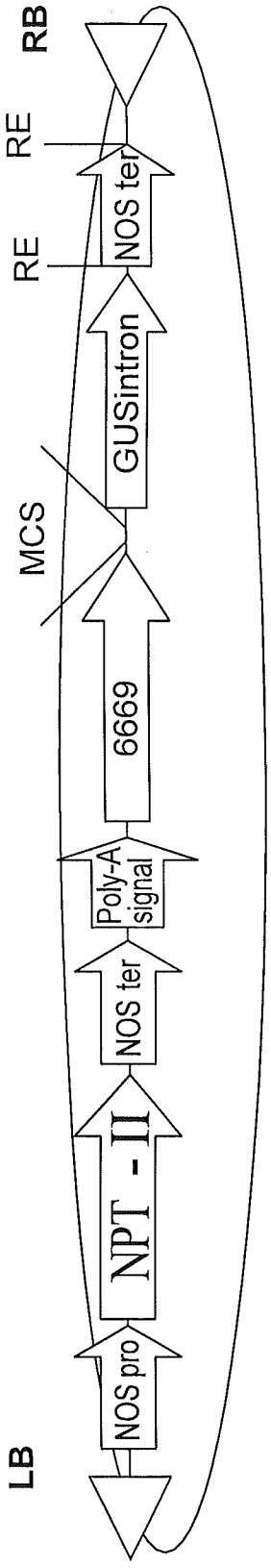

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oCOLE-06 (807 bp)
bNRB-01-01 (25 bp)
eFMV-03 (194 bp)
e35S-05 (293 bp)
oVS1-02 (405 bp)
prAct2-01 (1408 bp)
iAct2-01 (453 bp)
cRepA-03 (1074 bp)
cEVO18010081 (264 bp)
tNOS-05-01 (253 bp)
20944 EVO
11966 bp
eFMV-07 (542 bp)
cVirG-01 (726 bp)
uAtRNAligase-01 (255 bp)
uAtL-EF1aA1 (55 bp)
prAtEF1aA1-02 (1160 bp)
cSpec-03 (789 bp)
iAtEF1aA1u-01 (613 bp)
bNLB-03 (130 bp)
xAtCTP2-01 (228 bp)
bNLB-01-01 (25 bp)
cCP4EPSPSCTP2-01 (1596 bp)
tPsE9-01 (643 bp)

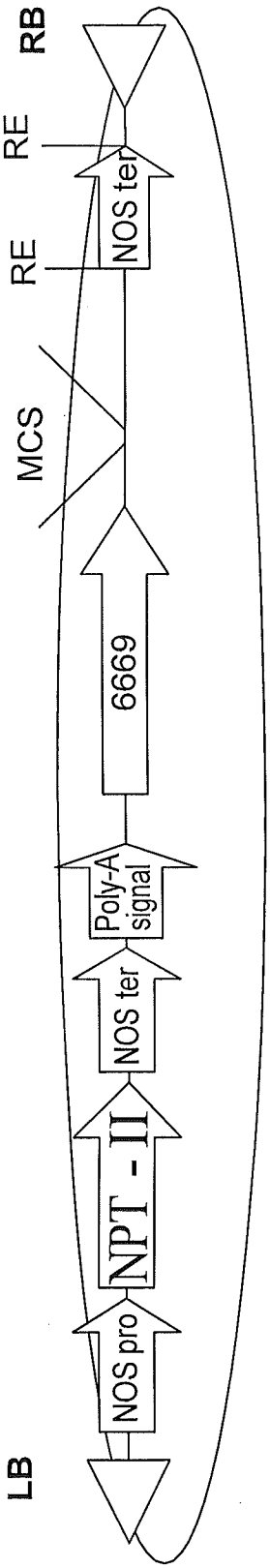
FIG. 4


bNRB-04 (140 bp)
oCOLE-06 (807 bp)
bNRB-01-01 (25 bp)
eFMV-03 (194 bp)
e35S-05 (293 bp)
oVS1-02 (405 bp)
prAct2-01 (1408 bp)
iAct2-01 (453 bp)
cRepA-03 (1074 bp)
tNOS-05-01 (253 bp)
eFMV-07 (542 bp)
20944 Empty
11799 bp
uAtRNAligase-01 (255 bp)
cVirG-01 (726 bp)
TATA-box (11 bp)
uAtL-EF1aA1 (55 bp)
prAtEF1aA1-02 (1160 bp)
cSpec-03 (789 bp)
iAtEF1aA1u-01 (613 bp)
bNLB-03 (130 bp)
xAtCTP2-01 (228 bp)
bNLB-01-01 (25 bp)
tPsE9-01 (643 bp)
cCP4EPSPSCTP2-01 (1596 bp)



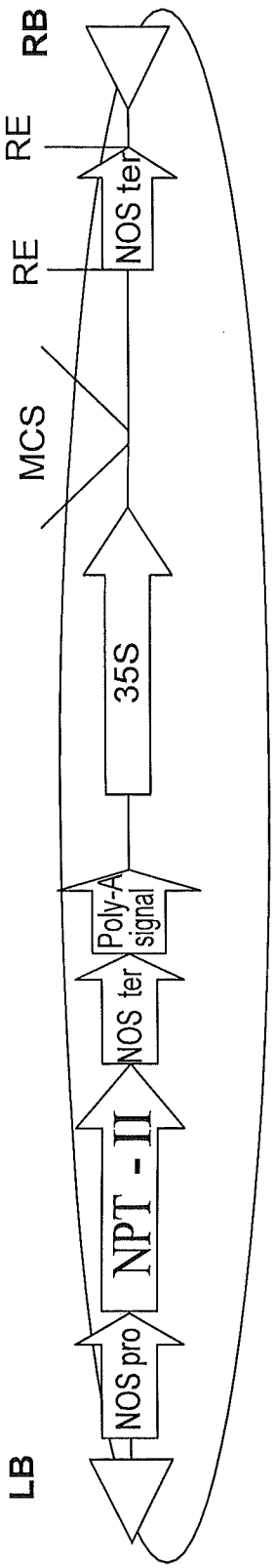
pQYN_6669

FIG. 5



pQFN, pQFNc

FIG. 6



pQXNc

FIG. 7

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2012/065959

A. CLASSIFICATION OF SUBJECT MATTER
IPC(8) - A01H 1/06 (2013.01)
USPC - 800/301
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC(8) - A01H 1/06, 5/00; C07H 21/00; C07K 14/415; C12N 15/11, 15/82 (2013.01)
USPC - 435/320.1; 506/17; 536/23.1; 800/301

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
CPC - C12N 15/113, 15/8218, 15/8285; 2310/14 (2013.01)

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
PatBase, Google Patents, PubMed, NCBI Blast, Google

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	US 2010/0180352 A1 (REN et al) 15 July 2010 (15.07.2010) entire document	1-5, 9-16, 19-24, 29-31
Y	VERCAUTEREN et al. 'Arabidopsis thaliana Genes Expressed in the Early Compatible Interaction with Root-Knot Nematodes.' MPMI Vol. 14, No. 3, 2001, pp. 288–299. entire document	1-5, 9-16, 19-24, 29-31
Y	US 2009/0012029 A1 (HUSSEY et al) 08 January 2009 (08.01.2009) entire document	20, 21
A	US 2005/0091713 A1 (ATKINSON et al) 28 April 2005 (28.04.2005) entire document	1-5, 9-16, 19-24, 29-31
A	WO 2010/121956 A1 (CARDOZA et al) 28 October 2010 (28.10.2008) entire document	1-5, 9-16, 19-24, 29-31

☐ Further documents are listed in the continuation of Box C. ☐

* Special categories of cited documents:
"A" document defining the general state of the art which is not considered to be of particular relevance
"E" earlier application or patent but published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed
"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
14 March 2013	24 APR 2013
Name and mailing address of the ISA/US Mail Stop PCT, Attn: ISA/US, Commissioner for Patents P.O. Box 1450, Alexandria, Virginia 22313-1450 Facsimile No. 571-273-3201	Authorized officer: Blaine R. Copenheaver PCT Helpdesk: 571-272-4300 PCT OSP: 571-272-7774

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2012/065959

Box No. I Nucleotide and/or amino acid sequence(s) (Continuation of item 1.c of the first sheet)

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application, the international search was carried out on the basis of a sequence listing filed or furnished:

   a. (means)

   ☐ on paper

   ☒ in electronic form

   b. (time)

   ☐ in the international application as filed

   ☒ together with the international application in electronic form

   ☐ subsequently to this Authority for the purposes of search

2. ☐ In addition, in the case that more than one version or copy of a sequence listing has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that in the application as filed or does not go beyond the application as filed, as appropriate, were furnished.

3. Additional comments:

SEQ ID NOs: 15 and 29 were searched

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2012/065959

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☒ Claims Nos.: 6-8, 17, 18, 25-28, 32-37
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

See Extra Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-5, 9-16, 19-24, and 29-31, limited to a method of controlling a nematode plant pest, having incorporated into its genome a recombinant nucleic acid molecule that modulates the expression of one or more polypeptides selected to be SEQ ID NO:29; wherein the recombinant nucleic molecule comprises a nucleotide sequence operatively linked to a promoter functional in a plant or plant cell, and wherein the nucleotide sequence is selected be SEQ ID NO:15.

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2012/065959

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees need to be paid.

Group I+: claims 1-5, 9-16, 19-24, and 29-31 are drawn to a method of controlling a nematode plant pest, comprising contacting the nematode plant pest with a transgenic plant, or part thereof, having incorporated into its genome a recombinant nucleic acid molecule that modulates the expression of one or more polypeptides selected from the group consisting of SEQ ID NOs:29-42, SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046, and any combination thereof, thereby controlling the nematode plant pest.

The first invention is restricted to a method of controlling a nematode plant pest, comprising contacting the nematode plant pest with a transgenic plant, or part thereof, having incorporated into its genome a recombinant nucleic acid molecule that modulates the expression of one or more polypeptides selected to be SEQ ID NO:29; wherein the recombinant nucleic molecule comprises a nucleotide sequence operatively linked to a promoter functional in a plant or plant cell, and wherein the nucleotide sequence is selected be SEQ ID NO:15.

The exact claims searched will depend on Applicant's election. An exemplary election would be a method of controlling a nematode plant pest, comprising contacting the nematode plant pest with a transgenic plant, or part thereof, having incorporated into its genome a recombinant nucleic acid molecule that modulates the expression of one or more polypeptides selected to be SEQ ID NO:30; wherein the recombinant nucleic molecule comprises a nucleotide sequence operatively linked to a promoter functional in a plant or plant cell, and wherein the nucleotide sequence is selected be SEQ ID NO:16.

The inventions listed in Groups I+ do not relate to a single general inventive concept under PCT Rule 13.1, because under PCT Rule 13.2 they lack the same or corresponding special technical features for the following reasons:

The Group I+ formulas do not share a significant structural element that is responsible controlling the nematode plant pest, requiring the selection of alternatives where "one or more polypeptides selected from the group consisting of SEQ ID NOs:29-42, SEQ ID NOs:135-209, SEQ ID NOs:243-260, SEQ ID NOs:665-1046, and any combination thereof".

Further, Group I+ share the technical feature of a method of controlling a nematode plant pest, comprising contacting the nematode plant pest with a transgenic plant or seed, or part thereof, having incorporated into its genome a recombinant nucleic acid molecule that modulates the expression of one or more polypeptides, thereby controlling the nematode plant pest; a recombinant nucleic acid molecule comprising a nucleotide sequence operatively linked to a promoter functional in a plant; a recombinant nucleic acid molecule capable of producing a double stranded RNA comprising an antisense strand and a sense strand, wherein the antisense strand is complementary to a portion of the nucleotide sequence encoding a polypeptide, thereby controlling the genes to be overexpressed in the transgenic plant, the portion consisting essentially of about 18 to about 25 consecutive nucleotides. However, these shared technical features do not represent a contribution over the prior art.

Specifically, US 2011/0247096 A1 to McCaig discloses a method of controlling a nematode plant pest (methods to overcome, or at least alleviate, nematode infestation of valuable agricultural crops, Para. [0019]), comprising contacting the nematode plant pest with a transgenic plant or seed, or part thereof (after penetrating soybean roots, SCN juveniles move through the root until they contact vascular tissue, which time they stop migrating and begin to feed, Para. [0007]; transgenic roots are generated after transformation with the binary vectors....rooted explant cultures transformed with vectors...exhibited a general trend of reduced cyst numbers (contacting nematode with transgenic plant) and female index relative to the known susceptible variety, Williams82, Para. [0069]), having incorporated into its genome a recombinant nucleic acid molecule that modulates the expression of one or more polypeptides (a recombinant expression vector comprising a root-specific promoter in operative association with a polynucleotide, Para. [0059]; expression of a transgene comprising a polynucleotide encoding Serine-Arginine-rich protein, AVR9-elicited_111B-like protein, a bHLH protein, or a Dirigent-like protein in roots can render soybean plants resistant to SCN (soybean cyst nematode) infection, Para. [0019]; nucleotides described herein can be directly transformed into the plastid genome; genes are inserted by homologous recombination into the several thousand copies of the circular plastid genome present in each plant cell, [0058]), thereby controlling the nematode plant pest (expression vector of the invention is employed in a method of making a nematode-resistant transgenic plant, Para. [0054]; render soybean plants resistant to SCN (soybean cyst nematode) infection, Para. [0019]); a recombinant nucleic acid molecule comprising a nucleotide sequence operatively linked to a promoter functional in a plant (a nematode-resistant transgenic plant comprising a recombinant expression vector comprising a root-specific promoter in operative association with a polynucleotide, Para. [0059]).

Further, WO 2010/121956 A1 to Cardoza et al. teaches a recombinant nucleic acid molecule (a recombinant nucleic acid molecule, Pg. 4, Ln. 25) capable of producing a double stranded RNA comprising an antisense strand and a sense strand (in a more preferred embodiment, the RNA oligonucleotides are double-stranded, Pg. 10, Lns. 1-2; a "double-stranded RNA" molecule or "dsRNA" molecule comprises a sense RNA fragment of a nucleotide sequence and an antisense RNA fragment of the nucleotide sequence, Pg. 25, Lns. 16-18), wherein the antisense strand is complementary to a portion of the nucleotide sequence encoding a polypeptide, thereby controlling the genes to be overexpressed in the transgenic plant (a recombinant nucleic acid molecule not occurring in a respective wild-type plant or part thereof (transgenic) wherein at least a part of said recombinant nucleic acid molecule is complementary to at least a part of a plant specific regulatory element regulating expression of a target gene in said plant or part thereof and wherein said recombinant nucleic acid molecule confers an increase of expression of said target gene... said recombinant nucleic acid molecules may be complementary to either the sense or the antisense strand of at least a part of said plant specific regulatory element, Pg. 4, Lns. 25-33, the portion consisting essentially of about 18 to about 25 consecutive nucleotides (in a more preferred embodiment, the RNA oligonucleotides are double-stranded; the length of such oligonucleotides may for example be between about 15 and about 30 bp, Pg. 10, Lns. 1-3). It would have been obvious to one of ordinary skill in the art at the time of the invention to modify the invention of McCaig to include a nucleic acid molecule capable of producing a double-stranded RNA as taught by Cardoza et al. for the regulator expression of the polynucleotides of McCaig as RNA-mediated gene expression is a well understood regulatory mechanism that is broadly applicable across many plant species and is easily customizable to the nucleic acid construct of choice.

Group I+ therefore lack unity under Rule 13 because they do not share a same or corresponding special technical feature.

FIG. 1

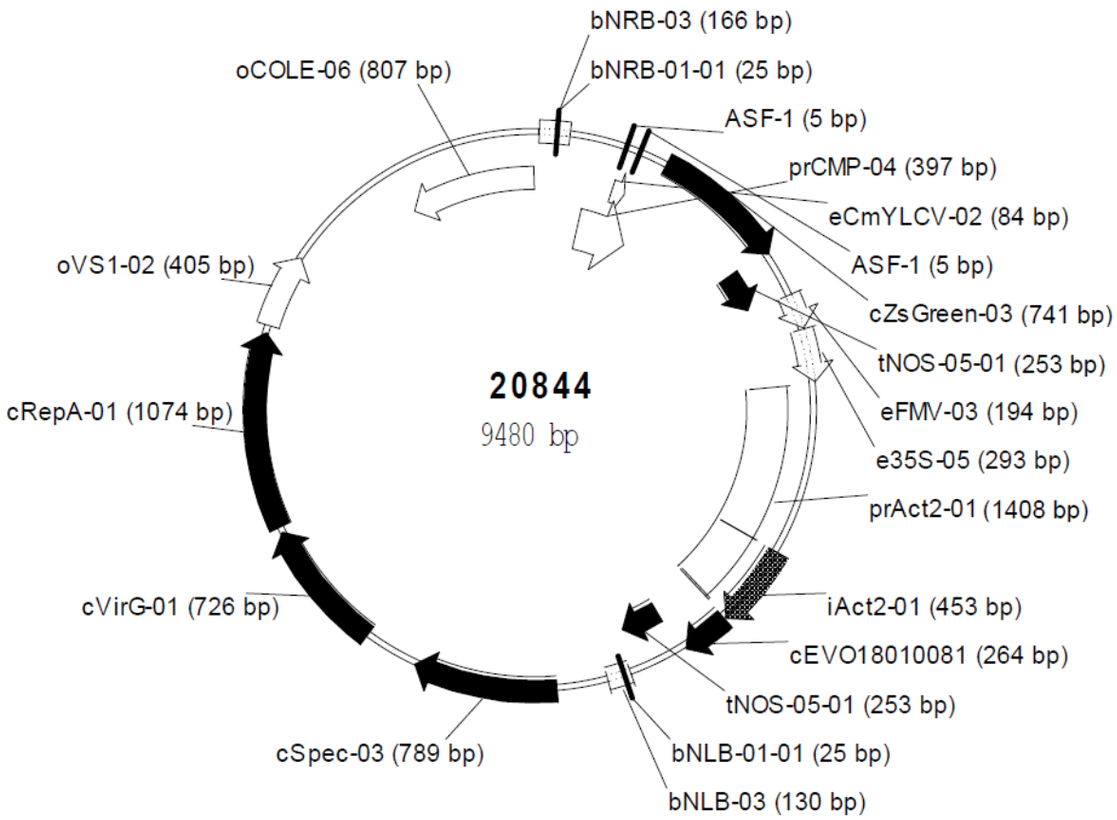

bNRB-03 (166 bp)
oCOLE-06 (807 bp)
bNRB-01-01 (25 bp)
ASF-1 (5 bp)
prCMP-04 (397 bp)
eCmYLCV-02 (84 bp)
oVS1-02 (405 bp)
ASF-1 (5 bp)
cZsGreen-03 (741 bp)
tNOS-05-01 (253 bp)
20844
9480 bp
cRepA-01 (1074 bp)
eFMV-03 (194 bp)
e35S-05 (293 bp)
prAct2-01 (1408 bp)
cVirG-01 (726 bp)
iAct2-01 (453 bp)
cEVO18010081 (264 bp)
tNOS-05-01 (253 bp)
cSpec-03 (789 bp)
bNLB-01-01 (25 bp)
bNLB-03 (130 bp)

FIG. 2

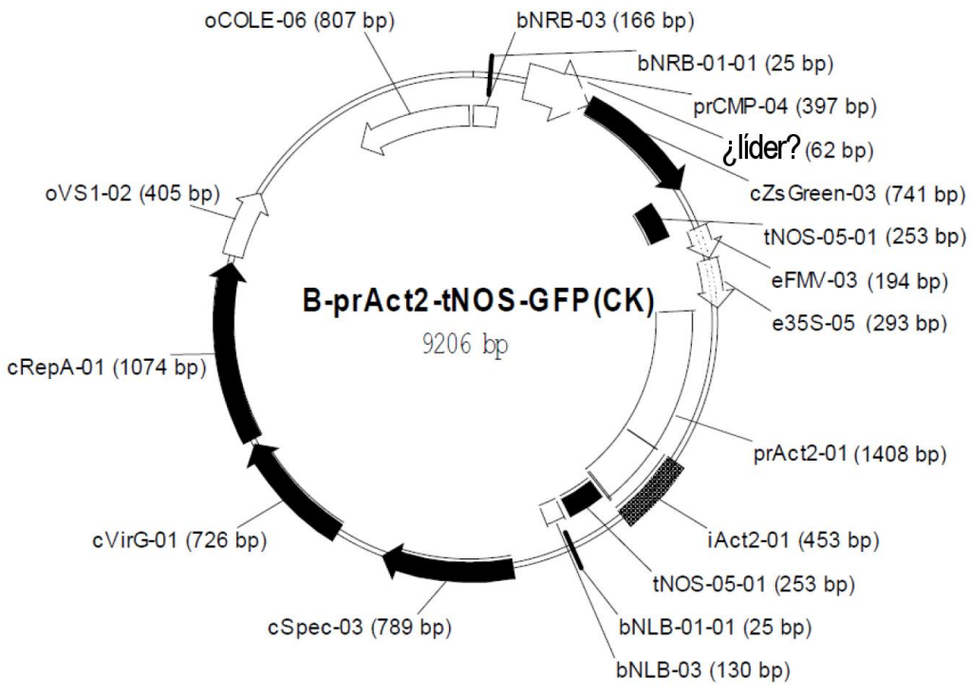

oCOLE-06 (807 bp)
bNRB-03 (166 bp)
bNRB-01-01 (25 bp)
prCMP-04 (397 bp)
¿líder? (62 bp)
cZsGreen-03 (741 bp)
tNOS-05-01 (253 bp)
eFMV-03 (194 bp)
e35S-05 (293 bp)
oVS1-02 (405 bp)
B-prAct2-tNOS-GFP(CK)
9206 bp
cRepA-01 (1074 bp)
prAct2-01 (1408 bp)
iAct2-01 (453 bp)
cVirG-01 (726 bp)
tNOS-05-01 (253 bp)
cSpec-03 (789 bp)
bNLB-01-01 (25 bp)
bNLB-03 (130 bp)

FIG. 3

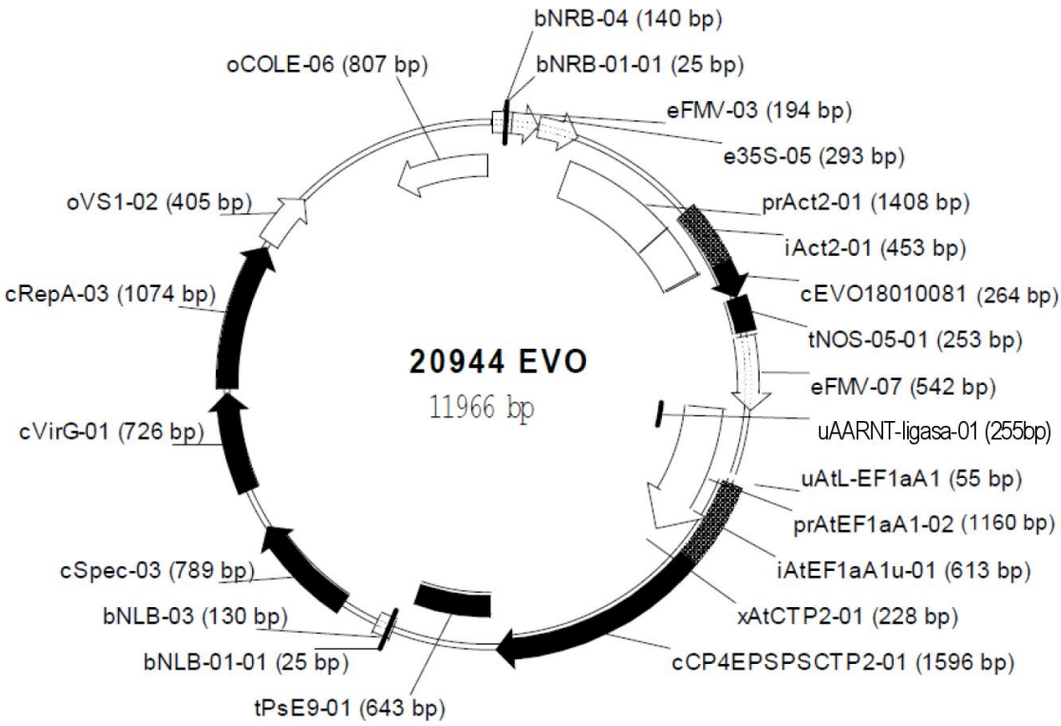
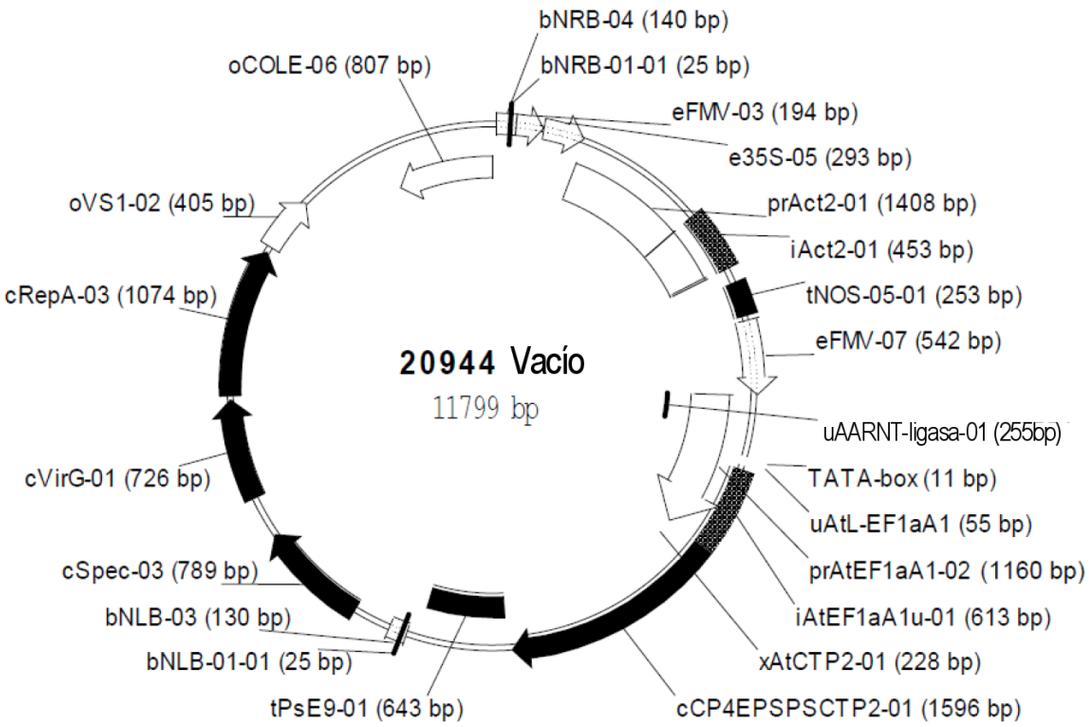
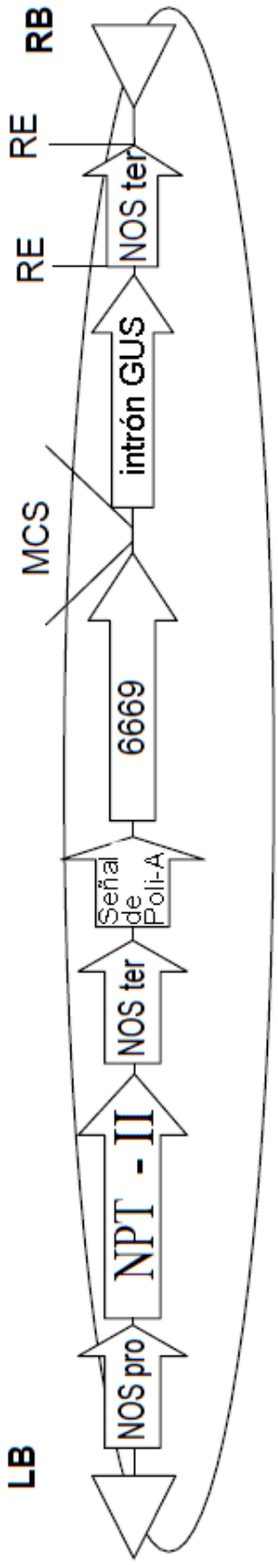

bNRB-04 (140 bp)
bNRB-01-01 (25 bp)
eFMV-03 (194 bp)
e35S-05 (293 bp)
prAct2-01 (1408 bp)
iAct2-01 (453 bp)
cEVO18010081 (264 bp)
tNOS-05-01 (253 bp)
eFMV-07 (542 bp)
uAARNT-ligasa-01 (255bp)
uAtL-EF1aA1 (55 bp)
prAtEF1aA1-02 (1160 bp)
iAtEF1aA1u-01 (613 bp)
xAtCTP2-01 (228 bp)
cCP4EPSPSCTP2-01 (1596 bp)
tPsE9-01 (643 bp)
bNLB-01-01 (25 bp)
bNLB-03 (130 bp)
cSpec-03 (789 bp)
cVirG-01 (726 bp)
cRepA-03 (1074 bp)
oVS1-02 (405 bp)
oCOLE-06 (807 bp)
20944 EVO
11966 bp

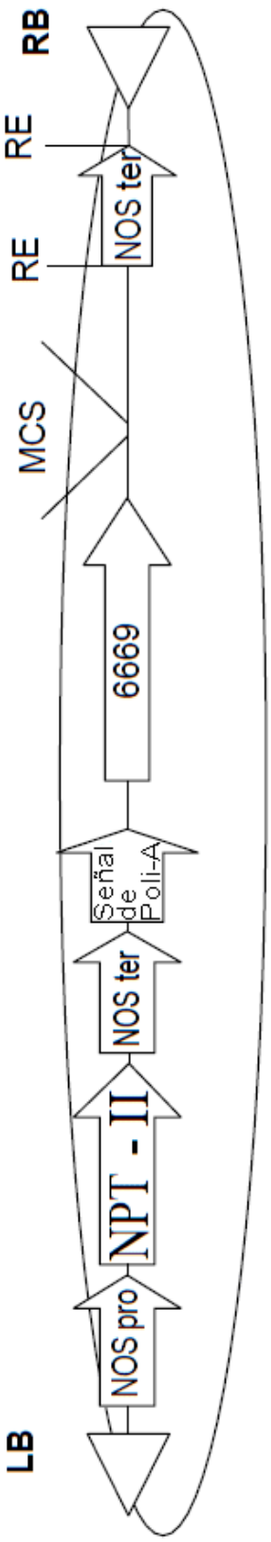
FIG. 4


bNRB-04 (140 bp)
oCOLE-06 (807 bp)
bNRB-01-01 (25 bp)
eFMV-03 (194 bp)
e35S-05 (293 bp)
oVS1-02 (405 bp)
prAct2-01 (1408 bp)
iAct2-01 (453 bp)
cRepA-03 (1074 bp)
tNOS-05-01 (253 bp)
eFMV-07 (542 bp)
20944 Vacío
11799 bp
uAARNT-ligasa-01 (255bp)
cVirG-01 (726 bp)
TATA-box (11 bp)
uAtL-EF1aA1 (55 bp)
cSpec-03 (789 bp)
prAtEF1aA1-02 (1160 bp)
bNLB-03 (130 bp)
iAtEF1aA1u-01 (613 bp)
bNLB-01-01 (25 bp)
xAtCTP2-01 (228 bp)
tPsE9-01 (643 bp)
cCP4EPSPSCTP2-01 (1596 bp)



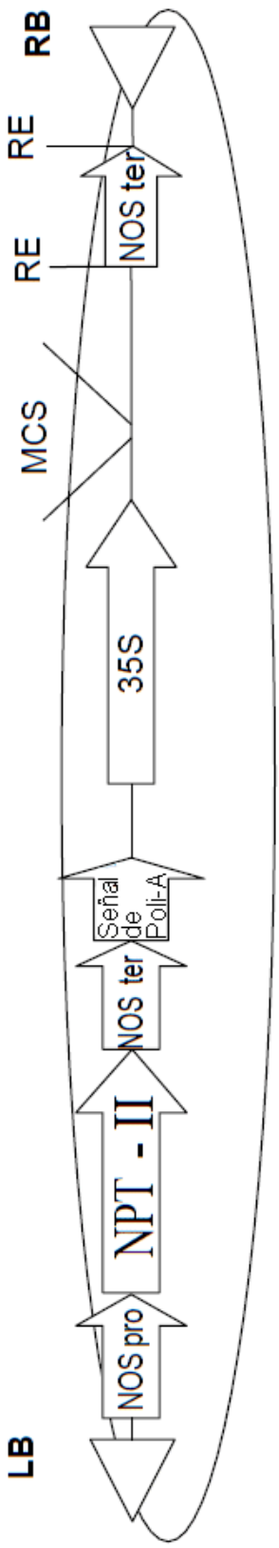
pQYN_6669

FIG. 5



pQFN, pQFNc

FIG. 6



pQXNc

FIG. 7

4915

COLOMBIA

PODER

El (los) Gregory W. Warren
SYNGENTA PARTICIPATIONS AG

Nombran por el presente a **XIMENA CASTELLANOS A. y/o MARGARITA CASTELLANOS A.** abogadas con oficinas en la Carrera 9 No. 93-09, Bogotá-Colombia para

y para obtener la protección de mi (nuestra) propiedad Industrial y con este fin autorizamos a dichos apoderados para que nos representen ante cualesquiera autoridades o personas de los órdenes administrativo, contencioso –administrativo y judicial en todo lo relacionado con los siguientes actos y gestiones:
a) Obtención de patentes de invención, modelos y dibujos industriales; registro de marcas de fabrica, de servicio, colectivas o defensivas y de denominaciones de origen, depósito de nombres y enseñas comerciales; su renovación, prórroga, inscripción de traspaso y cambio de nombre o domicilio, cancelación voluntaria y el registro de licencias de uso de esos derechos; b) Para la obtención de registros sanitarios; c) Acciones de oposición, observación, cancelación, nulidad, medidas cautelares y en general los juicios civiles, penales, administrativos o contencioso - administrativos que promovamos o se nos promuevan, pudiendo en todos los actos y gestiones arriba mencionados sustituir éste mandato, transigir, desistir, recibir, cancelar, renunciar, aceptar notificaciones y nombrar apoderados judiciales y extrajudiciales.

Dado y firmado hoy 24 de Marzo de 2004

en Research Triangle Park, Carolina del Norte 27709
por Gregory W. Warren

(El notario debe suscribir el documento en la pagina siguiente)

(Se requiere legalización consular)

POWER OF ATTORNEY

I (we) the undersigned Gregory W. Warren
Syngenta Participations AG

hereby grant(s) Power of Attorney to **XIMENA CASTELLANOS A. and /or MARGARITA CASTELLANOS** a. attorneys residing at Carrera 9 No. 93-09, Bogota- Colombia, to prosecute
and to obtain the protection of my (our Industrial Property, for which purpose we authorize the said attorneys to represent us before any authorities, or persons, specially those, administrative, contentious and judicial, in all matters concerning the following:

a) Obtention of patents, models and designs, registration of trademarks, service, collective and defensive marks, and of designations of origin; the deposit of trade names and ensigns; its renewal, extension, recordal of assignments, change of name or domicile, voluntary cancellation, and the registration of licenses of use of the above rights; b) For the obtention of Sanitary registrations; c) Actions of opposition, cancellation, nullity, infringement, granting of licenses; and in general the civil, criminal and administrative suits related to those rights; actions and suits instituted by us or against us; and that in all the above matters they may substitute this power of attorney, compromise, desist, cancel, receive, renounce, accept notifications and appoint attorneys in fact, in or out of court.

Given and signed this 24th March 2004

in Research Triangle Park, North Carolina 27709

by Gregory W. Warren Gregory W. Warren

(Notary shall execute on the other side)

(Consular legalization required)

ALVARO CASTELLANOS M. & CIA.

ABOGADOS COLOMBIA

Carrera 9 No. 93-09- P.O.Box 6349 - Bogotá, Colombia
Tels.: (571) 610 74 20 / 60 / 80 - Fax (571) 610 07 06 - e-mail acastell@impsat.net.co

XC/cm

COLOMBIA

CERTIFICADO NOTARIAL (Sociedad)

Hoy 24 de Marzo del año 2004
compareció (eron) personalmente Gregory W. Warren
a quienes conozco como la(s) personas que firma(n) en representación de la Sociedad (Compañía denominada
Certifico : Syngenta Participations AG

a) Que es una sociedad/Compañía legalmente constituida y existente de acuerdo con las leyes de
b) Que el domicilio de dicha Sociedad/Compañía es Basel,Suiza
c) Que el objeto u objetos para los cuales se otorga el presente poder están comprendidos dentro del objeto social de la mencionada Sociedad /Compañía.
d) Que el Sr. Gregory W. Warren

esta autorizado para otorgar el presente poder. Lo anterior esta probado por medio de los siguientes documentos, que certifico he visto*

(Ciudad) REsearch Triangle Park

(Estado) Carolina del Norte 27709

Hoy del 24 de Marzo de 2004

(Notario Público) LANEISHA C. HAYES

*Los documentos debe identificarse con fecha y origen.

LANEISHA C. HAYES NOTARY PUBLIC WAKE COUNTY, N.C.

NOTARIAL (Corporation)

On this 24th day of March of 2004 personally appeared Gregory W. Warren whom I know to be the person(s) who signed this document as representative(s) of the Corporation /Company named Syngenta Participations AG
I certify:

a) That Syngenta Participations AG is a corporation (Company legally constituted and in existence in accordance with the laws of Basel, Switzerland
b) That the domicile of said Corporation/Company is Basel, Switzerland
c) That the purpose or purposes for which the present Power of Attorney is granted are comprised within the object set forth in the charter of the mentioned Corporation/Company.
d) That Mr. Gregory W. Warren

is (are) authorized to grant the present Power of Attorney. The aforementioned was duly proven through the following documents and I duly certify having seen them*: on the 24th day of March, 2004 in Research Triangle Park, North Carolina 27709.

(City) Research Triangle Park

(State) North Carolina, 27709

this 24th day of March of the year 2004

(Notary Public) Laneisha C. Hayes

*Documents must be identified with date and origin
3/24/04 - Research Triangle Park, North Carolina 27709 - Syngenta Biotech, Inc.

ALVARO CASTELLANOS M. & CIA.
ABOGADOS COLOMBIA

Carrera 9 No. 93-09- P.O.Box 6349 - Bogotá, Colombia
Tels.: (571) 610 74 20 / 60 / 80 - Fax (571) 610 07 06 - e-mail acastell@impsat.net.co

XC/cm

Wake County Register of Deeds
Post Office Box 1897
Raleigh, North Carolina 27602-1897

Laura M. Riddick
Register Of Deeds

STATE OF NORTH CAROLINA

WAKE COUNTY

CERTIFICATE OF REGISTER OF DEEDS THAT NOTARY PUBLIC WAS ACTING NOTARY AT TIME OF SIGNATURE

I, LAURA M. RIDDICK, REGISTER OF DEEDS OF THE AFORESAID COUNTY AND STATE, DO HEREBY CERTIFY THAT Laneisha C. Hayes WAS, AT THE TIME OF SIGNING THE FOREGOING (OR ANNEXED) CERTIFICATE, A DULY COMMISSIONED AND QUALIFIED NOTARY PUBLIC IN AND FOR THE COUNTY OF WAKE, STATE OF NORTH CAROLINA, AND AS SUCH FULL FAITH AND CREDIT IS DUE TO HIS OFFICIAL ACTS; AND, FURTHER, THAT HIS SIGNATURE THERETO IS IN HIS OWN PROPER HANDWRITING.

IN TESTIMONY WHEREOF, I HAVE HEREUNTO SET MY HAND AND SEAL OF OFFICE THIS, THE 30TH DAY OF MARCH, 2004.

Laura M. Riddick
REGISTER OF DEEDS

(SEAL) LAURA M. RIDDICK REGISTER OF DEEDS SEAL WAKE COUNTY, N.C.

DEPUTY / ~~ASSISTANT~~

APOSTILLE
(Convention de La Haye 5 octobre 1961)

1. COUNTRY: **UNITED STATES OF AMERICA**
2. This Public Document has been signed by CARLA N. BROWN
3. acting in the capacity of DEPUTY REGISTER OF DEEDS
~~LAURA M. RIDDICK, REGISTER OF DEEDS~~
4. bears the seal/stamp of COUNTY OF WAKE, NORTH CAROLINA

CERTIFIED

5. at Raleigh, North Carolina
6. the 1ST DAY OF APRIL, 2004
7. by Deputy Secretary of State, State of North Carolina
8. No. 8117
9. Seal/Stamp:



10. Signature

Rodney S. Maddox

----------TRADUCCION OFICIAL No. -040417----------

de un documento escrito en INGLES, el cual para su identificación lleva el sello de la Traductora e Intérprete oficial, Res. 2755/68 y 01144/97 de Minjusticia, al igual que la presente.----------

----------(Anexos a un poder otorgado por Syngenta Participations AG)

(fdo) illegible

3/24/04 Research Triangle Park, NC 27709

ESTADO DE CAROLINA DEL NORTE

CONDADO DE WAKE

Yo, Laura M.Riddick, Registrador de Escrituras del condado y estado antes mencionados, certifico por medio del presente que Laneisha C. Hayes, al momento de firmar este documento era un Notario Público debidamente comisionado y habilitado en y para el Condado de Wake, Estado de Carolina del Norte, y como tal debe dares plena fe y crédito a sus actos oficiales, y además, que su firma en el mismo es de su propia letra.

En testimonio de lo cual, he impuesto aquí mi firma y sello de oficio, hoy día 30 de Marzo de 2004.

Laura M. Riddick, Registrador de Escrituras

Por (fdo) ilegible

DORA [illegible] DE BERNAL
TRADUCTORA E INTÉRPRETE OFICIAL
RES. 02[illegible] Y 01144/97 - MINJUSTICIA
REP. DE COLOMBIA

Delegado

APOSTILLA

(Convención de La Haya de octubre 5, 1961)

1. País: Estados Unidos de América

2. Este documento público ha sido firmado por CARLA N. BROWN

3. actuando en su carácter de Delegado del Registrador de Escrituras

4. lleva el sello de Laura M. Riddick, Registrador de Escrituras

Condado de Wake, Carolina del Norte

CERTIFICADO

5. En Raleigh.Carolina del Norte

6. el día 1 de Abril de 2004

7. por el Secretario de Estado Delegado, Estado de Carolina del Norte

8. No. 8117

9. Sello: (sello en oblea ocre)

10. Firma

(fdo) Rodney S. Maddox

ES TRADUCCION FIEL Y COMPLETA, a la cual me remito,

Bogotá, Abril 15, 2004

DORA DUQUE DE BERNAL
TRADUCTORA E INTERPRETE OFICIAL
RES. 02755/68 Y 01144/97 - MINJUSTICIA
REP. DE COLOMBIA

MINISTERIO DE
RELACIONES E...

Dora Duque

...EL
DOCUMENTO DESEMPEÑA
LAS FUNCIONES INDICADAS

...L TEXTO

2:42

...S

Met Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Asn Asn Cys Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Asn
355 360 365

Ser Asn Ala Ile Leu Tyr Ala Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Ala Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ser Glu
435 440 445

Ala Glu Asn Lys Phe His Thr Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
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Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
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Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
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<213> Mandioca

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His Glu Asn Arg Asn Gly Thr Phe Gln Trp Ile Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asn Thr His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
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Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Asp Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Gln Gln
195 200 205

Ile Val Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Met Ala Ala Leu Glu Arg
245 250 255

Asn Glu Val Glu Ile Ser Pro Ser Thr Leu Tyr Ala Leu Ala Cys Ile
260 265 270

Phe Glu Glu Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Val Ile Asp Leu Ala Ile Lys Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Gly Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Gln Asn Thr Ile Val Leu
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Glu Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
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35 40 45

Val Lys Tyr Glu Phe Lys Thr Asn Thr His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Arg Gln Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Glu
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Gln Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Ser Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Leu Glu Lys
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Leu Ala Cys Val
260 265 270

Leu Glu Glu Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Ser Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Leu Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Gly Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Cys Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
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35 40 45

Val Lys Tyr Glu Phe Arg Thr Asp Ala His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Ser Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val

85 90 95

Gln Pro Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Cys Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Gln Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Ala Thr Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Leu Ile

225 230 235 240

Val Gly Leu Asn Asp Thr Ile Glu Asn Leu Leu Ala Ser Leu Asp Arg
245 250 255

Asn Glu Pro Glu Ile Ser Pro Ser Thr Leu Tyr Ala Leu Ala Cys Val
260 265 270

Met Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val

370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Asp Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
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35 40 45

Val Lys Tyr Glu Phe Lys Thr Gln Thr Asn Val Pro Lys Leu Gly Val
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Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Ile
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
100 105 110

Val Gly Ser Phe Gln Gly Glu Glu Ile His Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Glu Asp Ile Val Trp Gly Gly Trp Asp Ile
130 135 140

Ser Asn Leu Asn Leu Ala Asp Ala Met Gly Arg Ala Arg Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Asp
180 185 190

Arg Ala Asn Asn Ile Ile Lys Gly Thr Lys Lys Glu Gln Leu Gln Gln
195 200 205

Val Ile Lys Asp Ile Lys Glu Phe Lys Glu Thr Thr Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Ile Val
225 230 235 240

Val Gly Leu Asn Asp Thr Thr Glu Asn Leu Leu Ala Ser Val Asp Lys
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Leu Ala Cys Val
260 265 270

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Asn
355 360 365

Ser Asn Ala Ile Leu Tyr Gly Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Met
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ser Glu
435 440 445

Gln Glu Asp Lys Phe His Ser Phe His Ala Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Ser Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
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35 40 45

Val Lys Tyr Gln Phe Lys Thr Gln Thr His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Cys Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Arg Glu Gln Val Gln Gln
195 200 205

Ile Ile Ser Asp Ile Lys Glu Phe Lys Glu Lys Ser Lys Val Asp Glu
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Ser Leu Leu Ala Ser Leu Asp Lys
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Arg Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Gly Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
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35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Thr Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Arg Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

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

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Glu Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Leu Lys Gly Thr Lys Lys Glu Gln Met Gln Gln
195 200 205

Ile Ile Lys Asp Ile Lys Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ile
225 230 235 240

Val Gly Leu Asn Asp Thr Val Glu Asn Leu Phe Ala Ser Leu Asp Arg
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Met Ala Cys Val
260 265 270

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
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Pro Gly Leu Ile Asp Leu Ala Ile Lys Arg Asn Ser Leu Ile Gly Gly
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Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp
305 310 315 320

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Arg Asn Thr Ile Val Leu
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ser Glu
435 440 445

Ala Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Ser Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
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485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
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His Glu Leu Lys Asn Gly Ser Tyr Gln Trp Thr Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Asn Thr Gln Thr His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val

85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Arg Glu Gln Val Gln Gln
195 200 205

Val Ile Asn Asp Ile Lys Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val

225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Ser Leu Leu Asp Ser Leu Asp Lys
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Arg Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Gly Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val

370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Thr Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
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<210> 825

<211> 510
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<400> 825

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Glu Asp Glu Ile His Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
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His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Thr
35 40 45

Val Gln Tyr Glu Phe Lys Thr Asp Val His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Met Glu Gln
195 200 205

Ile Val Lys Asp Ile Arg Glu Phe Lys Glu Lys Thr Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Ser Leu Leu Ala Ser Leu Glu Arg
245 250 255

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

Phe Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Val Ile Asp Leu Ala Ile Lys Gly Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Gly Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 826
<211> 510
<212> PRT
<213> Algodón

<400> 826

Met Phe Ile Glu Asn Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Asn Glu Ile Gln Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Lys Asn Gly Thr Tyr Gln Trp Val Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Ile His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Lys Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Ile Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asn Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Glu
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Gln Gln
195 200 205

Val Ile Lys Asp Ile Lys Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ile
225 230 235 240

Val Gly Leu Asn Asp Thr Val Glu Ser Leu Met Ala Ser Leu Glu Lys
245 250 255

Asn Glu Ser Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Gln Arg Asn Cys Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Gly Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ala Asp
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Ser
485 490 495

Ile Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 827
<211> 510
<212> PRT
<213> Roble

<400> 827

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Asn Glu Ile His Ser Val Tyr Asn Tyr Asp Thr Thr Glu Leu Val
20 25 30

His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Ile His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe His Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Phe Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Gln Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Ala Thr Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ile
225 230 235 240

Val Gly Leu Asn Asp Thr Glu Glu Ser Leu Leu Ala Ser Val Glu Lys
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Leu Ala Cys Val
260 265 270

Tyr Glu Asn Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Thr Asn Thr Ile Val Leu
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Ser Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 828
<211> 510
<212> PRT
<213> Pimiento

<400> 828

Met Phe Ile Glu Asn Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Ser Val Ile His Ser Val Tyr Asp Tyr Gln Thr Thr Glu Leu Val
20 25 30

His Glu Glu Lys Asn Gly Thr Tyr Gln Trp Thr Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Val His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val

85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Ile
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Val Lys Gly Thr Lys Lys Glu Gln Ile Asp Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Asn Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ala

225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Phe Thr Ala Val Asp Arg
245 250 255

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

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Phe Ile Asp Leu Ala Ile Lys Arg Asn Thr Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val

370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 829

<211> 510
<212> PRT
<213> Tabernaemontana

<400> 829

Met Phe Ile Glu Ser Phe Lys Val Asp Ser Ala Asn Val Lys Tyr Ser
1 5 10 15

Glu Ser Glu Ile His Ser Ile Tyr Asn Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Arg Asp Gly Ala Tyr Gln Trp Ile Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Thr Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ser Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Glu Pro Asp Phe Ile Ala Ala Asn Gln Gly Ala
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Met Gln Gln
195 200 205

Ile Ile Lys Asp Ile Gln Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Phe Ala Ala Leu Asp Arg
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Ser Arg Ile Gln Leu Lys Ser Glu
435 440 445

Ala Glu Ala Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 830
<211> 510
<212> PRT
<213> Algodón, Gossypium raimondii

<400> 830

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Asn Glu Ile Gln Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Lys Asn Gly Thr Tyr Gln Trp Val Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Ile His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Lys Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asn Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Glu
180 185 190

Arg Ala Asn Asn Val Met Lys Gly Thr Lys Lys Glu Gln Val Gln Gln
195 200 205

Val Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ile
225 230 235 240

Val Gly Leu Asn Asp Thr Val Glu Ser Leu Met Ala Ser Leu Glu Lys
245 250 255

Asn Glu Ser Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Gln Arg Asn Cys Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Gly Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ala Asp
435 440 445

Gly Glu Gly Lys Phe His Thr Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Ser
485 490 495

Ile Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 831
<211> 510
<212> PRT
<213> Tomate

<400> 831

Met Phe Ile Glu Asn Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Ser Glu Ile His Ser Val Tyr Asp Tyr Gln Thr Thr Glu Leu Val
20 25 30

His Glu Glu Lys Asn Gly Thr Phe Gln Trp Thr Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Val His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Ala Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Ile
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Met Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Ile Asp Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Asn Asn Lys Val Asp Arg
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Ser Val Ala
225 230 235 240

Val Gly Phe Asn Asp Thr Met Glu Asn Leu Phe Ala Ser Val Asp Arg
245 250 255

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

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Arg Asn Thr Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Arg Asn Thr Ile Val Leu
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 832
<211> 246
<212> PRT
<213> Solanum phureja

<400> 832

Met Phe Ile Glu Asn Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Ser Glu Ile His Ser Val Tyr Asp Tyr Gln Thr Thr Glu Leu Val
20 25 30

His Glu Glu Lys Asn Gly Thr Phe Gln Trp Thr Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Val His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Ala Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val

85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Ile
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Ile Asp Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Asn Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Ser Val Ala

225 230 235 240

Val Gly Leu Asn Trp Pro
245

<210> 833
<211> 510
<212> PRT
<213> Castaño

<400> 833

Met Phe Ile Glu Ser Phe Lys Val Asp Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Asn Glu Ile His Ser Leu Tyr Asn Tyr Asp Thr Thr Glu Leu Val
20 25 30

His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Ile His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe His Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Phe Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Gln Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Ala Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ile
225 230 235 240

Val Gly Leu Asn Asp Thr Glu Glu Asn Leu Leu Ala Ser Val Glu Lys
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Leu Ala Cys Val
260 265 270

Tyr Glu Asn Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Thr Asn Thr Ile Val Leu
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Ser Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 834
<211> 510

<212> PRT
<213> Flaveria

<400> 834

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Asp Asp Glu Ile His Ser Leu Tyr Asn Tyr Asp Thr Thr Glu Leu Val
20 25 30

His Glu Glu Lys Asn Gly Ala Tyr Gln Trp Val Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Gln Thr Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Glu Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Ser Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Glu
180 185 190

Arg Ala Asp Asn Val Ile Lys Gly Thr Lys Asn Glu Gln Ile Gln Lys
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Ala Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Met
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Ser Leu Phe Ala Ser Leu Asp Lys
245 250 255

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

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Val Ile Asp Leu Ala Ile Lys Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Asp Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 835
<211> 510
<212> PRT
<213> Kiwi

<400> 835

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Gly Glu Ile His Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Arg Asn Gly Asn Tyr Gln Trp Ile Val Lys Pro Lys Thr
35 40 45

Val Gln Tyr Glu Phe Lys Thr Asp Thr His Val Pro Lys Leu Gly Val
50 55 60

Leu Leu Val Gly Trp Gly Gly Asn Asn Gly Cys Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Ile
115 120 125

Leu Pro Met Val Asn Pro Asp Glu Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Arg Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

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

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Arg
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ile
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Phe Ala Ser Leu Glu Lys
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Leu Glu Asn Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Arg Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Asp
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Ile Gly Leu Ser Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 836
<211> 510
<212> PRT
<213> Platanus

<400> 836

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Asp His Glu Ile Gln Ser Ile Tyr Ser Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Val Val Lys Pro Lys Thr
35 40 45

Val Gln Tyr Glu Phe Lys Thr Asp Thr Cys Val Pro Lys Leu Gly Val

50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe Asp Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ser Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Arg Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asn Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Glu Gln

195 200 205

Ile Met Lys Asp Ile Arg Glu Phe Lys Glu Ala Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Ser Ala Ser Leu Asp Lys
245 250 255

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

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe

340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Gly Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Ile
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys

485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 837
<211> 510
<212> PRT
<213> Platanus

<400> 837

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Asp His Glu Ile Gln Ser Val Tyr Ser Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Lys Asn Gly Thr Tyr Gln Trp Leu Val Lys Pro Lys Thr
35 40 45

Val Gln Tyr Glu Phe Lys Thr Asp Thr Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Arg Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Ser Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Gln Gln
195 200 205

Ile Met Lys Asp Ile Arg Glu Phe Lys Glu Ala Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Leu Glu Lys
245 250 255

Asn Glu Val Glu Ile Ser Pro Ser Thr Leu Tyr Ala Leu Ala Cys Val
260 265 270

Phe Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Gly Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Ile
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Ile Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 838
<211> 331

<212> PRT
<213> Vinca

<400> 838

Met Phe Ile Glu Ser Phe Lys Val Asp Ser Ala Asn Val Lys Tyr Thr
1 5 10 15

Glu Ser Glu Ile His Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Arg Asp Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Thr Leu Val Pro Lys Leu Gly Ile
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Arg Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

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

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Glu Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Leu Lys Gly Thr Lys Lys Glu Gln Met Gln Gln
195 200 205

Ile Ile Lys Asp Ile Lys Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val
225 230 235 240

Val Gly Leu Asn Asp Thr Val Glu Asn Leu Phe Ala Ala Leu Asp Arg
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

Phe Leu Val Gly Ala Gly Ile Lys Pro Ile Leu
325 330

<210> 839
<211> 510
<212> PRT
<213> Amsonia

<400> 839

Met Phe Ile Glu Ser Phe Lys Val Asp Ser Ala Asn Val Lys Tyr Thr
1 5 10 15

Glu Ser Glu Ile His Ser Val Tyr Asp Tyr Gln Thr Thr Glu Leu Val
20 25 30

His Glu Asn Arg Asp Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Thr Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Val Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Glu Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asn Met Ser Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Met Leu Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val
225 230 235 240

Val Gly Leu Asn Asp Thr Val Glu Asn Leu Phe Ala Ala Leu Asp Arg
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Arg Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ser Glu
435 440 445

Ala Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 840
<211> 510
<212> PRT
<213> Haya

<400> 840

Met Phe Ile Glu Ser Phe Lys Val Asp Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Asn Glu Ile His Ser Val Tyr Asn Tyr Asp Thr Thr Glu Leu Val
20 25 30

His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Ile Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Glu Thr His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val

85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe His Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val His Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Phe Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ala
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Gln Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Ala Thr Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ile

225 230 235 240

Val Gly Leu Asn Asp Thr Glu Glu Ser Leu Leu Ala Ser Val Asp Lys
245 250 255

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

Leu Glu Asn Val Ala Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Glu Leu Ala Ile Lys Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val

370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Thr Asn Thr Ile Val Leu
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Ser Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 841

<211> 510
<212> PRT
<213> Algodón, Gossypium raimondii

<400> 841

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Asp Asn Ala Ile Gln Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Arg Asp Gly Thr Tyr Gln Trp Val Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Arg Thr Asp Ile His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Arg Trp Gly Val Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Glu Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Glu
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Gln Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Phe Glu Lys
245 250 255

Asn Glu Ser Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Phe Glu Asp Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Gln Arg Asn Cys Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Gly Ile Leu Tyr Gln Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Ile Gly Leu Ser Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 842
<211> 510
<212> PRT
<213> Kiwi

<400> 842

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Gly Glu Ile His Ser Val Tyr Ser Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Val Val Lys Pro Lys Thr
35 40 45

Val Gln Tyr Glu Phe Lys Thr Asp Thr His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Cys Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Ile
115 120 125

Leu Pro Met Val Asn Pro Asp Glu Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Arg Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Glu Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Ser Lys Lys Glu Gln Val Asp Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Arg
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ile
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Phe Ala Ala Leu Glu Lys
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Leu Glu Asn Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Arg Arg Asn Cys Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Asp
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Ile Gly Leu Ser Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 843
<211> 510
<212> PRT
<213> Phlya

<400> 843

Met Phe Ile Glu Ser Phe Lys Val Asp Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Gly Glu Ile His Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Thr
35 40 45

Val Glu Tyr Gln Phe Lys Thr Asp Thr His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp Asp Ile
130 135 140

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

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu His Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Pro
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Gln Gln
195 200 205

Val Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ile
225 230 235 240

Val Gly Leu Asn Asp Thr Ser Glu Ser Leu Met Ala Ala Val Glu Arg
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Met Ile Asp Leu Ala Ile Gln His Asn Thr Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Gly Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Gln
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 844
<211> 510
<212> PRT
<213> Tomate

<400> 844

Met Phe Ile Glu Asn Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Ile
1 5 10 15

Glu Asn Glu Ile His Ser Val Tyr Asp Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Glu Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Thr His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Glu Lys Val

85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asn Met Asn Leu Ala Asp Ala Met Val Arg Ala Lys Val Phe Glu
145 150 155 160

Val Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Glu Ala
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Glu Gln
195 200 205

Ile Val Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Ile Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val

225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ala Val Asp Arg
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu His Ala Ile Ala Cys Ile
260 265 270

Met Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Arg Asn Thr Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Ser Gly Glu His Pro Asp His Val Val

370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Met Ser Glu Ile Phe Met Gly Gly Lys Ser Thr Ile Val Met
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 845

<211> 364
<212> PRT
<213> Catharanthus

<400> 845

Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Glu Ile Asp
1 5 10 15

Leu Gln Asn Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro Leu Pro
20 25 30

Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser Arg Ala
35 40 45

Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Met Gln Gln Ile Ile
50 55 60

Lys Asp Ile Gln Glu Phe Lys Glu Lys Asn Lys Val Asp Lys Val Val
65 70 75 80

Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Leu Val Val Gly
85 90 95

Leu Asn Asp Thr Met Glu Asn Leu Phe Ala Ala Leu Asp Arg Asn Glu
100 105 110

Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Leu Ala Cys Val Leu Glu
115 120 125

Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val Pro Ala
130 135 140

Leu Ile Asp Leu Ala Ile Lys Arg Asn Ser Leu Ile Gly Gly Asp Asp
145 150 155 160

Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp Phe Leu
165 170 175

Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn His Leu
180 185 190

Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe Arg Ser
195 200 205

Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala Ser Asn
210 215 220

Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val Val Ile
225 230 235 240

Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp Glu Tyr
245 250 255

Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Leu His Asn
260 265 270

Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp Leu Val
275 280 285

Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ser Glu Ala Glu
290 295 300

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

Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn Ala Leu
325 330 335

Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys Val Gly
340 345 350

Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
355 360

<210> 846
<211> 510
<212> PRT
<213> Cacao

<400> 846

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Asp Asn Glu Ile Leu Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Val Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Thr His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Ala
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Glu Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Thr Val Pro
165 170 175

Ile Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Glu
180 185 190

Arg Ala Asn Asn Ile Ile Lys Gly Thr Lys Lys Glu Gln Val Gln Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Arg
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ile
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Ser Leu Leu Gly Ser Leu Glu Lys
245 250 255

Asn Glu Ser Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Ser Val
260 265 270

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Gln Arg Asn Cys Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Gly Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Gln Asn Thr Ile Val Leu
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Ile Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 847
<211> 511
<212> PRT
<213> Trébol

<400> 847

Met Phe Ile Glu Asn Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Thr Glu Ile Glu Ser Val Tyr Ser Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Gln Lys Asn Thr Asn Asp Thr Tyr Glu Trp Val Val Lys Pro Lys
35 40 45

Thr Val Lys Tyr Glu Phe Lys Thr Gln Thr Asn Leu Pro Lys Leu Gly
50 55 60

Val Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Ser Leu Thr Gly
65 70 75 80

Gly Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Asn
85 90 95

Ile Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile
100 105 110

Arg Val Gly Ser Phe Gln Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser
115 120 125

Leu Leu Pro Met Val Asn Pro Glu Asp Ile Val Trp Gly Gly Trp Asp
130 135 140

Ile Ser Asp Met Asn Leu Ala Asp Ala Met Gly Arg Ala Lys Val Phe
145 150 155 160

Asp Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val
165 170 175

Pro Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly
180 185 190

Asp Arg Ala Asn Asn Ile Ile Lys Gly Thr Lys Lys Glu Gln Leu Gln
195 200 205

Gln Val Ile Lys Asp Ile Lys Glu Phe Lys Glu Ala Asn Lys Val Asp
210 215 220

Lys Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Ile
225 230 235 240

Val Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Val Asp
245 250 255

Lys Asn Glu Ser Glu Ile Ser Pro Ser Thr Leu Phe Ala Leu Ala Cys
260 265 270

Val Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe
275 280 285

Val Pro Gly Leu Ile Asp Leu Ala Ile Lys Arg Asn Ser Leu Ile Gly
290 295 300

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

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

Asn His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr
340 345 350

Phe Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val
355 360 365

Asn Ser Asn Ala Ile Leu Tyr Gly Pro Gly Glu His Pro Asp His Val
370 375 380

Val Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met
385 390 395 400

Asp Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val
405 410 415

Met His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu
420 425 430

Asp Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ser
435 440 445

Glu His Glu Asp Lys Phe His Thr Phe His Pro Val Ala Thr Ile Leu
450 455 460

Ser Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val
465 470 475 480

Asn Ala Leu Ser Lys Gln Arg Ser Met Leu Glu Asn Ile Leu Arg Ala
485 490 495

Cys Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 848
<211> 510
<212> PRT
<213> Euonymus

<400> 848

Met Phe Ile Glu Asn Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Thr Glu Ile His Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Lys Asn Gly Ser Tyr Gln Trp Thr Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Thr Ser Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val

85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Val Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Glu Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Met Pro Tyr Met Glu His Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Asp Ser
180 185 190

Arg Ala Asn Asn Ile Ile Lys Gly Thr Lys Lys Glu Gln Val Gln Gln
195 200 205

Val Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Thr Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ile

225 230 235 240

Val Gly Leu Asn Asp Thr Ile Glu Asn Leu Phe Ala Ser Leu Asp Lys
245 250 255

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

Leu Glu Asn Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Gly Ile Leu Phe Glu Pro Gly Glu His Pro Asp His Val Val

370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Arg Asn Thr Ile Val Leu
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Asp
435 440 445

Asp Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 849

<211> 510
<212> PRT
<213> Flaveria

<400> 849

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Asp Asp Glu Ile His Ser Leu Tyr Asn Tyr Asp Thr Thr Glu Leu Ile
20 25 30

His Glu Glu Lys Asn Gly Ala Tyr Gln Trp Val Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Lys Thr Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Glu Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Phe Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Ser Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Glu
180 185 190

Arg Ala Asp Asn Val Ile Lys Gly Thr Lys Asn Glu Gln Ile Gln Lys
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Ala Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Met
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Ser Leu Phe Ala Ser Leu Asp Lys
245 250 255

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

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Val Ile Asp Leu Ala Ile Lys Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Asp Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 850
<211> 510
<212> PRT
<213> Flaveria

<400> 850

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Asp Asp Glu Ile His Ser Leu Tyr Asn Tyr Asp Thr Thr Glu Leu Ile
20 25 30

His Glu Glu Lys Asn Gly Ala Tyr Gln Trp Val Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Gln Thr Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Glu Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Phe Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Ser Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Glu
180 185 190

Arg Ala Asp Asn Val Ile Lys Gly Thr Lys Asn Glu Gln Ile Gln Lys
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Ala Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Met
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Ser Leu Phe Ala Ser Leu Asp Lys
245 250 255

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

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Val Ile Asp Leu Ala Ile Lys Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Asp Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 851
<211> 510
<212> PRT
<213> Flaveria

<400> 851

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Asp Glu Ile His Ser Leu Tyr Asn Tyr Asp Thr Thr Glu Leu Leu
20 25 30

His Glu Glu Lys Asp Gly Ala Tyr Gln Trp Val Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Gln Thr Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Glu Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Ser Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Glu
180 185 190

Arg Ala Asp Asn Val Ile Lys Gly Thr Lys Asn Glu Gln Ile Gln Lys
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Ala Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Met
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Ser Leu Phe Ala Ser Leu Asp Lys
245 250 255

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

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Val Ile Asp Leu Ala Ile Lys Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Asp Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 852
<211> 510
<212> PRT
<213> Álamo

<400> 852

Met Phe Ile Glu Lys Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Asp Glu Ile His Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Lys Asn Gly Ser Tyr Gln Trp Thr Val Lys Pro Lys Thr
35 40 45

Val Gln Tyr Glu Phe Lys Thr Asp Ile His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val

85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Ala Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Gln Gln
195 200 205

Ile Ile Glu Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Ile Val

225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ala Val Glu Lys
245 250 255

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

Tyr Glu Asn Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Val Asp Leu Ala Ile Lys Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Gly Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val

370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Gly Glu
435 440 445

Ala Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 853

<211> 510
<212> PRT
<213> Clementina

<400> 853

Met Phe Ile Glu Asn Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Asp Asn Glu Ile His Ser Val Tyr Asp Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Val His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Thr Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Ile
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Arg Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Leu Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Met Leu Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Arg
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ile
225 230 235 240

Val Gly Leu Asn Asp Thr Val Glu Asn Leu Leu Ala Ser Leu Asp Lys
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Leu Glu Asn Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Arg Arg Asn Cys Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Gly Ile Leu Tyr Gly Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Val Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 854
<211> 510
<212> PRT
<213> Coffea

<400> 854

Met Phe Ile Glu Asn Phe Lys Val Asp Ser Pro Asn Val Lys Tyr Ser
1 5 10 15

Glu Ser Glu Ile His Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Arg Asp Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser
35 40 45

Val Gln Tyr Glu Phe Arg Thr Asp Ile His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Glu Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asn Leu Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Leu Ile Lys Gly Thr Lys Lys Glu Gln Val Glu Gln
195 200 205

Val Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Ile Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ala
225 230 235 240

Val Gly Leu Asn Asp Thr Thr Glu Asn Leu Leu Ala Ala Leu Asp Arg
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Met
260 265 270

Tyr Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Arg Asn Cys Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Gly Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Ser Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 855
<211> 510
<212> PRT
<213> Flaveria

<400> 855

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Asp Asp Glu Ile His Ser Leu Tyr Asn Tyr Asp Thr Thr Glu Leu Ile
20 25 30

His Glu Glu Lys Asn Gly Ala Tyr Gln Trp Val Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Lys Thr Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Glu Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Phe Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Ser Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Glu
180 185 190

Arg Ala Asp Asn Val Ile Lys Gly Thr Lys Asn Glu Gln Ile Gln Lys
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Ala Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Met
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Ser Leu Phe Ala Ser Leu Asp Lys
245 250 255

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

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Val Ile Asp Leu Ala Ile Lys Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Asp Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 856
<211> 510
<212> PRT
<213> Flaveria

<400> 856

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Asp Asp Glu Ile His Ser Leu Tyr Asn Tyr Asp Thr Thr Glu Leu Ile
20 25 30

His Glu Glu Lys Asn Gly Ala Tyr Gln Trp Val Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Lys Thr Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Glu Lys Val

85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Phe Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Ser Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Glu
180 185 190

Arg Ala Asp Asn Val Ile Lys Gly Thr Lys Asn Glu Gln Ile Gln Lys
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Ala Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Met

225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Ser Leu Phe Ala Ser Leu Asp Lys
245 250 255

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

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Val Ile Asp Leu Ala Ile Lys Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val

370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Asp Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Gly Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 857

<211> 510
<212> PRT
<213> Naranja

<400> 857

Met Phe Ile Glu Asn Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Asp His Glu Ile His Ser Val Tyr Asp Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Val His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ser Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Thr Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Ile
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Arg Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Met Leu Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Arg
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ile
225 230 235 240

Val Gly Leu Asn Asp Thr Val Glu Asn Leu Leu Ala Ser Leu Asp Lys
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Leu Glu Asn Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Arg Arg Asn Cys Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Gly Ile Leu Tyr Gly Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Val Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 858
<211> 510
<212> PRT
<213> Girasol

<400> 858

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Ser
1 5 10 15

Glu Asp Glu Ile His Ser Leu Tyr Asn Tyr Asp Thr Thr Glu Leu Val
20 25 30

His Glu Glu Lys Asn Gly Ala Tyr Gln Trp Val Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Gln Thr Asn Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Glu Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Ser Met Asn Leu Ala Asp Ser Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Val Phe Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Glu
180 185 190

Arg Ala Asp Asn Val Ile Lys Gly Thr Lys Asn Glu Gln Ile Gln Lys
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Ala Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Met
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Ser Leu Phe Ala Ser Leu Asp Arg
245 250 255

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

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Val Ile Asp Leu Ala Ile Lys Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Thr Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 859
<211> 510
<212> PRT
<213> Tabaco

<400> 859

Met Phe Ile Glu Asn Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Asn Glu Ile Arg Ser Val Tyr Asp Tyr Gln Thr Thr Glu Leu Val
20 25 30

His Glu Glu Lys Asn Gly Ser Tyr Gln Trp Thr Val Lys Pro Lys Cys
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Thr Asn Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Ile Ile Ala Asn Lys Glu Gly Ile Ser Trp Ala Thr Lys Glu Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asn Met Asn Leu Ala Asp Ala Met Val Arg Ala Lys Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Asn Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Glu Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Asp Gln
195 200 205

Ile Val Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Ile Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ile
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ala Val Asp Arg
245 250 255

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

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Arg Asn Thr Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Ala Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 860
<211> 510
<212> PRT
<213> Ambrosia

<400> 860

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Asp Glu Ile His Ser Leu Tyr Asn Tyr Asp Thr Thr Glu Leu Val
20 25 30

His Glu Glu Lys Asn Gly Ala Tyr Gln Trp Val Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Gln Thr Asn Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Glu Lys Val

85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Ser Met Asn Leu Ala Asp Ser Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Phe Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Glu
180 185 190

Arg Ala Asp Asn Val Ile Lys Gly Thr Lys Asn Glu Gln Ile Gln Lys
195 200 205

Val Ile Lys Asp Ile Arg Glu Phe Lys Glu Ala Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Met

225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Ser Leu Phe Ala Ser Leu Asp Arg
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Phe Ala Ile Ala Cys Ile
260 265 270

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Val Ile Asp Leu Ala Ile Lys Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val

370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Thr Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 861

<211> 510
<212> PRT
<213> Cirsium

<400> 861

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Pro Asp Glu Ile His Ser Leu Tyr Asn Tyr Asp Thr Thr Glu Leu Val
20 25 30

His Glu Glu Lys Asp Gly Ala Phe Gln Trp Val Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Gln Thr His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Ser Met Asn Leu Ala Asp Ser Met Ala Arg Ala Arg Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Phe Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asp Asn Val Ile Lys Gly Thr Lys Asn Glu Gln Ile Gln Lys
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Ala Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Phe Ala Ser Ile Asp Lys
245 250 255

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

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Val Ile Asp Leu Ala Ile Gln Arg Asn Thr Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Thr Asn Thr Ile Val Leu
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Ser Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 862
<211> 510
<212> PRT
<213> Euonymus

<400> 862

Met Phe Ile Glu Asn Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Thr Glu Ile His Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Lys Asn Gly Ser Tyr Gln Trp Thr Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Thr Ser Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Val Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Glu Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Met Pro Tyr Met Glu His Met Ile Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Asp Ser
180 185 190

Arg Ala Asn Asn Ile Ile Lys Gly Thr Lys Lys Glu Gln Val Gln Gln
195 200 205

Val Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Thr Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ile
225 230 235 240

Val Gly Leu Asn Asp Thr Ile Glu Asn Leu Phe Ala Ser Leu Asp Lys
245 250 255

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

Leu Glu Asn Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Gly Ile Leu Phe Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Asp
435 440 445

Asp Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 863
<211> 510
<212> PRT
<213> Flaveria

<400> 863

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Asp Asp Glu Ile His Ser Leu Tyr Asn Tyr Asp Thr Thr Glu Leu Ile
20 25 30

His Glu Gly Glu Asn Gly Ala Tyr Gln Trp Val Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Leu Gln Thr Gln Thr Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Glu Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Phe Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Ser Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Glu
180 185 190

Arg Ala Asp Asn Val Ile Lys Gly Thr Lys Asn Glu Gln Ile Gln Lys
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Ala Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Met
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Ser Leu Phe Ala Ser Leu Asp Lys
245 250 255

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

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Val Ile Asp Leu Ala Ile Lys Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Asp Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 864
<211> 510
<212> PRT
<213> Flor del mono

<400> 864

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Asp Asp Ile Gln Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Ser Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Thr His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val

85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp Asp Ile
130 135 140

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

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu His Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Ala Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Gln Gln
195 200 205

Leu Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Arg
210 215 220

Ile Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val

225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Met Ala Ser Val Asp Lys
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Phe Ala Ile Ala Cys Val
260 265 270

Leu Glu Asn Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Glu Met Ala Ile Gln Arg Asn Cys Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Gly Ile Leu Phe Glu Pro Gly Glu His Pro Asp His Val Val

370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Gly Lys Phe His Thr Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 865

<211> 510
<212> PRT
<213> Parthenium

<400> 865

Met Phe Ile Glu Asn Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Ser
1 5 10 15

Glu Asp Glu Ile His Ser Leu Tyr Asn Tyr Asp Thr Thr Glu Leu Val
20 25 30

His Glu Glu Lys Asn Gly Ala Tyr Gln Trp Val Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Gln Thr His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Glu Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Ser Met Asn Leu Ala Asp Ser Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Phe Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Glu
180 185 190

Arg Ala Asp Asn Val Ile Lys Gly Thr Lys Asn Glu Gln Ile Gln Lys
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Thr Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Met
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Ser Leu Phe Ala Ser Leu Asp Lys
245 250 255

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

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Val Ile Asp Leu Ala Ile Lys Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Thr Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 866
<211> 510
<212> PRT
<213> Prunus

<400> 866

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Asn Glu Ile His Ser Val Tyr Ser Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Glu Arg Lys Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Ile His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Arg Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Leu Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ala
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Gln Gln
195 200 205

Ile Ile Glu Asp Ile Arg Glu Phe Lys Glu Gln Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val
225 230 235 240

Val Gly Leu Asn Asp Thr Val Glu Asn Leu Leu Gly Ser Val Asp Lys
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Arg Arg Asn Cys Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Gly Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Ala Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ser Glu
435 440 445

Ala Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Ser Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 867
<211> 327
<212> PRT
<213> Phlya

<400> 867

Met Phe Ile Glu Ser Phe Lys Val Asp Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Gly Glu Ile His Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Leu
20 25 30

His Glu Asn Arg Asn Gly Ala Tyr Gln Trp Thr Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Thr His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Glu Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

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

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu His Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ala
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Glu Gln
195 200 205

Leu Ile Glu Asp Ile Arg Glu Phe Lys Glu Gln Asn Lys Val Asp Ser
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val
225 230 235 240

Val Gly Leu Asn Asp Thr Thr Glu Asn Leu Met Ala Ser Leu Glu Arg
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Phe Gly Leu Ala Cys Val
260 265 270

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Glu Leu Ala Ile Gln Arg Asn Cys Leu Ile Gly Gly
290 295 300

Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Arg
305 310 315 320

Phe Ser Cys Trp Ser Trp Tyr
325

<210> 868
<211> 446
<212> PRT
<213> Pteridium

<400> 868

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Ala
1 5 10 15

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
20 25 30

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
35 40 45

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
50 55 60

Leu Pro Met Val Asn Pro Glu Asp Ile Val Phe Gly Gly Trp Asp Ile
65 70 75 80

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
85 90 95

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Thr Val Pro
100 105 110

Ile Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Glu

115 120 125

Arg Ala Asn Asn Ile Ile Lys Gly Thr Lys Lys Glu Gln Val Gln Gln
130 135 140

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Arg
145 150 155 160

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ile
165 170 175

Val Gly Leu Asn Asp Thr Met Glu Ser Leu Leu Gly Ser Leu Glu Lys
180 185 190

Asn Glu Ser Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Ser Val
195 200 205

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
210 215 220

Pro Gly Leu Ile Asp Leu Ala Ile Gln Arg Asn Cys Leu Ile Gly Gly
225 230 235 240

Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp
245 250 255

Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn

260 265 270

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
275 280 285

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
290 295 300

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

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
325 330 335

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Gln Asn Thr Ile Val Leu
340 345 350

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
355 360 365

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

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

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn

405 410 415

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
420 425 430

Ile Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
435 440 445

<210> 869
<211> 510
<212> PRT
<213> Ambrosia

<400> 869

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Ala
1 5 10 15

Glu Asp Glu Ile His Ser Leu Tyr Asn Tyr Asp Thr Thr Glu Leu Val
20 25 30

His Glu Glu Lys Asn Gly Ser Tyr Gln Trp Val Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Gln Thr His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Glu Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Ser Met Asn Leu Ala Asp Ser Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Phe Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Glu
180 185 190

Arg Ala Asp Asn Val Ile Lys Gly Thr Lys Asn Glu Gln Ile Gln Lys
195 200 205

Val Ile Lys Asp Ile Arg Glu Phe Lys Glu Ala Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Met
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Ser Leu Phe Ala Ser Leu Asp Arg
245 250 255

Asn Glu Ser Glu Ile Ser Pro Ser Thr Leu Phe Ala Ile Ala Cys Ile
260 265 270

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Val Ile Asp Leu Ala Ile Lys Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Thr Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 870
<211> 510
<212> PRT
<213> Aristolochia

<400> 870

Met Phe Ile Glu Asn Phe Arg Val Glu Ser Pro Asn Val Lys Tyr Ile
1 5 10 15

Asp Gly Glu Ile Gln Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Arg Asn Gly Val Tyr Gln Trp Ile Val Lys Pro Lys Thr
35 40 45

Val Gln Tyr Glu Phe Lys Thr Asp Thr Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Phe Asp Leu Gln Lys Gln Val Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Glu Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Ala Asn Lys Val Asp Lys
210 215 220

Val Val Ile Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val
225 230 235 240

Val Gly Leu Asn Asp Thr Thr Glu Asn Leu Leu Ala Ala Leu Asp Arg
245 250 255

Asn Glu Ser Glu Ile Ser Pro Ser Thr Leu Tyr Ala Leu Ala Cys Val
260 265 270

Met Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Thr Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Gly Ile Leu Tyr Ala Pro Gly Glu His Pro Asp His Val Ile
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Val Gln Leu Lys Ala Glu
435 440 445

Gly Glu Ala Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Ile Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 871
<211> 511
<212> PRT
<213> Senecio

<400> 871

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Asp Thr Glu Ile His Ser Leu Tyr Asn Tyr Asp Thr Thr Glu Leu Val
20 25 30

His Glu Glu Asn Asn Asn Gly Ala Phe Gln Trp Val Val Lys Pro Lys
35 40 45

Thr Val Lys Tyr Glu Phe Lys Thr Gln Thr His Val Pro Lys Leu Gly
50 55 60

Val Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala
65 70 75 80

Gly Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Glu Lys
85 90 95

Val Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile
100 105 110

Arg Val Gly Ser Phe Asn Gly Glu Glu Ile His Ala Pro Phe Lys Ser
115 120 125

Leu Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp
130 135 140

Ile Ser Lys Met Asn Leu Ala Asp Ser Met Ala Arg Ala Gln Val Leu
145 150 155 160

Asp Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val
165 170 175

Pro Leu Pro Gly Ile Tyr Asp Ala Asp Phe Ile Ala Ala Asn Gln Gly
180 185 190

Ser Arg Ala Asp Asn Val Ile Lys Gly Thr Lys Asn Glu Gln Ile Gln
195 200 205

Lys Leu Ile Lys Asp Ile Arg Glu Phe Lys Glu Ser Asn Lys Val Asp
210 215 220

Lys Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val
225 230 235 240

Val Val Gly Leu Asn Asp Thr Met Glu Ser Leu Phe Ala Ser Leu Asp
245 250 255

Arg Asn Glu Ser Glu Ile Ser Pro Ser Thr Leu Phe Ala Ile Ala Cys
260 265 270

Ile Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe
275 280 285

Val Pro Gly Val Ile Glu Leu Ala Ile Lys Arg Asn Ser Leu Ile Gly
290 295 300

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

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

Asn His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr
340 345 350

Phe Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val
355 360 365

Ser Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val
370 375 380

Val Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met
385 390 395 400

Asp Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Ser Thr Ile Val
405 410 415

Met His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu
420 425 430

Asp Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Glu Leu Lys Ser
435 440 445

Glu Thr Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu
450 455 460

Ser Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val
465 470 475 480

Asn Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala
485 490 495

Cys Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 872
<211> 510
<212> PRT
<213> Tripterygium

<400> 872

Met Phe Ile Glu Asn Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Gly Thr Glu Ile His Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Leu
20 25 30

His Glu Asn Arg Asn Gly Ser Tyr Gln Trp Thr Val Lys Pro Lys Thr

35 40 45

Val Gln Tyr Glu Phe Lys Thr Asp Thr Ser Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Ala Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Glu Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu His Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Asp Ser

180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Gln Gln
195 200 205

Val Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Thr Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ile
225 230 235 240

Val Gly Leu Asn Asp Thr Ile Glu Asn Leu Phe Ala Ser Leu Glu Lys
245 250 255

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

Leu Glu Asn Ile Pro Phe Val Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Asn Asn Ser Leu Ile Gly Gly
290 295 300

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

Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn

325 330 335

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Gly Ile Leu Phe Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Arg Asn Thr Ile Val Leu
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Ile Lys Ala Glu
435 440 445

Asp Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn

465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 873
<211> 510
<212> PRT
<213> Artemisia

<400> 873

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Ser
1 5 10 15

Glu Asp Glu Ile His Ser Val Tyr Asp Tyr Asp Thr Thr Glu Leu Val
20 25 30

His Glu Glu Lys Asn Gly Ala Tyr Gln Trp Val Val Arg Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Gln Thr Asn Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Ser Met Asn Leu Ala Asp Ala Met Ala Arg Ala Arg Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Phe Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asp Asn Val Ile Lys Gly Thr Lys Asn Glu Gln Ile Gln Lys
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Ala Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Met Phe Ala Ser Leu Asp Arg
245 250 255

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

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Val Ile Glu Leu Ala Ile Lys His Asn Thr Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Ala Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Thr Asn Thr Ile Val Met
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Glu Leu Lys Ser Glu
435 440 445

Ala Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 874
<211> 510
<212> PRT
<213> Papa

<400> 874

Met Phe Ile Glu Asn Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Ile
1 5 10 15

Glu Asn Glu Ile His Ser Val Tyr Asp Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Glu Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Thr His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Glu Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asn Met Asn Leu Ala Asp Ala Met Val Arg Ala Lys Val Phe Glu
145 150 155 160

Val Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Glu Ala
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Asp Gln
195 200 205

Ile Val Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Ile Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ala Val Asp Arg
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu His Ala Ile Ala Cys Ile
260 265 270

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Arg Asn Thr Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Ser Ile Leu Tyr Glu Ser Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Met Ser Glu Ile Phe Met Gly Gly Lys Ser Thr Ile Val Met
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ser Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 875
<211> 510
<212> PRT
<213> Rosa

<400> 875

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Glu Tyr Thr
1 5 10 15

Glu Asn Glu Ile His Ser Val Tyr Thr Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Arg Lys Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Val His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Arg Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Gln Glu Gln Val Gln Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Met
225 230 235 240

Glu Gly Leu Asn Asp Thr Val Glu Asn Leu Leu Gly Ser Val Asp Lys
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Met Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Arg Arg Asn Thr Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Gly Ile Leu Phe Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Ala Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Leu Gly Gly Arg Asn Thr Ile Val Met
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ser Glu
435 440 445

Asp Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 876
<211> 510
<212> PRT
<213> Solanum phureja

<400> 876

Met Phe Ile Glu Asn Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Ile
1 5 10 15

Glu Asn Glu Ile His Ser Val Tyr Asp Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Glu Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser

35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Thr His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Glu Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Ile Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asn Met Asn Leu Ala Asp Ala Met Val Arg Ala Lys Val Phe Glu
145 150 155 160

Val Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Glu Ala

180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Asp Gln
195 200 205

Ile Val Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Ile Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ala Val Asp Arg
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu His Ala Ile Ala Cys Ile
260 265 270

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Arg Asn Thr Leu Ile Gly Gly
290 295 300

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

Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn

325 330 335

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Ser Ile Leu Tyr Glu Ser Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Met Ser Glu Ile Phe Met Gly Gly Lys Ser Thr Ile Val Met
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn

465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 877
<211> 510
<212> PRT
<213> Triphysaria

<400> 877

Met Phe Ile Asp Ser Phe Lys Val Asp Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Thr Glu Ile His Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Glu Ala Ile Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Thr Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Glu Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Glu Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

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

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Gln Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asn Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

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

Leu Ile Lys Asp Ile Arg Glu Phe Lys Glu Gln Asn Lys Val Asp Arg
210 215 220

Ile Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ala
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Met Ala Ser Val Asp Arg
245 250 255

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

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Glu Leu Ala Ile Gln Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Gly Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 878
<211> 510
<212> PRT
<213> Manzana

<400> 878

Met Phe Ile Asp Ser Phe Lys Val Glu Ser Pro Asn Val Ala Tyr Thr
1 5 10 15

Glu Asn Glu Ile His Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Arg Asn Gly Ala Tyr Gln Trp Ile Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Val His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Leu Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ala
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Leu Gln Gln
195 200 205

Val Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Arg
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val
225 230 235 240

Val Gly Leu Asn Asp Thr Val Glu Asn Leu Leu Gly Ser Val Asp Lys
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Leu Glu Asn Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Arg Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Gly Ile Leu Tyr Gly Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Leu Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Gln Asn Thr Ile Val Leu
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ser Glu
435 440 445

Ala Glu Ala Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Ser Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 879
<211> 510
<212> PRT
<213> Aquilegia

<400> 879

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Asp Asp Glu Ile His Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Lys Asn Gly Ser Tyr Gln Trp Val Val Lys Pro Lys Ser
35 40 45

Val Gln Tyr Glu Phe Lys Thr Asp Thr His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp Asp Ile
130 135 140

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

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn His Val Ile Lys Gly Thr Lys Lys Glu Gln Met Gln Gln
195 200 205

Val Ile Lys Asp Ile Arg Glu Phe Lys Glu Ala Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ile
225 230 235 240

Val Gly Leu Asn Asp Thr Val Glu Ser Leu Leu Ala Ser Leu Asp Lys
245 250 255

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

Tyr Glu Asp Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Val Ile Asp Leu Ala Ile Lys Arg Asn Val Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Gly Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Ile
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Ser Thr Ile Val Met
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Ala
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ser Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 880
<211> 510
<212> PRT
<213> Arnica

<400> 880

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Asp Glu Ile His Ser Val Tyr Asn Tyr Asp Thr Thr Glu Leu Val
20 25 30

His Glu Glu Lys Asp Gly Ala Tyr Gln Trp Leu Val Lys Pro Lys Thr

35 40 45

Val Lys Tyr Glu Phe Lys Thr Gln Thr Arg Leu Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Glu Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Ser Met Asn Leu Ala Asp Ser Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Val Pro Gly Ile Phe Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ala

180 185 190

Arg Ala Asp Asn Cys Ile Lys Gly Thr Lys Asn Glu Gln Ile Gln Lys
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Ala Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Met
225 230 235 240

Phe Gly Leu Asn Asp Thr Met Glu Ser Leu Phe Ala Ser Leu Asp Lys
245 250 255

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

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Val Ile Asp Leu Ala Ile Lys Arg Asn Thr Leu Ile Gly Gly
290 295 300

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

Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn

325 330 335

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Thr Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn

465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 881
<211> 510
<212> PRT
<213> Cirsium

<400> 881

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Ser Asp Glu Ile His Ser Leu Tyr Asn Tyr Asp Thr Thr Glu Leu Val
20 25 30

His Glu Glu Lys Asp Gly Ala Phe Gln Trp Val Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Gln Thr Pro Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Ser Met Asn Leu Ala Asp Ser Met Ala Arg Ala Arg Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Phe Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asp Asn Val Ile Lys Gly Asn Lys Asn Glu Gln Ile Gln Lys
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Ala Asn Lys Val Glu Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Phe Ala Ser Ile Asp Lys
245 250 255

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

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Val Ile Asp Leu Ala Ile Gln Arg Asn Thr Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Thr Asn Thr Ile Val Leu
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Ser Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 882
<211> 510
<212> PRT
<213> Cleome spinosa

<400> 882

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Asn Glu Ile His Ser Val Tyr Asp Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Val Asn Gly Ala Tyr Gln Trp Ile Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Val His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Arg Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Ser Val Ile Lys Gly Ser Lys Lys Glu Gln Val Asp Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Ser Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ile
225 230 235 240

Ala Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Val Asp Lys
245 250 255

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

Phe Glu Gly Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Met Ala Ile Arg Arg Asn Cys Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Gly Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Ala Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Ser Thr Ile Val Met
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Gly Lys Phe His Thr Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 883
<211> 512
<212> PRT
<213> Aizoáceas

<400> 883

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Asn Glu Ile Glu Ser Val Tyr Asn Tyr Asp Thr Thr Glu Leu Val
20 25 30

His Glu Asn Arg Lys Asp Ala Gly Gly Tyr Gln Trp Ile Val Lys Pro
35 40 45

Lys Thr Val Gln Tyr His Phe Lys Thr Asp Thr Arg Val Pro Lys Leu
50 55 60

Gly Val Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr
65 70 75 80

Gly Gly Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp
85 90 95

Lys Ile Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser
100 105 110

Ile Arg Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys
115 120 125

Ser Leu Leu Pro Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp
130 135 140

Asp Ile Ser Asp Met Asn Leu Ala Asp Ala Met Thr Arg Ala Arg Val
145 150 155 160

Phe Asp Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu His Met
165 170 175

Val Pro Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln
180 185 190

Gly Ser Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val
195 200 205

Glu Arg Val Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val
210 215 220

Asp Lys Val Val Val Leu Trp Thr Gly Asn Thr Glu Arg Tyr Ser Asn
225 230 235 240

Val Val Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Leu
245 250 255

Glu Lys Asn Glu Ser Glu Ile Ser Pro Ser Thr Leu Tyr Ala Leu Ala
260 265 270

Cys Ile Glu Glu Asn Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr
275 280 285

Phe Val Pro Gly Leu Ile Asp Leu Ala Ile Lys Lys Asn Ser Leu Ile
290 295 300

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

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

Tyr Asn His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln
340 345 350

Thr Phe Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met
355 360 365

Val Ala Ser Asn Gly Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His
370 375 380

Val Val Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala
385 390 395 400

Met Asp Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Thr Asn Thr Ile
405 410 415

Val Met His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile
420 425 430

Leu Asp Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys
435 440 445

Ala Glu Glu Glu Asp Lys Phe His Ser Phe His Pro Val Ala Thr Ile
450 455 460

Leu Ser Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val
465 470 475 480

Val Asn Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg
485 490 495

Ala Cys Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 884
<211> 510
<212> PRT
<213> Pimiento

<400> 884

Met Phe Ile Glu Asn Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Asn Glu Ile Gln Ser Val Tyr Ile Tyr Asp Thr Thr Glu Leu Val
20 25 30

His Glu Ala Arg Asn Gly Asn Tyr Gln Trp Ile Val Lys Pro Asn Ser

35 40 45

Val Gln Tyr Gln Phe Lys Thr Asp Ile His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Glu Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asn Met Asn Leu Ala Asp Ala Met Val Arg Ala Lys Val Phe Asp
145 150 155 160

Val Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Glu Ala

180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Asp Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Ile Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ile
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ala Val Asp Arg
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu His Ala Ile Ala Cys Ile
260 265 270

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Gln Arg Asn Thr Leu Ile Gly Gly
290 295 300

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

Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn

325 330 335

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Ser Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Ser Thr Ile Val Met
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn

465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 885
<211> 510
<212> PRT
<213> Platanus

<400> 885

Met Phe Ile Glu Gly Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Asp Asp Glu Ile Gln Ser Val Tyr Ser Tyr Glu Ser Thr Glu Leu Val
20 25 30

His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Thr
35 40 45

Val Gln Tyr Glu Phe Lys Thr Asp Ile Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Ile Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Leu Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Arg Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Val Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Leu Glu Gln
195 200 205

Ile Met Lys Asp Ile Arg Glu Phe Lys Glu Ala Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Leu Glu Lys
245 250 255

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

Tyr Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Val Ile Asp Leu Ala Ile Lys Ser Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Gly Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Ile
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Ile Lys Ala Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 886
<211> 510
<212> PRT
<213> Valeriana

<400> 886

Met Phe Ile Glu Ser Phe Lys Val Asp Ser Pro Asn Val Thr Tyr Thr
1 5 10 15

Glu Asn Glu Ile His Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Leu
20 25 30

His Glu Asn Lys Asn Gly Ala Tyr Gln Trp Thr Val Lys Pro Lys Ser
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Thr His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Ser Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Glu Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Gln Gln
195 200 205

Val Ile Lys Asp Ile Arg Glu Phe Lys Glu Ala Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ile
225 230 235 240

Val Gly Leu Asn Asp Thr Glu Glu Asn Leu Phe Ala Ser Leu Glu Lys
245 250 255

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

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Arg Lys Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Gln
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Val Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ser Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 887
<211> 510
<212> PRT
<213> B. rapa, Canola

<400> 887

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Asn Glu Ile Gln Ser Val Tyr Asp Tyr Glu Thr Thr Glu Val Val
20 25 30

His Glu Asn Val Asn Gly Ala Tyr Gln Trp Ile Val Lys Pro Lys Val
35 40 45

Val Lys Tyr Asp Phe Lys Thr Asp Thr Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Lys Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Val Pro Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp Asp Ile
130 135 140

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

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Asn Ile Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Asn Gly Thr Lys Lys Glu Gln Val Asp Gln
195 200 205

Ile Ile Lys Asp Met Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Met Asn Ser Val Asp Arg
245 250 255

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

Leu Glu Gly Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Asn Asn Val Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Gly Ile Leu Phe Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Ala Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Met
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ser Glu
435 440 445

Lys Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 888
<211> 510
<212> PRT
<213> B. rapa, Canola

<400> 888

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Asn Glu Ile His Ser Val Tyr Asp Tyr Glu Thr Thr Glu Val Val
20 25 30

His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Val Val Lys Pro Lys Thr

35 40 45

Val Lys Tyr Asp Phe Lys Thr Asp Thr Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Lys Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Arg Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu His Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser

180 185 190

Arg Ala Asn Ser Val Ile Lys Gly Thr Lys Lys Glu Gln Val Asp Gln
195 200 205

Ile Ile Lys Asp Met Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

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

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Val Glu Lys
245 250 255

Asn Glu Ser Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Leu Glu Gly Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Glu Leu Ala Ile Thr Lys Asn Cys Leu Ile Gly Gly
290 295 300

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

Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn

325 330 335

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Gly Ile Leu Phe Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Met
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ala Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn

465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 889
<211> 510
<212> PRT
<213> Palma aceitera

<400> 889

Met Phe Ile Glu Lys Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Gly
1 5 10 15

Glu His Glu Ile Glu Ser Val Tyr His Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Arg Asp Gly Ser Tyr Gln Trp Ile Val Lys Pro Lys Thr
35 40 45

Val Arg Phe Asp Phe Lys Thr Asp Thr Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Ala Gly Trp Gly Gly Asn Asn Gly Ala Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Tyr Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Ile Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Glu Gly Thr Lys Lys Glu Gln Val Gln Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Glu Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ile
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Leu Asp Arg
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Leu Ala Cys Val
260 265 270

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Gly Ile Leu Tyr Gly Pro Gly Glu His Pro Asp His Val Ile
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Arg Asn Thr Ile Val Leu
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Ser Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Ile Gly Leu Ser Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 890
<211> 510
<212> PRT
<213> Canola, trigo

<400> 890

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Asn Glu Ile His Ser Val Tyr Asp Tyr Glu Thr Thr Glu Val Val
20 25 30

His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Val Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Asp Phe Lys Thr Asp Thr Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Lys Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Arg Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu His Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Ser Val Ile Lys Gly Thr Lys Lys Glu Gln Val Asp Gln
195 200 205

Ile Ile Lys Asp Met Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

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

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Val Glu Lys
245 250 255

Asn Glu Ser Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Leu Glu Gly Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Glu Leu Ala Ile Ser Lys Asn Cys Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Gly Ile Leu Phe Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Met
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ala Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Ala Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 891
<211> 510
<212> PRT
<213> Diente de león

<400> 891

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Asp Glu Ile His Ser Val Tyr Asn Tyr Asp Thr Thr Glu Leu Val
20 25 30

His Glu Glu Lys Asn Gly Ala Tyr Gln Trp Val Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Gln Ala Asn Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Ser Met Asn Leu Ala Asp Ser Met Ala Arg Ala Arg Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Ile Pro
165 170 175

Leu Pro Gly Ile Phe Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asp Asn Val Ile Lys Gly Asn Lys Asn Glu Gln Ile Gln Lys
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Ala Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val
225 230 235 240

Val Gly Leu Asn Asp Thr Val Glu Asn Leu Phe Ala Ser Ile Asp Lys
245 250 255

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

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Val Ile Asp Leu Ala Ile Gln Lys Asn Thr Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Thr Asn Thr Ile Val Leu
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Glu Leu Lys Ser Glu
435 440 445

Thr Gln Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 892
<211> 112
<212> PRT
<213> Epimedium

<400> 892

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Asn Glu Val Gln Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Ser Arg Asn Gly Val Tyr Gln Trp Val Val Lys Pro Lys Thr

35 40 45

Val Gln Tyr Glu Phe Lys Thr Asp Thr His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Arg Gln Gly Ile Ser Trp Ala Thr Lys Glu Lys Tyr
85 90 95

Asn Arg Leu Ile Ile Leu Ala Pro Ser Leu Lys His Arg Ala Ser Gly
100 105 110

<210> 893
<211> 510
<212> PRT
<213> Euonymus

<400> 893

Met Phe Ile Glu Asn Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Thr Glu Ile His Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Arg Asn Gly Ser Tyr Gln Trp Thr Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Thr Ser Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Lys Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Tyr His Gly Glu Glu Val Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Glu Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Met Pro Tyr Met Glu His Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Asp Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Gln Gln
195 200 205

Val Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Thr Lys Val Asp Arg
210 215 220

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

Val Gly Leu Asn Asp Thr Thr Glu Asn Leu Phe Ala Ala Leu Asp Arg
245 250 255

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

Leu Glu Asn Ile Pro Phe Val Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Gly Ile Leu Phe Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Thr Asn Thr Ile Val Met
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Ser Arg Ile Gln Leu Lys Ala Glu
435 440 445

Asp Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 894
<211> 510
<212> PRT
<213> Euphorbia

<400> 894

Met Phe Ile Glu Lys Phe Gln Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Asn Asp Glu Val His Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Ser Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Gln Phe Lys Thr Asp Leu Asn Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Cys Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Lys Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Arg Val Phe Glu
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Glu Gln
195 200 205

Ile Arg Lys Asp Ile Arg Glu Phe Lys Glu Lys Thr Lys Val Asp Arg
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ala
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Val Asp Lys
245 250 255

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

Tyr Glu Asp Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Met Arg Asn Cys Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Gly Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Asp
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 895
<211> 510
<212> PRT
<213> Lechuga

<400> 895

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Ala
1 5 10 15

Glu Asp Glu Ile His Ser Leu Tyr Asn Tyr Asp Thr Thr Glu Leu Ile
20 25 30

His Glu Glu Lys Asn Gly Ala Tyr Gln Trp Val Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Gln Thr His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Ser Met Asn Leu Ala Asp Ser Met Ala Arg Ala Arg Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Phe Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asp Asn Val Ile Lys Gly Asn Lys Asn Glu Gln Ile Gln Lys
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Ala Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val
225 230 235 240

Val Gly Leu Asn Asp Thr Val Glu Asn Leu Phe Lys Ser Ile Asp Lys
245 250 255

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

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Val Ile Asp Leu Ala Ile Ser Lys Asn Thr Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Thr Asn Thr Ile Val Leu
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Thr Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 896
<211> 510
<212> PRT
<213> Álamo

<400> 896

Met Phe Ile Glu Lys Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Ile

1 5 10 15

Glu Asp Glu Ile His Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Arg Asn Gly Ser Tyr Gln Trp Thr Val Lys Pro Lys Thr
35 40 45

Val Gln Tyr Glu Phe Lys Thr Asp Ile Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Lys Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Leu Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp

145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Leu Gln Lys
195 200 205

Ile Met Glu Asp Ile Arg Glu Phe Lys Glu Ala Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Ile Val
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ala Val Glu Lys
245 250 255

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

Asn Glu Asn Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Arg Asn Ser Leu Ile Gly Gly

290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Gly Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Gln Asn Thr Ile Val Met
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Gly Glu

435 440 445

Ala Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 897
<211> 510
<212> PRT
<213> Rábano

<220>
<221> misc_feature
<222> (36)..(36)
<223> Xaa puede ser cualquier aminoácido de origen natural

<220>
<221> misc_feature
<222> (41)..(41)
<223> Xaa puede ser cualquier aminoácido de origen natural

<220>

<221> misc_feature
<222> (52)..(52)
<223> Xaa puede ser cualquier aminoácido de origen natural

<400> 897

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Asn Glu Ile His Ser Val Tyr Asp Tyr Glu Thr Thr Glu Val Val
20 25 30

His Glu Asn Xaa Asn Gly Thr Tyr Xaa Trp Val Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Xaa Phe Lys Thr Asp Thr Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Lys Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Arg Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu His Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Ser Val Ile Lys Gly Thr Lys Lys Glu Gln Val Asp Gln
195 200 205

Ile Ile Lys Asp Met Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

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

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Val Glu Lys
245 250 255

Asn Glu Ser Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Leu Glu Gly Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Glu Leu Ala Ile Ser Lys Asn Cys Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Gly Ile Leu Phe Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Met
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ala Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 898
<211> 510
<212> PRT
<213> Tragopogon

<400> 898

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Ser Asn Val Lys Tyr Thr
1 5 10 15

Glu Asn Glu Ile Gln Ser Leu Tyr Asn Tyr Asp Thr Thr Glu Leu Val
20 25 30

His Glu Glu Lys Asp Gly Ala Tyr Gln Trp Val Val Arg Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Gln Thr Asn Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Ser Met Asn Leu Ala Asp Ser Met Ala Arg Ala Arg Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Phe Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asp Asn Ile Ile Lys Gly Thr Lys Asn Glu Gln Ile Gln Lys
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Ala Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val
225 230 235 240

Val Gly Leu Asn Asp Thr Val Glu Asn Leu Phe Ala Ser Ile Asp Lys
245 250 255

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

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Val Ile Asp Leu Ala Ile Lys Lys Asn Thr Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Thr Asn Thr Ile Val Leu
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ser Glu
435 440 445

Thr Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 899
<211> 510
<212> PRT
<213> B. juncea

<400> 899

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Asn Glu Ile Gln Ser Val Tyr Asp Tyr Glu Thr Thr Glu Val Val
20 25 30

His Glu Asn Val Asn Gly Ala Tyr Gln Trp Ile Val Lys Pro Lys Val
35 40 45

Val Lys Tyr Asp Phe Lys Thr Asp Thr Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Lys Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Val Pro Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp Asp Ile
130 135 140

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

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Asn Ile Val Pro
165 170 175

Leu Pro Gly Ile Phe Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Asp Gln
195 200 205

Ile Ile Lys Asp Met Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ile
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Met Asn Ser Val Asp Arg
245 250 255

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

Leu Glu Gly Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Asn Asn Val Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Gly Ile Leu Phe Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Ala Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Met
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ser Glu
435 440 445

Lys Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 900
<211> 510
<212> PRT
<213> Canola

<400> 900

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Asn Glu Ile His Ser Val Tyr Asp Tyr Glu Thr Thr Glu Val Val
20 25 30

His Glu Asn Val Asn Gly Ala Tyr Gln Trp Ile Val Lys Pro Lys Val
35 40 45

Val Lys Tyr Asp Phe Lys Thr Asp Thr Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Lys Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val

85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Val Pro Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp Asp Ile
130 135 140

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

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Asn Ile Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Asp Gln
195 200 205

Ile Ile Lys Asp Met Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ile

225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Met Asn Ser Val Asp Arg
245 250 255

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

Leu Glu Gly Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Asn Asn Val Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Gly Ile Leu Phe Glu Pro Gly Glu His Pro Asp His Val Val

370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Ala Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Met
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ser Glu
435 440 445

Lys Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 901

<211> 510
<212> PRT
<213> Euonymus

<400> 901

Met Phe Ile Glu Asn Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Thr Glu Ile His Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Arg Asn Gly Ser Tyr Gln Trp Thr Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Thr Ser Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Lys Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Tyr His Gly Glu Glu Val Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Glu Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Met Pro Tyr Met Glu His Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Asp Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Gln Gln
195 200 205

Val Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Thr Lys Val Asp Arg
210 215 220

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

Val Gly Leu Asn Asp Thr Thr Glu Asn Leu Phe Ala Ala Leu Asp Arg
245 250 255

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

Leu Glu Asn Ile Pro Phe Val Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Val Asp Leu Ala Ile Lys Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Gly Ile Leu Phe Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Thr Asn Thr Ile Val Met
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Ser Arg Ile Gln Leu Lys Ala Glu
435 440 445

Asp Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 902
<211> 510
<212> PRT
<213> Fresa

<400> 902

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Glu Tyr Thr
1 5 10 15

Glu Asn Glu Ile His Ser Val Tyr Thr Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Arg Lys Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Val His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Arg Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Ile Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Gln Glu Gln Val Gln Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Ser Val Ile
225 230 235 240

Glu Gly Leu Asn Asp Thr Val Glu Asn Leu Leu Gly Ser Val Glu Lys
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Met Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Arg Arg Asn Thr Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Gly Ile Leu Phe Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Ala Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Leu Gly Gly Arg Asn Thr Ile Val Met
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ser Glu
435 440 445

Ala Glu Ala Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 903
<211> 510
<212> PRT
<213> Thellungiella parvulum

<400> 903

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Asn Glu Ile Gln Ser Val Tyr Asp Tyr Glu Thr Thr Glu Val Val
20 25 30

His Glu Asn Ile Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Val
35 40 45

Val Lys Tyr Asp Phe Lys Thr Asp Thr Arg Val Pro Asn Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Lys Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp Asp Ile
130 135 140

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

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Asn Ile Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

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

Ile Ile Lys Asp Met Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

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

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Met Asn Ser Val Asp Arg
245 250 255

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

Leu Glu Gly Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Asn Asn Val Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Gly Ile Leu Phe Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Ala Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Met
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ser Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 904
<211> 510
<212> PRT
<213> Thellungiella parvulum

<400> 904

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Asn Glu Ile His Ser Val Tyr Asp Tyr Gln Thr Thr Glu Leu Val
20 25 30

His Glu Ser Lys Asn Gly Ala Tyr Gln Trp Ile Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Thr His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Glu Lys Val

85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Glu Glu Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Phe Met Glu His Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn His Leu Ile Lys Gly Thr Lys Lys Gln Gln Leu Glu Gln
195 200 205

Val Ile Lys Asp Ile Arg Asp Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val

225 230 235 240

Ala Gly Leu Asn Asp Thr Thr Glu Asn Leu Met Ser Ser Leu Asp Asn
245 250 255

Asn Glu Ser Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Ile Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Glu Leu Ala Ile Lys Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Gly Ile Leu Tyr Glu Ser Gly Glu His Pro Asp His Val Val

370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Met
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Thr Thr Arg Ile Glu Phe Lys Ala Glu
435 440 445

Thr Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Ser Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 905

<211> 61
<212> PRT
<213> Pepino

<400> 905

Met Phe Ile Asp Ser Phe Lys Val Glu Ser Pro Asn Val Thr Tyr Ser
1 5 10 15

Asp His Glu Ile His Ser Ile Tyr Asn Tyr Glu Thr Thr Glu Leu Leu
20 25 30

His Glu Asn Arg Asn Gly Thr Tyr His Gly Leu Ser Asn Pro Asn Pro
35 40 45

Phe Asn Ile Asn Ser Arg Leu Ile Phe Val Ser Pro Asn
50 55 60

<210> 906
<211> 446
<212> PRT
<213> Thellungiella halophilum

<400> 906

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
1 5 10 15

Val Ile Ala Asn Lys Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
20 25 30

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
35 40 45

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
50 55 60

Leu Pro Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp Asp Ile
65 70 75 80

Ser Asp Met Asn Leu Ala Asp Ala Met Gly Arg Ala Lys Val Leu Asp
85 90 95

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Asn Ile Val Pro
100 105 110

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
115 120 125

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

Ile Ile Lys Asp Met Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
145 150 155 160

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ile
165 170 175

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Met Asn Ser Val Asp Arg
180 185 190

Asp Glu Ser Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
195 200 205

Leu Glu Gly Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
210 215 220

Pro Gly Leu Ile Asp Leu Ala Ile Lys Asn Asn Val Leu Ile Gly Gly
225 230 235 240

Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp
245 250 255

Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn
260 265 270

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Val Pro Gln Thr Phe
275 280 285

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
290 295 300

Ser Asn Gly Ile Leu Phe Glu Pro Gly Glu His Pro Asp His Val Val
305 310 315 320

Val Ile Lys Tyr Val Pro Tyr Val Ala Asp Ser Lys Arg Ala Met Asp
325 330 335

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Met
340 345 350

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
355 360 365

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ser Glu
370 375 380

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

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
405 410 415

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
420 425 430

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
435 440 445

<210> 907
<211> 510
<212> PRT

<213> Eschscholzia

<400> 907

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Asn Thr Ile His Ser Val Tyr Asn Tyr Glu Thr Thr Gln Leu Val
20 25 30

His Glu Asn Lys Asn Gly Ala Tyr Gln Trp Thr Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Asn Thr Asp Thr Asn Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Leu Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Leu Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Leu Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Ile Ile Lys Gly Thr Lys Lys Glu Gln Val Gln Glu
195 200 205

Ile Ile Lys His Met Arg Glu Phe Lys Glu Ala Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ile
225 230 235 240

Val Gly Leu Asn Asp Thr Thr Glu Asn Leu Leu Ala Ser Leu Glu Arg
245 250 255

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

Tyr Glu Asn Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys His Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Gly Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Ile
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Ser Thr Ile Val Met
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Thr Thr Arg Ile Gln Leu Lys Ser Glu
435 440 445

Ala Glu Asp Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 908
<211> 510
<212> PRT
<213> Primula

<400> 908

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Asp Glu Ile His Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val

20 25 30

His Glu Ser Arg Asn Gly Ser Tyr Gln Trp Ile Val Lys Pro Lys Ser
35 40 45

Ile Gly Tyr Gln Phe Lys Thr Leu Thr Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Trp Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ser Met Ala Arg Ala Arg Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu His Met Val Pro

165 170 175

Leu Pro Gly Ile Phe Asn Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

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

Val Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Ser Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ile
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Met Ala Ser Val Asp Lys
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Glu Leu Ala Ile Gln Arg Asn Thr Leu Ile Gly Gly
290 295 300

Asp Asp Phe Lys Ser Gly Gln Thr Lys Ile Lys Ser Val Leu Val Asp

305 310 315 320

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Thr Asn Thr Ile Val Met
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ser Val Ile Leu Ser

450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ser Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 909
<211> 510
<212> PRT
<213> Amorphophallus

<400> 909

Met Phe Ile Glu Lys Phe Arg Val Glu Ser Pro Asn Val Lys Tyr Gly
1 5 10 15

Ala His Glu Ile Glu Ser Val Tyr Ser Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Leu Arg Asp Gly Ser Tyr Gln Trp Val Val Lys Pro Lys Ser
35 40 45

Val Arg Tyr Gln Phe Lys Thr Asp Thr Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ala Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Val Thr Lys Asp Lys Ile
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ala Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Val Lys Gly Ser Lys Lys Glu Gln Val Gln Gln
195 200 205

Val Ile Lys Asp Ile Arg Glu Phe Lys Glu Arg Glu Lys Val Asp Gln
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val
225 230 235 240

Val Gly Leu Asn Asp Thr Thr Asp Asn Leu Leu Ala Ala Leu Asp Arg
245 250 255

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

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Lys Asn Ser Met Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Gly Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Ile
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Ala Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Ile Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 910
<211> 510
<212> PRT
<213> Arabidopsis lyrata

<400> 910

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Asn Glu Ile His Ser Val Tyr Asp Tyr Gln Thr Thr Glu Leu Val
20 25 30

His Glu Asn Lys Asn Gly Ala Phe Gln Trp Thr Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Thr His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Glu Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Glu Glu Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Leu Met Glu His Met Val Pro
165 170 175

Leu Pro Gly Ile Phe Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

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

Val Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val
225 230 235 240

Val Gly Leu Asn Asp Thr Thr Glu Asn Leu Met Ser Ser Leu Glu Lys
245 250 255

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

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Glu Leu Ala Ile Glu Arg Asn Cys Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Gly
355 360 365

Ser Asn Gly Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Met
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Thr Thr Arg Ile Gln Phe Met Ala Glu
435 440 445

Thr Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Leu Leu Ser
450 455 460

Tyr Leu Ser Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 911
<211> 509
<212> PRT

<213> Remolacha

<400> 911

Met Phe Ile Asp Asn Phe Lys Val Glu Ser Pro Asn Val Thr Tyr Thr
1 5 10 15

Glu Asn Glu Ile His Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Arg Lys Gly Cys Gly Tyr Gln Trp Ile Val Lys Pro Lys
35 40 45

Ser Val Lys Tyr Glu Phe Lys Thr Asp Thr His Val Pro Lys Leu Gly
50 55 60

Val Met Leu Val Gly Trp Gly Gly Asn Asn Gly Cys Thr Leu Thr Gly
65 70 75 80

Gly Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys
85 90 95

Ile Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile
100 105 110

Arg Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser
115 120 125

Leu Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp
130 135 140

Ile Ser Asp Met Asn Leu Ala Asp Ala Met Thr Arg Ala Lys Val Leu
145 150 155 160

Asp Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu His Met Ile
165 170 175

Pro Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Asp
180 185 190

Ser Arg Ala Asn Asn Ile Ile Lys Gly Thr Lys Lys Glu Gln Val Glu
195 200 205

Gln Val Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp
210 215 220

Lys Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val
225 230 235 240

Val Glu Gly Leu Asn Gly Thr Thr Glu Asn Leu Leu Ala Ser Val Glu
245 250 255

Arg Asn Glu Ser Glu Ile Ser Pro Ser Thr Leu Phe Ala Leu Ala Cys
260 265 270

Val Leu Glu Asn Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe
275 280 285

Val Pro Gly Leu Ile Glu Leu Ala Thr Lys Asn Asn Ser Leu Ile Gly
290 295 300

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

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

Asn His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr
340 345 350

Phe Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val
355 360 365

Ala Ser Asn Gly Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val
370 375 380

Val Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met
385 390 395 400

Asp Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val
405 410 415

Leu His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu
420 425 430

Asp Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Glu Phe Lys Ala
435 440 445

Glu Thr Glu Asp Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu
450 455 460

Ser Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val
465 470 475 480

Asn Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala
485 490 495

Cys Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu
500 505

<210> 912
<211> 510
<212> PRT
<213> Chelidonium

<400> 912

Met Phe Ile Glu Asn Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Ser
1 5 10 15

Glu Asn Glu Val Glu Ser Val Tyr Phe Tyr Glu Thr Thr Glu Leu Val

20 25 30

His Glu Asn Lys Asn Gly Thr Tyr Gln Trp Thr Val Lys Pro Lys Thr
5 35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Thr Lys Val Pro Lys Leu Gly Val
50 55 60
10

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

15

Ile Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

20 Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
25 115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Leu Gly Gly Trp Asp Ile
130 135 140
30

Ser Asp Met Asn Leu Ala Asp Ser Met Ser Arg Ala Arg Val Phe Asp
145 150 155 160

35

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro

165 170 175

Leu Pro Gly Val Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Leu Gln Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Thr Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ile
225 230 235 240

Val Gly Leu Asn Asp Thr Thr Glu Asn Leu Leu Ala Ser Leu Glu Lys
245 250 255

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

Tyr Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Val Ile Asp Leu Ala Ile Lys His Asn Thr Leu Ile Gly Gly
290 295 300

Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp

305 310 315 320

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Gly Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Ile
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Ser Thr Ile Val Met
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ser Glu
435 440 445

Ala Glu Glu Lys Tyr His Ser Phe His Pro Val Ala Thr Ile Leu Ser

450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 913
<211> 510
<212> PRT
<213> Eucalyptus

<400> 913

Met Phe Ile Glu Ser Phe Lys Val Asp Ser Pro Asn Val Thr Tyr Gly
1 5 10 15

Asp Ala Glu Ile His Ser Val Tyr Asp Tyr Gln Thr Thr Glu Leu Val
20 25 30

His Glu Asn Arg Asn Gly Ala Tyr Gln Trp Thr Val Lys Pro Lys Ser
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Thr Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Asn Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile His Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Ile Gly Gly Trp Asp Ile
130 135 140

Ser Lys Met Asn Leu Ala Asp Ala Met Ala Arg Ala Arg Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu His Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Glu Ala
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Ser Lys Lys Glu Gln Val Gln Gln
195 200 205

Ile Ile Lys Asp Met Arg Asp Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Met Asn Ser Met Glu Lys
245 250 255

Asn Glu Ser Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Leu Glu Asn Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Gln Arg Asn Val Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 914
<211> 510
<212> PRT
<213> Arabidopsis

<400> 914

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Asn Glu Ile His Ser Val Tyr Asp Tyr Gln Thr Thr Glu Leu Val
20 25 30

His Glu Asn Lys Asn Gly Ala Phe Gln Trp Thr Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Thr His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Glu Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Glu Glu Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Met Arg Pro Phe Met Glu His Met Val Pro
165 170 175

Leu Pro Gly Ile Phe Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

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

Val Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val
225 230 235 240

Val Gly Leu Asn Asp Thr Thr Glu Asn Leu Met Ser Ser Leu Asp Lys
245 250 255

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

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Glu Leu Ala Ile Lys Arg Asn Cys Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Gly
355 360 365

Ser Asn Gly Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Cys Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Met
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Thr Thr Arg Ile Gln Phe Met Ser Glu
435 440 445

Asn Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Leu Leu Ser
450 455 460

Tyr Leu Ser Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Val Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 915
<211> 510
<212> PRT

<213> B. rapa

<400> 915

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Asn Glu Ile His Ser Val Tyr Asp Tyr Glu Thr Thr Glu Val Val
20 25 30

His Glu Asn Arg Asn Gly Ser Tyr Gln Trp Ile Val Lys Pro Lys Thr
35 40 45

Val Gln Tyr Asp Phe Lys Thr Asp Thr Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Lys Glu Gly Ile Ser Trp Ala Thr Lys Asp Gly Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Arg Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu His Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Ser Val Ile Glu Gly Thr Lys Lys Glu Gln Val Asp His
195 200 205

Ile Ile Lys Asp Met Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

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

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Val Glu Lys
245 250 255

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

Leu Glu Gly Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Glu Leu Ala Ile Ser Arg Asn Cys Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Gly Ile Leu Phe Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Ala Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Met
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ala Lys
435 440 445

Gly Glu Gly Lys Tyr His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 916
<211> 510
<212> PRT
<213> B. rapa

<400> 916

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Lys Val Lys Tyr Thr
1 5 10 15

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

20 25 30

His Glu Ser Lys Asn Gly Ala Tyr Gln Trp Thr Val Lys Pro Lys Thr
5 35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Thr His Val Pro Lys Leu Gly Val
50 55 60
10

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

15

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Glu Lys Val
85 90 95

20 Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
25 115 120 125

Leu Pro Met Val Asn Pro Glu Glu Ile Val Phe Gly Gly Trp Asp Ile
130 135 140
30

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

35

Ile Asp Leu Gln Lys Gln Leu Arg Pro Phe Met Glu His Met Val Pro

165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn His Leu Ile Lys Gly Thr Lys Lys Glu Gln Leu Glu Gln
195 200 205

Val Ile Lys Asp Ile Arg Asp Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val
225 230 235 240

Ala Gly Leu Asn Asp Thr Thr Glu Asn Leu Met Ser Ser Leu Asp Lys
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Glu Leu Ala Ile Lys Arg Asn Ser Leu Ile Gly Gly
290 295 300

Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp

305 310 315 320

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Gly Ile Leu Phe Asp Ser Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Met
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Thr Thr Arg Ile Glu Leu Lys Ala Asp
435 440 445

Asn Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Leu Leu Ser

450 455 460

Tyr Leu Ser Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 917
<211> 510
<212> PRT
<213> Mijo

<400> 917

Met Phe Ile Glu Ser Phe Arg Val Glu Ser Pro Asn Val Arg Tyr Gly
1 5 10 15

Pro Ser Glu Ile Glu Ser Glu Tyr Arg Tyr Asp Thr Thr Glu Leu Val
20 25 30

His Glu Gly Lys Asp Gly Ala Ser Arg Trp Val Val Arg Pro Lys Ser
35 40 45

Val Lys Tyr Asn Phe Arg Thr Ser Thr Ala Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

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

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Asp Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Cys
225 230 235 240

Ala Gly Leu Asn Asp Thr Val Glu Asn Leu Leu Ala Ser Val Asp Lys
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Met Glu Gly Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Asn Asn Cys Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Glu Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 918
<211> 510
<212> PRT
<213> Phalaenopsis

<400> 918

Met Phe Val Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Gly
1 5 10 15

Glu Gln Glu Ile His Ser Ile Tyr Asn Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Ser Arg Asn Gly Ser Tyr Ala Trp Ile Val Lys Pro Lys Thr
35 40 45

Val Gln Tyr Glu Phe Lys Thr Asp Thr Leu Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Ala
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Asn Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Ile Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Glu Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asn Leu Asn Leu Ala Asp Ser Met Thr Arg Ala Arg Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Asp Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Ser Glu Gln Val Gln Gln
195 200 205

Val Ile Lys Asp Ile Arg Glu Phe Lys Asp Lys Asn Asn Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asp Val Met
225 230 235 240

Val Gly Leu Asn Asp Thr Thr Glu Asn Leu Leu Ala Ser Leu Glu Arg
245 250 255

Asn Glu Thr Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Met Glu Asn Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Phe Ala Ile Gln Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Thr
355 360 365

Ser Asn Gly Ile Leu Tyr Gln Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Ser Arg Ile Gln Phe Lys Ala Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Ile Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 919
<211> 511
<212> PRT

<213> Silene

<400> 919

Met Phe Ile Glu Asn Phe Lys Val Glu Ser Pro Asn Val Glu Tyr Ser
1 5 10 15

Asp Gly Glu Ile Arg Ser Val Tyr Asp Tyr Gln Thr Thr Glu Leu Val
20 25 30

His Glu Asn Arg Lys Gly Ser Gly Tyr Gln Trp Ile Val Lys Pro Lys
35 40 45

Ser Val Lys Tyr Gln Phe Lys Thr Asp Thr Arg Val Pro Lys Leu Gly
50 55 60

Val Met Leu Val Gly Trp Gly Gly Asn Asn Gly Cys Thr Leu Thr Gly
65 70 75 80

Gly Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys
85 90 95

Ile Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile
100 105 110

Arg Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser
115 120 125

Leu Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp
130 135 140

Ile Ser Asn Leu Asn Leu Ala Asp Ala Met Thr Arg Ala Lys Val Leu
145 150 155 160

Asp Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu His Met Val
165 170 175

Pro Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Asp
180 185 190

Ser Arg Ala Asn Asn Ile Ile Lys Gly Thr Lys Lys Glu Gln Val Asp
195 200 205

Gln Val Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp
210 215 220

Lys Val Val Val Leu Trp Thr Gly Asn Thr Glu Arg Tyr Ser Asn Val
225 230 235 240

Gln Val Gly Leu Asn Asp Thr Met Glu Asn Phe Leu Ala Ser Val Glu
245 250 255

Lys Asn Glu Ser Glu Ile Ser Pro Ser Thr Leu Tyr Ala Leu Ala Cys
260 265 270

Ile Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe
275 280 285

Val Pro Gly Leu Ile Asp Leu Ala Ile Lys Asn Asn Ser Leu Ile Gly
290 295 300

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

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

Asn His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr
340 345 350

Phe Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val
355 360 365

Ala Ser Asn Gly Ile Leu Phe Glu Pro Gly Glu His Pro Asp His Val
370 375 380

Val Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met
385 390 395 400

Asp Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val
405 410 415

Met His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu
420 425 430

Asp Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala
435 440 445

Glu Asn Glu Glu Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu
450 455 460

Ser Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val
465 470 475 480

Asn Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala
485 490 495

Cys Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 920
<211> 510
<212> PRT
<213> Sorgo, caña de azúcar

<400> 920

Met Phe Ile Glu Ser Phe Arg Val Glu Ser Pro His Val Arg Tyr Gly
1 5 10 15

Pro Thr Glu Ile Glu Ser Glu Tyr Arg Tyr Asp Thr Thr Glu Leu Val

20 25 30

His Glu Gly Lys Asp Gly Ala Ser Arg Trp Val Val Arg Pro Lys Ser
35 40 45

Val Lys Tyr Asn Phe Arg Thr Ser Thr Ala Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Leu Val Phe Gly Gly Trp Asp Ile
130 135 140

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

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro

165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Glu Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Ile Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Cys
225 230 235 240

Thr Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Val Asp Lys
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Met Glu Gly Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Asn Asn Cys Leu Ile Gly Gly
290 295 300

Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp

305 310 315 320

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Asp Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser

450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 921
<211> 510
<212> PRT
<213> Pasto varilla

<400> 921

Met Phe Ile Glu Ser Phe Arg Val Glu Ser Pro Asn Val Arg Tyr Gly
1 5 10 15

Pro Ser Glu Ile Glu Ser Glu Tyr Arg Tyr Asp Thr Thr Glu Leu Val
20 25 30

His Glu Gly Lys Asp Gly Ala Ser Arg Trp Val Val Arg Pro Lys Ser
35 40 45

Val Lys Tyr Asn Phe Arg Thr Ser Thr Ala Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

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

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Asp Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Cys
225 230 235 240

Ala Gly Leu Asn Asp Thr Val Glu Asn Leu Leu Ala Ser Val Asp Lys
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Met Glu Gly Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Asn Asn Cys Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Glu Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Ile Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 922
<211> 510
<212> PRT
<213> Thellungiella halophilum

<400> 922

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Asn Glu Ile His Ser Val Tyr Asp Tyr Glu Thr Thr Glu Val Val
20 25 30

His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Asp Phe Lys Thr Asp Thr Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Lys Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Arg Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu His Met Ile Pro
165 170 175

Leu Pro Gly Ile Tyr Asn Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

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

Ile Ile Lys Asp Met Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

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

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Met Ala Ser Val Glu Lys
245 250 255

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

Leu Glu Gly Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Glu Leu Ala Ile Ser Arg Asn Cys Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Gly Ile Leu Phe Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Ala Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Met
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ala Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Met Glu Tyr Lys
500 505 510

<210> 923
<211> 462
<212> PRT

<213> Amborella

<400> 923

Met Phe Ile Glu Ser Phe Arg Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Asp Lys Ile Glu Ser Val Tyr Glu Tyr Glu Thr Thr Glu Val Val
20 25 30

His Glu Asn Arg Asn Gly Lys Tyr Glu Trp Val Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr His Phe Asn Thr Asp Thr Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Ile Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Met Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Leu Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ser Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Arg Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Gln Lys
195 200 205

Ile Ile Asn Asp Ile Arg Glu Phe Lys Glu Thr Asn Lys Val Asp Met
210 215 220

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

Glu Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ala Val Asp Arg
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu His Ala Met Ala Cys Val
260 265 270

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Glu Leu Ala Ile Lys Thr Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Gly Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Ile
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala His
435 440 445

Glu Gly Glu Val Pro Leu Leu Pro Pro Gly Cys His His Pro
450 455 460

<210> 924
<211> 249
<212> PRT
<213> Thellungiella halophilum

<400> 924

Met Phe Ile Glu Ser Phe Lys Val Asp Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Asn Glu Ile His Ser Val Tyr Asp Tyr Gln Thr Thr Glu Leu Val
20 25 30

His Glu Asn Lys Asn Gly Ala Tyr Gln Trp Thr Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asn Thr His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly

65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Glu Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Ala Glu Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

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

Ile Asp Leu Gln Lys Gln Leu Arg Pro Phe Met Glu His Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn His Leu Ile Lys Gly Thr Lys Lys Gln Gln Leu Glu Gln
195 200 205

Val Ile Lys Asp Ile Arg Asp Phe Lys Glu Lys Asn Thr Val Asp Arg

210 215 220

Val Val Val Leu Trp Thr Arg Thr Gln Lys Asp Thr Ala Met Cys Trp
225 230 235 240

Leu Val Leu Thr Thr Arg Arg Arg Ile
245

<210> 925
<211> 510
<212> PRT
<213> Arabidopsis

<400> 925

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Asn Glu Ile Asn Ser Val Tyr Asp Tyr Glu Thr Thr Glu Val Val
20 25 30

His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Val Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Asp Phe Lys Thr Asp Thr Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Lys Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Glu Asp Val Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Arg Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Asn Met Ile Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Ser Val Ile Lys Gly Thr Lys Lys Glu Gln Val Asp His
195 200 205

Ile Ile Lys Asp Met Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Leu Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ile
225 230 235 240

Val Gly Leu Asn Asp Thr Thr Glu Asn Leu Leu Ala Ser Val Glu Lys
245 250 255

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

Leu Glu Gly Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Glu Leu Ala Ile Ser Lys Asn Cys Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Gly Ile Leu Phe Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Ala Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Arg Asn Thr Ile Val Leu
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ala Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Met Glu Tyr Lys
500 505 510

<210> 926
<211> 510
<212> PRT
<213> Canola

<400> 926

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Asn Glu Ile His Ser Val Tyr Asp Tyr Glu Thr Thr Glu Val Val
20 25 30

His Glu Asn Arg Asn Gly Ser Tyr Gln Trp Ile Val Lys Pro Lys Thr
35 40 45

Val Gln Tyr Asp Phe Lys Thr Asp Thr Arg Val Pro Thr Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Lys Glu Gly Ile Ser Trp Ala Thr Lys Asp Gly Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Arg Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu His Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Ser Val Ile Lys Gly Thr Lys Lys Glu Gln Val Asp His
195 200 205

Ile Ile Lys Asp Met Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

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

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Val Glu Lys
245 250 255

Asn Glu Ser Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Leu Glu Gly Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Glu Leu Ala Ile Ser Lys Asn Cys Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Gly Ile Leu Phe Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Ala Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Met
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ala Lys
435 440 445

Gly Glu Gly Lys Tyr His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 927
<211> 510
<212> PRT
<213> Mijo menor

<400> 927

Met Phe Ile Glu Ser Phe Arg Val Glu Ser Pro Asn Val Arg Tyr Gly
1 5 10 15

Pro Ser Glu Ile Glu Ser Glu Tyr Arg Tyr Asp Thr Thr Glu Leu Val
20 25 30

His Glu Gly Lys Asp Gly Ala Ser Arg Trp Val Val Arg Pro Lys Ser
35 40 45

Val Lys Tyr Asn Phe Arg Thr Ser Thr Ala Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

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

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Asp Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Ile Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Cys
225 230 235 240

Ala Gly Leu Asn Asp Thr Val Glu Asn Leu Leu Ala Ser Val Asp Lys
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Met Glu Gly Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Asn Asn Cys Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Glu Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 928
<211> 510
<212> PRT
<213> Nasturtium

<400> 928

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Asn Tyr Ser
1 5 10 15

Glu Asn Glu Ile His Ser Val Tyr Asp Tyr Gln Thr Thr Asp Leu Val
20 25 30

His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser

35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Thr Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Thr Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Glu Lys Val
85 90 95

Gln Arg Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile His Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Met Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu His Leu Val Pro
165 170 175

Leu Pro Gly Ile Tyr Glu Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser

180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Gln Gln
195 200 205

Ile Ile Lys Asp Ile Ser Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Ser Val Val
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Leu Glu Lys
245 250 255

Asn Glu Glu Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Leu Glu Asn Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Lys Asn Ser Leu Ile Gly Gly
290 295 300

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

Phe Leu Val Ser Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn

325 330 335

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gln Glu Gly Lys Phe His Pro Phe His Pro Val Ala Thr Leu Leu Ser
450 455 460

Tyr Leu Ser Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn

465 470 475 480

Ala Leu Ser Lys Gln Arg Ser Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 929
<211> 510
<212> PRT
<213> Phalaenopsis

<400> 929

Met Phe Val Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Gly
1 5 10 15

Glu Gln Glu Ile His Ser Ile Tyr Asn Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Ser Arg Asn Gly Ser Tyr Ala Trp Ile Val Lys Pro Lys Thr
35 40 45

Val Gln Tyr Glu Phe Lys Thr Asp Thr Leu Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Ala
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Asn Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Ile Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Glu Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asn Leu Asn Leu Ala Asp Ser Met Thr Arg Ala Arg Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Asp Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Ser Glu Gln Val Gln Gln
195 200 205

Val Ile Lys Asp Ile Arg Glu Phe Lys Asp Lys Asn Asn Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asp Val Met
225 230 235 240

Val Gly Leu Asn Asp Thr Thr Glu Asn Leu Leu Ala Ser Leu Glu Arg
245 250 255

Asn Glu Thr Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Met Glu Asn Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Phe Ala Ile Gln Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Thr
355 360 365

Ser Asn Gly Ile Leu Tyr Gln Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Ile
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Ser Arg Ile Gln Phe Lys Ala Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Ile Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 930
<211> 510
<212> PRT
<213> Amapola

<400> 930

Met Phe Ile Glu Asn Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Glu Gly Ile Glu Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Ile
20 25 30

His Glu Asn Lys Asn Gly Ala Tyr Gln Trp Thr Val Lys Pro Lys Ser
35 40 45

Val Gln Tyr Gln Phe Lys Thr Asp Thr Lys Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Met Ile Ala Asn Lys Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Leu Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ser Arg Ala Arg Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Ile Ile Lys Gly Thr Lys Lys Glu Gln Val Gln Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Ala Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ile
225 230 235 240

Val Gly Leu Asn Asp Thr Glu Glu Ser Leu Val Ala Ser Val Glu Lys
245 250 255

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

Tyr Glu Asn Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys His Asn Thr Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Gly Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Ile
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Ser Thr Ile Val Met
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ser Glu
435 440 445

Lys Glu Gly Lys Phe His Ser Phe His Pro Val Ser Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 931
<211> 510
<212> PRT
<213> Rábano

<400> 931

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Asn Glu Ile His Ser Val Tyr Asp Tyr Glu Thr Thr Glu Val Val
20 25 30

His Glu Asn Val Asn Gly Ala Tyr Gln Trp Ile Val Lys Pro Lys Val
35 40 45

Val Lys Tyr Asp Phe Lys Thr Asp Thr Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Lys Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Val Pro Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp Asp Ile
130 135 140

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

Ile Asp Leu Gln Lys Gln Leu Arg Pro Phe Met Glu Asn Ile Val Pro
165 170 175

Leu Pro Gly Ile Phe Asp Pro Asp Phe Val Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Asp Gln
195 200 205

Ile Ile Lys Asp Met Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Gly Asn Thr Glu Arg Tyr Ser Asn Val Ile
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Met Lys Ser Val Glu Arg
245 250 255

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

Leu Glu Gly Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Asn Asn Val Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Gly Ile Leu Phe Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Ala Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Met
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ser Glu
435 440 445

Lys Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 932
<211> 510
<212> PRT
<213> Pasto varilla

<400> 932

Met Phe Ile Glu Ser Phe Arg Val Glu Ser Pro Asn Val Arg Tyr Gly
1 5 10 15

Pro Ser Glu Ile Glu Ser Glu Tyr Arg Tyr Asp Thr Thr Glu Leu Val
20 25 30

His Glu Gly Lys Asp Gly Ala Ser Arg Trp Val Val Arg Pro Lys Ser

35 40 45

Val Lys Tyr His Phe Arg Thr Ser Thr Ala Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

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

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser

180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Asp Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Cys
225 230 235 240

Thr Gly Leu Asn Asp Thr Val Glu Asn Leu Leu Lys Ser Val Asp Lys
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Thr Glu Gly Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Asn Asn Cys Leu Ile Gly Gly
290 295 300

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

Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn

325 330 335

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Glu Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn

465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 933
<211> 510
<212> PRT
<213> Trigo

<400> 933

Met Phe Ile Glu Ser Phe Arg Val Glu Ser Pro Asn Val Arg Tyr Gly
1 5 10 15

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

His Glu Ser His Asp Gly Ala Ser Lys Trp Val Val Arg Pro Lys Ser
35 40 45

Val Asn Tyr His Phe Lys Thr Asn Thr Asn Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Met Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Leu Val Phe Gly Gly Trp Asp Ile
130 135 140

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

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Ile Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Met Glu Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ser
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Val Asp Lys
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Met Glu Gly Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Asn Asn Cys Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Asp Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 934
<211> 510
<212> PRT
<213> Trigo

<400> 934

Met Phe Ile Glu Ser Phe Arg Val Glu Ser Pro Asn Val Arg Tyr Gly
1 5 10 15

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

His Glu Ser His Asp Gly Ala Ser Lys Trp Val Val Arg Pro Lys Ser
35 40 45

Val Asn Tyr His Phe Lys Thr Asn Thr Thr Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Met Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Leu Val Phe Gly Gly Trp Asp Ile
130 135 140

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

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Ile Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Met Glu Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ser
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Val Asp Lys
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Met Glu Gly Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Asn Asn Cys Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Asp Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 935
<211> 380
<212> PRT
<213> Cleome gynandra

<400> 935

Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp Asp Ile Ser Asp
1 5 10 15

Met Asn Leu Ala Asp Ala Met Ala Arg Ala Arg Val Leu Asp Ile Asp
20 25 30

Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Asn Ile Val Pro Leu Pro
35 40 45

Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser Arg Ala
50 55 60

Asn Asn Val Val Lys Gly Cys Lys Lys Glu Gln Val Asp Gln Ile Ile
65 70 75 80

Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys Val Val
85 90 95

Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ile Val Gly
100 105 110

Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Val Asp Lys Asn Glu
115 120 125

Ser Glu Ile Ser Pro Ser Thr Leu Tyr Gly Ile Ala Cys Val Met Glu
130 135 140

Gly Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val Pro Gly
145 150 155 160

Leu Ile Asp Met Ala Ile Arg Arg Asn Cys Leu Ile Gly Gly Asp Asp
165 170 175

Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp Phe Leu
180 185 190

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

Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe Arg Ser
210 215 220

Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala Ser Asn
225 230 235 240

Gly Ile Leu Phe Glu Pro Gly Glu His Pro Asp His Val Val Val Ile
245 250 255

Lys Tyr Val Pro Tyr Val Ala Asp Ser Lys Arg Ala Met Asp Glu Tyr
260 265 270

Thr Ser Glu Ile Phe Leu Gly Gly Lys Asn Thr Ile Val Met His Asn
275 280 285

Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp Leu Val
290 295 300

Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu Gly Glu
305 310 315 320

Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser Tyr Leu
325 330 335

Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn Ala Leu
340 345 350

Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys Val Gly
355 360 365

Leu Ser Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
370 375 380

<210> 936
<211> 304
<212> PRT
<213> Cebolla

<220>
<221> misc_feature
<222> (208)..(208)
<223> Xaa puede ser cualquier aminoácido de origen natural

<220>

<221> misc_feature
<222> (303)..(303)
<223> Xaa puede ser cualquier aminoácido de origen natural

<400> 936

Met Phe Ile Glu Asn Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Gly
1 5 10 15

Glu Asp Glu Ile Glu Ser Ile Tyr Asn Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Ser Arg Asn Gly Ser Tyr Gln Trp Ile Val Lys Pro Lys Thr
35 40 45

Val Gln Tyr Asn Phe Lys Thr Asp Val His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Ile
85 90 95

Gln Arg Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asn Met Asn Met Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Phe Asp Pro Asp Phe Ile Ala Ser Asn Gln Gly Ala
180 185 190

Arg Ala Asn His Thr Ile Lys Gly Thr Lys Lys Glu Gln Val Gln Xaa
195 200 205

Ile Ile Lys Asp Met Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Ile Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val
225 230 235 240

Val Gly Leu Asn Asp Thr Met Lys Asn Leu Met Ala Ser Leu Glu Lys
245 250 255

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

Met Glu Asn Val Pro Tyr Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Glu Met Ala Ile Gln Arg Asn Cys Leu Ile Xaa Trp
290 295 300

<210> 937
<211> 242
<212> PRT
<213> Petunia

<400> 937

Met Phe Ile Glu Asn Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Ser Glu Ile His Ser Leu Tyr Asp Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Glu Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Thr His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Glu Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asn Met Asn Leu Ala Asp Ala Met Val Arg Ala Lys Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Asn Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Glu Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Asp Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Ile Gln Lys Glu Gln Gln Cys Gly Trp
225 230 235 240

Trp Ser

<210> 938
<211> 510
<212> PRT
<213> Maíz

<400> 938

Met Phe Ile Glu Ser Phe Arg Val Glu Ser Pro His Val Arg Tyr Gly
1 5 10 15

Pro Thr Glu Ile Glu Ser Glu Tyr Arg Tyr Asp Thr Thr Glu Leu Val
20 25 30

His Glu Gly Lys Asp Gly Ala Ser Arg Trp Val Val Arg Pro Lys Ser
35 40 45

Val Lys Tyr Asn Phe Arg Thr Arg Thr Ala Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Tyr Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

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

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Ser Val Ile Lys Gly Thr Lys Lys Glu Gln Val Glu Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Ile Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Cys
225 230 235 240

Ala Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Val Asp Lys
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Met Glu Gly Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Asn Asn Cys Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Asp Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 939
<211> 510
<212> PRT
<213> Amapola

<400> 939

Met Phe Ile Glu Asn Phe Lys Val Glu Ser Pro Asn Leu Lys Tyr Thr
1 5 10 15

Glu Glu Gly Ile Glu Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Ile
20 25 30

His Glu Asn Lys Asn Gly Ala Tyr Gln Trp Thr Val Lys Pro Lys Ser
35 40 45

Val Gln Tyr Gln Phe Lys Thr Asp Thr Lys Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Met Ile Ala Asn Lys Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu

115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Leu Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ser Arg Ala Arg Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Ile Ile Lys Gly Thr Lys Lys Glu Gln Val Gln Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Ala Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ile
225 230 235 240

Val Gly Leu Asn Asp Thr Glu Glu Ser Leu Leu Ala Ser Val Glu Lys
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Leu Ala Cys Ile

260 265 270

Tyr Glu Asn Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys His Asn Thr Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Gly Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Ile
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Ser Thr Ile Val Met

405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ser Glu
435 440 445

Lys Glu Gly Lys Phe His Ser Phe His Pro Val Ser Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 940
<211> 510
<212> PRT
<213> Arabidopsis lyrata

<400> 940

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Asn Glu Ile His Ser Val Tyr Asp Tyr Glu Thr Thr Glu Val Val
20 25 30

His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser
35 40 45

Val Lys Tyr Asp Phe Ile Thr Glu Thr Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Lys Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Arg Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Asn Met Ile Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Ser Val Ile Lys Gly Thr Lys Lys Glu Gln Val Asp His
195 200 205

Ile Ile Lys Asp Met Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Leu Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ile
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Val Glu Lys
245 250 255

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

Leu Glu Gly Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Glu Leu Ala Ile Ser Lys Asn Cys Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Gly Ile Leu Phe Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Ala Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Arg Asn Thr Ile Val Met
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ala Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Met Glu Tyr Lys
500 505 510

<210> 941
<211> 510
<212> PRT
<213> Brachypodium

<400> 941

Met Phe Ile Glu Ser Phe Arg Val Glu Ser Pro Asn Val Arg Tyr Gly
1 5 10 15

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

His Glu Ser His Asp Gly Ala Ser Lys Trp Val Val Arg Pro Lys Ser
35 40 45

Val Asn Tyr His Phe Lys Thr Asn Thr Asn Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Met Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Leu Val Phe Gly Gly Trp Asp Ile
130 135 140

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

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Ile Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Met Glu Gln
195 200 205

Ile Ile Lys Asp Ile Arg Asp Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ser
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Val Asp Lys
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Met Glu Gly Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Asn Asn Cys Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Asp Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 942
<211> 510
<212> PRT
<213> Canola

<400> 942

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Glu Tyr Thr
1 5 10 15

Glu Asn Glu Ile His Ser Val Tyr Asp Tyr Glu Thr Thr Glu Val Val
20 25 30

His Glu Asn Arg Asn Gly Ser Tyr Gln Trp Ile Val Lys Pro Lys Thr
35 40 45

Ile Lys Tyr Asp Phe Lys Thr Asp Thr Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Lys Glu Gly Ile Ser Trp Ala Thr Lys Asp Gly Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Arg Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu His Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Ser Val Ile Lys Gly Thr Lys Lys Glu Gln Val Asp His
195 200 205

Ile Ile Lys Asp Met Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

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

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Val Glu Lys
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Leu Glu Gly Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Glu Leu Ala Ile Ser Arg Asn Cys Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Gly Ile Leu Phe Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Ala Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Met
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Arg Ala Lys
435 440 445

Gly Glu Gly Lys Tyr His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Gly Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 943
<211> 510
<212> PRT
<213> Centeno

<400> 943

Met Phe Ile Glu Ser Phe Arg Val Glu Ser Pro Asn Val Arg Tyr Gly
1 5 10 15

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

His Glu Ser His Asp Gly Ala Ser Lys Trp Val Val Arg Pro Lys Ser
35 40 45

Val Asn Tyr His Phe Lys Thr Asn Thr Asn Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Met Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu

115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

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

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Ile Thr Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Leu Lys Gly Thr Lys Lys Glu Gln Met Glu Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ser
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Val Asp Lys
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val

260 265 270

Met Glu Gly Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Asn Asn Cys Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Ser Thr Ile Val Leu

405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Asp Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 944
<211> 510
<212> PRT
<213> Thellungiella parvulum

<400> 944

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Asn Glu Ile His Ser Val Tyr Asp Tyr Glu Thr Thr Gln Val Val
20 25 30

His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Asp Phe Lys Thr Asp Thr Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Lys Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Arg Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu His Met Ile Pro
165 170 175

Leu Pro Gly Ile Tyr Asn Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Ser Val Ile Lys Gly Thr Lys Lys Glu Gln Val Asp His
195 200 205

Ile Ile Lys Asp Met Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

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

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Val Glu Lys
245 250 255

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

Leu Glu Gly Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Glu Leu Ala Ile Ser Lys Asn Cys Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Gly Ile Leu Phe Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Ala Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Met
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ala Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Met Glu Tyr Lys
500 505 510

<210> 945
<211> 511
<212> PRT
<213> Arabidopsis lyrata

<400> 945

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Arg Asn Val Lys Tyr Thr
1 5 10 15

Glu Asn Glu Ile His Ser Val Tyr Asp Tyr Glu Thr Thr Glu Val Val
20 25 30

His Glu Lys Thr Ile Asn Gly Ser Tyr Gln Trp Ile Val Lys Pro Lys
35 40 45

Thr Val Lys Tyr Asp Phe Lys Thr Asp Ile Arg Val Pro Lys Leu Gly
50 55 60

Val Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala
65 70 75 80

Gly Val Ile Ala Asn Lys Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys
85 90 95

Val Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile
100 105 110

Arg Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser
115 120 125

Leu Leu Pro Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp Asp
130 135 140

Ile Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Arg Val Leu
145 150 155 160

Asp Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Asn Ile Val
165 170 175

Pro Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly
180 185 190

Ser Arg Ala Asn His Val Ile Lys Gly Thr Lys Lys Glu Gln Val Asp
195 200 205

His Ile Ile Lys Asp Met Arg Glu Phe Lys Glu Lys Asn Gln Val Asp
210 215 220

Lys Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val
225 230 235 240

Val Val Gly Met Asn Asp Thr Met Glu Asn Leu Met Glu Ser Val Asp
245 250 255

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

Val Leu Glu Gly Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe
275 280 285

Val Pro Gly Leu Ile Asp Met Ala Ile Arg Asn Asn Val Leu Ile Gly
290 295 300

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

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

Asn His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr
340 345 350

Phe Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val
355 360 365

Ala Ser Asn Gly Ile Leu Phe Glu Pro Gly Glu His Pro Asp His Val
370 375 380

Val Val Ile Lys Tyr Val Pro Tyr Val Ala Asp Ser Lys Arg Ala Met
385 390 395 400

Asp Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val
405 410 415

Met His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu
420 425 430

Asp Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ser
435 440 445

Glu Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu
450 455 460

Ser Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val
465 470 475 480

Asn Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala
485 490 495

Cys Val Gly Leu Ala Pro Glu Asn Asn Met Ile Met Glu Phe Lys
500 505 510

<210> 946
<211> 510
<212> PRT
<213> B. juncea

<400> 946

Met Phe Ile Glu Ser Phe Arg Val Glu Ser Pro His Val Arg Tyr Gly
1 5 10 15

Ala Ala Glu Ile Glu Ser Asp Tyr Gln Tyr Asp Thr Thr Glu Leu Val
20 25 30

His Glu Ser His Asp Gly Ala Ser Arg Trp Val Val Arg Pro Lys Ser
35 40 45

Val Arg Tyr Asn Phe Arg Thr Thr Thr Thr Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Tyr Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Leu Val Phe Gly Gly Trp Asp Ile
130 135 140

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

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Met Glu Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Ser Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Cys
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Val Asp Lys
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Met Glu Gly Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Asn Asn Cys Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Lys Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Glu Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 947
<211> 511
<212> PRT
<213> Arabidopsis

<400> 947

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Asn Glu Ile His Ser Val Tyr Asp Tyr Glu Thr Thr Glu Val Val
20 25 30

His Glu Lys Thr Val Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys
35 40 45

Thr Val Lys Tyr Asp Phe Lys Thr Asp Ile Arg Val Pro Lys Leu Gly
50 55 60

Val Met Leu Val Gly Leu Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala
65 70 75 80

Gly Val Ile Ala Asn Lys Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys
85 90 95

Val Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile
100 105 110

Arg Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser

115 120 125

Leu Leu Pro Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp Asp
130 135 140

Ile Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Arg Val Leu
145 150 155 160

Asp Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Asn Ile Val
165 170 175

Pro Leu Pro Gly Ile Phe Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly
180 185 190

Ser Arg Ala Asn His Val Ile Lys Gly Thr Lys Lys Glu Gln Val Asp
195 200 205

His Ile Ile Lys Asp Met Arg Glu Phe Lys Glu Lys Asn Lys Val Asp
210 215 220

Lys Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val
225 230 235 240

Val Val Gly Met Asn Asp Thr Met Glu Asn Leu Met Glu Ser Val Asp
245 250 255

Arg Asp Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys

260 265 270

Val Leu Glu Gly Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe
275 280 285

Val Pro Gly Leu Ile Asp Met Ala Ile Arg Asn Asn Val Leu Ile Gly
290 295 300

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

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

Asn His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr
340 345 350

Phe Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val
355 360 365

Ala Ser Asn Gly Ile Leu Phe Glu Pro Gly Glu His Pro Asp His Val
370 375 380

Val Val Ile Lys Tyr Val Pro Tyr Val Ala Asp Ser Lys Arg Ala Met
385 390 395 400

Asp Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val

405 410 415

Met His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu
420 425 430

Asp Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ser
435 440 445

Glu Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu
450 455 460

Ser Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Ile
465 470 475 480

Asn Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala
485 490 495

Cys Val Gly Leu Ala Pro Glu Asn Asn Met Ile Met Glu Phe Lys
500 505 510

<210> 948
<211> 224
<212> PRT
<213> Centeno

<400> 948

Met Phe Ile Glu Ser Phe Arg Val Glu Ser Pro Asn Val Arg Tyr Gly
1 5 10 15

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

His Glu Ser His Asp Gly Ala Ser Lys Trp Val Val Arg Pro Lys Ser
35 40 45

Val Asn Tyr His Phe Lys Thr Asn Thr Asn Val Pro Arg Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Met Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

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

Ile Asp Leu Gln Lys Gln Leu Arg Pro Thr Trp Ser Pro Ser Arg Arg
165 170 175

Ser Pro Ala Ser Met Thr Arg Thr Ser Ser Leu Pro Thr Arg Ala Pro
180 185 190

Gly Leu Thr Met Ser Leu Arg Val Gln Arg Lys Ser Arg Trp Ser Arg
195 200 205

Leu Ser Lys Thr Leu Gly Ser Ser Arg Arg Arg Thr Arg Trp Thr Lys
210 215 220

<210> 949
<211> 495
<212> PRT
<213> Arnica

<400> 949

Thr Glu Asn Glu Ile His Ser Val Tyr Asn Tyr Asp Thr Thr Glu Leu
1 5 10 15

Val His Glu Glu Lys Asn Gly Ala Tyr Gln Trp Val Val Lys Pro Lys
20 25 30

Thr Val Lys Tyr Glu Phe Lys Thr Glu Thr Asn Val Pro Lys Leu Gly
35 40 45

Val Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala
50 55 60

Gly Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Glu Lys
65 70 75 80

Ile Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile
85 90 95

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

Leu Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp
115 120 125

Ile Ser Ser Met Asn Leu Ala Asp Ser Met Ala Arg Ala Lys Val Leu
130 135 140

Asp Ile Asp Leu Gln Lys Gln Leu Ser Pro Tyr Met Glu Ser Met Val
145 150 155 160

Pro Leu Pro Gly Ile Phe Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly
165 170 175

Ala Arg Ala Asp Asn Cys Ile Lys Gly Thr Lys Asn Glu Gln Ile Gln
180 185 190

Lys Val Ile Lys Asp Ile Arg Glu Phe Lys Glu Ala Asn Lys Val Asp
195 200 205

Lys Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val
210 215 220

Met Val Gly Leu Asn Asp Thr Met Glu Ser Leu Phe Ala Ser Leu Asp
225 230 235 240

Arg Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Phe Ala Ile Ala Cys
245 250 255

Ile Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe
260 265 270

Val Pro Gly Val Ile Asp Leu Ala Ile Lys Arg Asn Thr Leu Ile Gly
275 280 285

Gly Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val
290 295 300

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

Asn His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr
325 330 335

Phe Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val
340 345 350

Ser Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val
355 360 365

Val Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met
370 375 380

Asp Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Ser Thr Ile Val
385 390 395 400

Leu His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu
405 410 415

Asp Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ser
420 425 430

Glu Thr Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu
435 440 445

Ser Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val
450 455 460

Asn Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala
465 470 475 480

Cys Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
485 490 495

<210> 950
<211> 510
<212> PRT
<213> Cebada

<400> 950

Met Phe Ile Glu Ser Phe Arg Val Glu Ser Pro Lys Val Arg Tyr Gly
1 5 10 15

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

His Glu Ser His Asp Gly Ala Ser Lys Trp Val Val Arg Pro Lys Ser
35 40 45

Val Asn Tyr His Phe Lys Thr Asn Thr Thr Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Met Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Leu Val Phe Gly Gly Trp Asp Ile
130 135 140

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

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Ile Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Met Glu Gln
195 200 205

Val Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ser
225 230 235 240

Val Gly Leu Asn Asp Thr Thr Glu Asn Leu Leu Ala Ser Val Asp Lys
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Met Glu Gly Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Asn Asp Cys Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Asp Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 951
<211> 510
<212> PRT
<213> Avena

<400> 951

Met Phe Ile Glu Ser Phe Arg Val Glu Ser Pro Asn Val Arg Tyr Gly
1 5 10 15

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

His Glu Ser His Asn Gly Ala Ser Lys Trp Val Val Arg Pro Lys Ser
35 40 45

Val Asn Tyr His Phe Lys Thr Asp Thr Asn Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Met Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Ser Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile

130 135 140

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

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Ile Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Met Glu Gln
195 200 205

Val Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

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

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Val Asp Lys
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Met Glu Gly Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val

275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Asn Asn Cys Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp

420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Asp Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 952
<211> 510
<212> PRT
<213> Arroz

<400> 952

Met Phe Ile Glu Ser Phe Arg Val Glu Ser Pro His Val Arg Tyr Gly
1 5 10 15

Ala Ala Glu Ile Glu Ser Asp Tyr Gln Tyr Asp Thr Thr Glu Leu Val
20 25 30

His Glu Ser His Asp Gly Ala Ser Arg Trp Ile Val Arg Pro Lys Ser
35 40 45

Val Arg Tyr Asn Phe Arg Thr Thr Thr Thr Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Tyr Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Leu Val Phe Gly Gly Trp Asp Ile
130 135 140

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

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Met Glu Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Ser Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Cys
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Val Asp Lys
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Met Glu Gly Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Asn Asn Cys Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Leu Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Glu Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 953
<211> 505
<212> PRT
<213> Silene

<400> 953

Lys Val Glu Ser Pro Asn Val Glu Tyr Arg Asp Gly Glu Ile His Ser
1 5 10 15

Val Tyr Asn Tyr Gln Thr Thr Glu Leu Val His Glu Asn Pro Lys Gly
20 25 30

Thr Gly Tyr Gln Trp Thr Val Lys Pro Lys Ser Val Lys Tyr Glu Phe
35 40 45

Arg Thr Gln Thr His Val Pro Lys Leu Gly Val Met Leu Val Gly Trp
50 55 60

Gly Gly Asn Asn Gly Cys Thr Leu Thr Gly Gly Val Ile Ala Asn Arg
65 70 75 80

Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Ile Gln Gln Ala Asn Tyr
85 90 95

Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg Val Gly Ser Phe Asn
100 105 110

Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu Leu Pro Met Val Asn
115 120 125

Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile Ser Asn Met Asn Leu
130 135 140

Ala Asp Ala Met Thr Arg Ala Arg Val Leu Asp Ile Asp Leu Gln Lys
145 150 155 160

Gln Leu Arg Pro Tyr Met Glu His Met Val Pro Leu Pro Gly Ile Tyr
165 170 175

Asp Pro Asp Phe Ile Ala Ala Asn Gln Asp Ser Arg Ala Asn Asn Ile
180 185 190

Ile Lys Gly Thr Lys Lys Glu Gln Val Asp Gln Val Ile Lys Asp Ile
195 200 205

Arg Glu Phe Lys Glu Lys Thr Lys Val Asp Lys Val Val Val Leu Trp
210 215 220

Thr Gly Asn Thr Glu Arg Tyr Ser Asn Val Val Val Gly Leu Asn Asp
225 230 235 240

Thr Ile Glu Asn Leu Leu Ala Ala Val Asp Arg Asp Glu Ser Glu Ile
245 250 255

Ser Pro Ser Thr Leu Tyr Ala Leu Ala Cys Val Leu Glu Gln Val Pro
260 265 270

Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val Pro Gly Leu Ile Asp
275 280 285

Leu Ala Ile Lys Asn Asn Ser Leu Ile Gly Gly Asp Asp Phe Lys Ser
290 295 300

Gly Gln Thr Lys Ile Lys Ser Val Leu Val Asp Phe Leu Val Gly Ala
305 310 315 320

Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn His Leu Gly Asn Asn
325 330 335

Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe Arg Ser Lys Glu Ile
340 345 350

Ser Lys Ser Asn Val Val Asp Asp Met Val Ala Ser Asn Gly Ile Leu
355 360 365

Phe Glu Pro Gly Glu His Pro Asp His Val Val Val Ile Lys Tyr Val
370 375 380

Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp Glu Tyr Thr Ser Glu
385 390 395 400

Ile Phe Met Gly Gly Thr Asn Thr Ile Val Met His Asn Thr Cys Glu
405 410 415

Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp Leu Val Leu Leu Ala
420 425 430

Glu Leu Ser Thr Arg Ile Gln Leu Lys Gly Glu His Glu Asp Lys Phe
435 440 445

His Ser Phe His Pro Val Ala Thr Ile Leu Ser Tyr Leu Thr Lys Ala
450 455 460

Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn Ala Leu Ser Lys Gln
465 470 475 480

Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys Val Gly Leu Ala Pro
485 490 495

Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505

<210> 954
<211> 239
<212> PRT
<213> Tomate

<400> 954

Met Cys Ser Lys Pro Ile Thr Leu Val Leu Leu His Arg Pro Leu Leu
1 5 10 15

Phe Lys Leu Gly Pro Ser Met Gly Arg Arg Ser Met Leu Pro Leu Arg
20 25 30

Ala Tyr Phe Pro Trp Leu Ile His Pro Asp Asp Val Val Phe Gly Glu
35 40 45

Trp Asp Ile Ser Asn Met Asn Leu Ala Asp Asp Met Ala Arg Ala Asn
50 55 60

Val Phe Asp Ile Asp Leu Gln Lys Lys Leu Arg Pro Tyr Met Glu Ser
65 70 75 80

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

Gln Gly Ser Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln
100 105 110

Val Asp Gln Ile Ile Lys Asp Ile Arg Gln Phe Lys Glu Asn Asn Lys
115 120 125

Val Asp Lys Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser
130 135 140

Ser Val Val Val Gly Leu Asn Asp Thr Met Glu Asn Leu Phe Ala Ser
145 150 155 160

Val Asp Arg Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile
165 170 175

Ala Cys Ile Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn
180 185 190

Thr Phe Val Pro Gly Leu Ile Asp Leu Ala Ile Lys Arg Asn Thr Leu
195 200 205

Ile Gly Gly Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val
210 215 220

Leu Val Tyr Phe Leu Val Gly Ala Gly Ile Asn Gln His Gln Ser
225 230 235

<210> 955
<211> 510
<212> PRT
<213> Maíz

<400> 955

Met Phe Ile Glu Ser Phe Arg Val Glu Ser Pro His Val Arg Tyr Gly
1 5 10 15

Pro Thr Glu Ile Glu Ser Glu Tyr Arg Tyr Asp Thr Thr Glu Leu Val
20 25 30

His Glu Ala Lys Asp Gly Ala Ser Arg Trp Val Val Arg Pro Lys Ser
35 40 45

Val Lys Tyr Asn Phe Arg Thr Ser Thr Ala Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Tyr Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu

115 120 125

Leu Pro Met Val Asn Pro Asp Asp Leu Val Phe Gly Gly Trp Asp Ile
130 135 140

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

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Val Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Glu Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Cys
225 230 235 240

Ala Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Val Asp Lys
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val

260 265 270

Thr Glu Gly Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Asn Asn Cys Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Gly Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Ser Thr Ile Val Leu

405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Pro Glu
435 440 445

Gly Thr Asp Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 956
<211> 510
<212> PRT
<213> Avena

<400> 956

Met Phe Ile Glu Ser Phe Arg Val Glu Ser Pro Asn Val Arg Tyr Gly
1 5 10 15

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

His Glu Ser His Asn Gly Ala Ser Lys Trp Val Val Arg Pro Lys Ser
35 40 45

Val Asn Tyr His Phe Lys Thr Asp Thr Asn Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Met Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Ser Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

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

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Ile Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Met Glu Gln
195 200 205

Val Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

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

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Val Glu Lys
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Met Glu Gly Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Asn Asn Cys Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Asp Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 957
<211> 509
<212> PRT
<213> Centeno

<400> 957

Met Phe Ile Glu Ser Phe Arg Val Glu Ser Pro Asn Val Arg Tyr Gly
1 5 10 15

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

His Glu Ser His Asp Gly Ala Ser Lys Trp Val Val Arg Pro Lys Ser
35 40 45

Val Asn Tyr His Phe Lys Thr Asn Thr Asn Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Met Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

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

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Ile Thr Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Leu Lys Gly Thr Lys Lys Glu Gln Met Glu Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ser
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Val Asp Lys
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Met Glu Gly Val Pro Phe Ile Asn Gly Ala Ser Asp His Phe Val Pro
275 280 285

Gly Leu Ile Asp Leu Ala Ile Lys Asn Asn Cys Leu Ile Gly Gly Asp
290 295 300

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

Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn His
325 330 335

Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe Arg
340 345 350

Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser Ser
355 360 365

Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val Val
370 375 380

Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp Glu
385 390 395 400

Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Ser Thr Ile Val Leu His
405 410 415

Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp Leu
420 425 430

Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu Gly
435 440 445

Glu Asp Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser Tyr
450 455 460

Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn Ala
465 470 475 480

Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys Val
485 490 495

Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505

<210> 958
<211> 511
<212> PRT
<213> Poroto

<400> 958

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Asn Glu Ile His Ser Val Tyr Asp Tyr Glu Thr Thr Glu Val Val
20 25 30

His Glu Lys Thr Val Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys
35 40 45

Thr Val Lys Tyr Asp Phe Lys Thr Asp Ile Arg Val Pro Lys Leu Gly
50 55 60

Val Met Leu Val Gly Leu Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala
65 70 75 80

Gly Val Ile Ala Asn Lys Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys
85 90 95

Val Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile
100 105 110

Arg Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser
115 120 125

Leu Leu Pro Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp Asp
130 135 140

Ile Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Arg Val Leu
145 150 155 160

Asp Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Asn Ile Val
165 170 175

Pro Leu Pro Gly Ile Phe Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly
180 185 190

Ser Arg Ala Asn His Val Ile Lys Gly Thr Lys Lys Glu Gln Val Asp
195 200 205

His Ile Ile Lys Asp Met Arg Glu Phe Lys Glu Lys Asn Lys Val Asp
210 215 220

Lys Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Glu
225 230 235 240

Val Val Gly Met Asn Asp Thr Met Glu Asp Leu Met Glu Ser Val Asp
245 250 255

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

Val Leu Glu Gly Ile Pro Phe Ile Asn Gly Ser Pro Gln His Thr Phe
275 280 285

Val Pro Gly Leu Ile Asp Met Ala Ile Arg Asn Asn Val Leu Ile Gly
290 295 300

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

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

Asn His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr
340 345 350

Phe Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val
355 360 365

Ala Ser Asn Gly Ile Leu Phe Glu Pro Gly Glu His Pro Asp His Val
370 375 380

Val Val Ile Lys Tyr Val Pro Tyr Val Ala Asp Ser Lys Arg Ala Met
385 390 395 400

Asp Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val
405 410 415

Met His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu
420 425 430

Asp Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ser
435 440 445

Glu Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu
450 455 460

Ser Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Ile
465 470 475 480

Asn Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala
485 490 495

Cys Val Gly Leu Ala Pro Glu Asn Asn Met Ile Met Glu Phe Lys
500 505 510

<210> 959
<211> 501
<212> PRT
<213> Eschscholzia

<400> 959

Met Phe Ile Asp Asn Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Ser
1 5 10 15

Glu Asn Glu Ile His Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Lys Asn Gly Ala Tyr Gln Trp Thr Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Glu Thr Lys Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Ser Leu Thr Gly Gly
65 70 75 80

Leu Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu

115 120 125

Leu Pro Leu Val Asn Pro Asp Asp Ile Val Leu Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Ile Ile Lys Gly Thr Lys Lys Glu Gln Val Glu Gln
195 200 205

Ile Met Lys Asp Ile Arg Glu Phe Lys Glu Asn Ser Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ile
225 230 235 240

Val Gly Leu Asn Asp Asn Ile Glu Asn Leu Leu Gly Ser Leu Glu Arg
245 250 255

Asn Glu Ser Glu Ile Ser Pro Ser Thr Leu Phe Ala Leu Ala Cys Ile

260 265 270

Tyr Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Met Lys His Asn Thr Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Gly Ile Leu Tyr Glu Ala Gly Glu His Pro Asp His Val Ile
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Ser Thr Ile Val Met

405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ser Glu
435 440 445

Gly Glu Glu Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro
500

<210> 960
<211> 509
<212> PRT
<213> Lolium

<400> 960

Met Phe Ile Glu Ser Phe Arg Val Glu Ser Pro Asn Val Arg Tyr Gly
1 5 10 15

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

His Glu Ser His Asn Gly Ala Ser Lys Trp Val Val Arg Pro Lys Ser
35 40 45

Val Gly Tyr Gln Phe Arg Thr Asp Thr Asn Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Leu Gly Gly Asn Asn Gly Ser Thr Leu Met Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Ser Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

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

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Ile Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Met Gln Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Ala Val Ser
225 230 235 240

Val Gly Leu Asn Asp Thr Thr Glu Asn Leu Leu Ala Ser Val Glu Lys
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Met Glu Gly Val Pro Phe Val Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Asn Asn Cys Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Phe Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ser Glu
435 440 445

Gly Glu Asp Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr
500 505

<210> 961
<211> 485
<212> PRT
<213> Tabaco

<400> 961

Tyr Gln Thr Thr Glu Leu Val His Glu Glu Lys Asn Gly Ser Tyr Gln
1 5 10 15

Trp Thr Val Lys Pro Lys Cys Val Lys Tyr Glu Phe Lys Thr Asp Thr
20 25 30

Asn Val Pro Lys Leu Gly Val Met Leu Val Gly Trp Gly Gly Asn Asn
35 40 45

Gly Ser Thr Leu Thr Gly Gly Ile Ile Ala Asn Lys Glu Gly Ile Ser
50 55 60

Trp Ala Thr Lys Glu Lys Val Gln Gln Ala Asn Tyr Phe Gly Ser Leu
65 70 75 80

Thr Gln Ala Ser Thr Ile Arg Val Gly Ser Phe Asn Gly Glu Glu Ile
85 90 95

Tyr Ala Pro Phe Lys Ser Leu Leu Pro Met Val Asn Pro Asp Asp Val
100 105 110

Val Phe Gly Gly Trp Asp Ile Ser Asn Met Asn Leu Ala Asp Ala Met
115 120 125

Val Arg Ala Lys Val Phe Asp Ile Asp Leu Gln Asn Gln Leu Arg Pro
130 135 140

Tyr Met Glu Ser Met Val Pro Leu Pro Gly Ile Tyr Asp Pro Asp Phe
145 150 155 160

Ile Ala Ala Asn Gln Glu Ser Arg Ala Asn Asn Val Ile Lys Gly Thr
165 170 175

Lys Lys Glu Gln Val Asp Gln Ile Val Lys Asp Ile Arg Glu Phe Lys
180 185 190

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

Glu Arg Tyr Ser Asn Val Ile Val Gly Leu Asn Asp Thr Met Glu Asn
210 215 220

Leu Leu Ala Ala Val Asp Arg Asp Glu Ala Glu Ile Ser Pro Ser Thr
225 230 235 240

Leu Tyr Ala Ile Ala Cys Val Leu Glu Asn Val Pro Phe Ile Asn Gly
245 250 255

Ser Pro Gln Asn Thr Phe Val Pro Gly Leu Ile Asp Leu Ala Ile Lys
260 265 270

Arg Asn Thr Leu Ile Gly Gly Asp Asp Phe Lys Ser Gly Gln Thr Lys
275 280 285

Met Lys Ser Val Leu Val Asp Phe Leu Val Gly Ala Gly Ile Lys Pro
290 295 300

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

Leu Ser Ala Pro Gln Thr Phe Arg Ser Lys Glu Ile Ser Lys Ser Asn
325 330 335

Val Val Asp Asp Met Val Ser Ser Asn Ala Ile Leu Tyr Glu Ala Gly
340 345 350

Glu His Pro Asp His Val Val Val Ile Lys Tyr Val Pro Tyr Val Gly
355 360 365

Asp Ser Lys Arg Ala Met Asp Glu Tyr Thr Ser Glu Ile Phe Met Gly
370 375 380

Gly Asn Asn Thr Ile Val Leu His Asn Thr Cys Glu Asp Ser Leu Leu
385 390 395 400

Ala Ala Pro Ile Ile Leu Asp Leu Val Leu Leu Ala Glu Leu Ser Thr
405 410 415

Arg Ile Gln Leu Lys Ala Glu Gly Glu Gly Lys Phe His Ser Phe His
420 425 430

Pro Val Ala Thr Ile Leu Ser Tyr Leu Thr Lys Ala Pro Leu Val Pro
435 440 445

Pro Gly Thr Pro Val Val Asn Ala Leu Ser Lys Gln Arg Ala Met Leu
450 455 460

Glu Asn Ile Leu Arg Ala Cys Val Gly Leu Ala Pro Glu Asn Asn Met
465 470 475 480

Ile Leu Glu Tyr Lys
485

<210> 962
<211> 510
<212> PRT
<213> Gengibre

<400> 962

Met Phe Val Glu Lys Phe Arg Val Glu Ser Pro Asn Val Arg Tyr Gly
1 5 10 15

Glu Glu Glu Ile Glu Ala Val Tyr His Tyr Glu Thr Thr Asp Leu Val
20 25 30

His Glu Ser Arg Asp Gly Ala Tyr Gln Trp Ile Val Arg Pro Lys Arg
35 40 45

Val Arg Tyr Asp Phe Lys Thr Gln Thr Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Val Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asp Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

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

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Phe Glu Pro Asp Phe Val Ala Ala Asn Gln Gly Ala
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Ser Glu Gln Val Gln Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Gln Thr Gln Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ile
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Met Ala Ser Leu Glu Lys
245 250 255

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

Leu Glu Asn Val Pro Tyr Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Glu Met Ala Ile Gln Arg Asn Ser Leu Ile Gly Gly
290 295 300

Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Glu
305 310 315 320

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Gly Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Ile
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Glu Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ser Ala Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Ser Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Asn Leu Glu Tyr Lys
500 505 510

<210> 963
<211> 510
<212> PRT
<213> Taxus

<400> 963

Met Phe Ile Glu Ser Phe Arg Val Gln Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Glu Ser Ile Asp Ser Val Tyr Asp Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Thr Asn Gly Lys Tyr Glu Trp Val Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Asp Phe Lys Thr Asp Thr Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Cys Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Val Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Cys Arg
100 105 110

Ile Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asp Pro Asn Asp Ile Val Phe Gly Gly Trp Asp Ile

130 135 140

Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Glu
145 150 155 160

Val Asp Leu Gln Met Gln Leu Arg Pro Tyr Met Gln Asp Met Val Pro
165 170 175

Leu Pro Gly Ile Phe Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Glu
180 185 190

Arg Ala Asn Asn Ile Ile Lys Gly Ser Lys Lys Glu Gln Val Gln Gln
195 200 205

Ile Ile Gln Asp Ile Arg Glu Phe Lys Ala Lys Thr Lys Val Glu Lys
210 215 220

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

Val Gly Leu Asn Asp Thr Lys Glu Thr Leu Phe Ala Ser Leu Glu Lys
245 250 255

Asn Glu Ser Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Gln Glu Asn Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val

275 280 285

Pro Gly Leu Ile Asp Phe Ala Ile Glu Lys Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Gly Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Leu Ile Leu Asp

420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Lys Glu
435 440 445

Gly Glu Ala Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Ile Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 964
<211> 483
<212> PRT
<213> Momordica

<400> 964

Thr Thr Glu Leu Ile His Glu Asn Lys Asn Gly Ser Tyr Gln Trp Thr
1 5 10 15

Val Lys Pro Lys Ile Val Lys Tyr Glu Phe Lys Thr Asp Thr Arg Leu
20 25 30

Pro Lys Leu Gly Val Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser
35 40 45

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

Thr Lys Asp Lys Val Gln Pro Ala Asn Tyr Phe Gly Ser Leu Thr Gln
65 70 75 80

Ala Ser Ser Ile Arg Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala
85 90 95

Pro Phe Lys Ser Leu Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe
100 105 110

Gly Gly Trp Asp Ile Ser Asp Met Ser Leu Ala Asp Ala Met Ala Arg
115 120 125

Ala Lys Val Phe Asp Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met
130 135 140

Glu Ser Met Val Pro Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala
145 150 155 160

Ala Asn Gln Asp Ser Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys
165 170 175

Glu Gln Val Gln Lys Val Ile Asn Asp Ile Lys Glu Phe Lys Glu Lys
180 185 190

Ser Lys Val Asp Lys Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg
195 200 205

Tyr Ser Asn Val Val Val Gly Leu Asn Asp Thr Met Glu Ser Leu Leu
210 215 220

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

Ala Ile Ala Cys Val Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro
245 250 255

Gln Asn Thr Phe Val Pro Gly Leu Ile Asp Leu Ala Ile Arg Arg Asn
260 265 270

Ser Leu Ile Gly Gly Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys
275 280 285

Ser Val Leu Val Asp Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser
290 295 300

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

Ala Pro Gln Thr Phe Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val
325 330 335

Asp Asp Met Val Ser Ser Asn Gly Ile Leu Tyr Glu Pro Gly Glu His
340 345 350

Pro Asp His Ile Val Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser
355 360 365

Lys Arg Ala Met Asp Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys
370 375 380

Ser Thr Ile Val Leu His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala
385 390 395 400

Pro Ile Ile Leu Asp Leu Val Leu Leu Ala Glu Leu Ser Ser Arg Ile
405 410 415

Gln Leu Lys Ala Gly Gly Glu Glu Lys Phe His Ser Phe His Pro Val
420 425 430

Ala Thr Ile Leu Ser Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly
435 440 445

Thr Pro Val Val Asn Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn
450 455 460

Ile Leu Arg Ala Cys Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu
465 470 475 480

Glu Tyr Lys

<210> 965
<211> 510
<212> PRT
<213> Podocarpus

<400> 965

Met Phe Ile Glu Ser Phe Arg Val Gln Ser Pro Asn Val Lys Tyr Ser
1 5 10 15

Glu Glu Ser Ile Glu Ser Val Tyr Asp Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Arg Asn Gly Lys Tyr Glu Trp Val Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Gln Thr Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Cys Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Val Thr Lys Glu Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Cys Arg
100 105 110

Ile Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asp Pro Asn Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Gln Asp Met Met Pro
165 170 175

Leu Pro Gly Ile Phe Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Glu
180 185 190

Arg Ala Asn Asn Ile Ile Lys Gly Ser Lys Lys Glu Gln Val His Lys
195 200 205

Ile Ile Gln Asp Ile Arg Glu Phe Lys Ala Lys Thr Lys Val Asp Lys
210 215 220

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

Val Gly Leu Asn Asp Thr Lys Glu Thr Phe Leu Ala Ser Leu Glu Arg
245 250 255

Asn Glu Ser Glu Ile Ser Pro Ser Ser Leu Tyr Ala Leu Ala Cys Ile
260 265 270

Glu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Glu Lys Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Gly Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Leu Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Lys Glu
435 440 445

Gly Glu Glu Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 966
<211> 510
<212> PRT
<213> Curcuma

<400> 966

Met Phe Val Glu Lys Phe Arg Val Glu Ser Pro Asn Val Arg Tyr Gly
1 5 10 15

Glu Glu Glu Ile Glu Ser Val Tyr Tyr Tyr Asp Thr Thr Asp Leu Val
20 25 30

His Glu Ser Arg Asp Gly Ala Tyr Gln Trp Ile Val Arg Pro Lys Arg
35 40 45

Val Arg Tyr Asp Phe Lys Thr Gln Thr Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Val Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asp Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

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

Ile Asp Leu Gln Lys Gln Leu Lys Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Phe Glu Pro Asp Phe Val Ala Ala Asn Gln Gly Ala
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Ser Glu Gln Val Gln Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Gln Thr Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Gln Arg Tyr Ser Asn Glu Ile
225 230 235 240

Asp Gly Leu Asn Asp Thr Met Glu Asn Leu Met Ala Ser Leu Glu Lys
245 250 255

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

Leu Glu Asn Val Pro Tyr Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Glu Met Ala Ile Gln Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Gly Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Ile
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Glu Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ser Ala Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Asn Leu Glu Tyr Lys
500 505 510

<210> 967
<211> 510
<212> PRT
<213> Sciadopitys

<400> 967

Met Phe Ile Glu Lys Phe Arg Val Gln Ser Pro Asn Val Lys Tyr Thr

1 5 10 15

Glu Glu Ser Ile Glu Ser Val Tyr Asp Tyr Ser Thr Thr Glu Leu Val
20 25 30

His Glu Asn Ile Asn Gly Lys Tyr Glu Trp Val Val Lys Pro Lys Ser
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Ala Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Val Thr Lys Glu Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Cys Arg
100 105 110

Ile Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asp Pro Asn Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asn Leu Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp

145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met His Asp Met Ala Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Glu
180 185 190

Arg Ala Asp Asn Ile Ile Lys Gly Ser Lys Lys Asp Gln Val Gln Lys
195 200 205

Ile Ile Gln Asp Ile Arg Glu Phe Lys Ser Lys Thr Lys Val Asp Lys
210 215 220

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

Val Gly Leu Asn Asp Thr Lys Gln Thr Leu Leu Ala Ser Leu Glu Arg
245 250 255

Asn Glu Ser Glu Ile Ser Pro Ser Thr Leu Tyr Ala Met Ala Cys Ile
260 265 270

Gln Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Glu Leu Ala Ile Glu Lys Asn Ser Leu Ile Gly Gly

290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Ser Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Gly Pro Gly Glu His Pro Asp His Val Ile
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Leu Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Lys Glu

435 440 445

Gly Glu Pro Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ser Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 968
<211> 510
<212> PRT
<213> Cephalotaxus

<400> 968

Met Phe Ile Glu Lys Phe Arg Val Gln Ser Pro Asn Val Lys Tyr Ser
1 5 10 15

Glu Glu Ser Ile Glu Ser Val Tyr Asp Phe Glu Thr Thr Glu Leu Val
20 25 30

His Gln Asn Thr Asn Gly Lys Tyr Glu Trp Val Val Lys Pro Lys Ser
35 40 45

Val Lys Tyr Gln Phe Lys Thr Asp Thr Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Cys Arg
100 105 110

Ile Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asp Pro Asn Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Leu Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Gln Asp Met Val Pro
165 170 175

Leu Pro Gly Ile Phe Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Glu
180 185 190

Arg Ala Asn His Ile Ile Lys Gly Ser Lys Lys Glu Gln Val Gln Gln
195 200 205

Ile Val Gln Asp Ile Thr Glu Phe Lys Ala Lys Thr Lys Val Asp Arg
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Met
225 230 235 240

Val Gly Leu Asn Asp Thr Lys Glu Thr Leu Leu Ala Ser Leu Glu Arg
245 250 255

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

Gln Glu Asn Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Glu Leu Ala Ile Glu Lys Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Gly Pro Gly Glu His Pro Asp His Val Ile
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Leu Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Lys Glu
435 440 445

Asp Glu Ala Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 969
<211> 510
<212> PRT
<213> Cephalotaxus

<400> 969

Met Phe Ile Glu Ser Phe Arg Val Gln Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Glu Ser Ile Glu Ser Val Tyr Asp Tyr Ala Thr Thr Glu Leu Val
20 25 30

His Glu Asn Thr Asn Gly Arg Tyr Glu Trp Val Val Arg Pro Lys Thr
35 40 45

Val Thr Tyr Asp Phe Arg Thr Asp Thr Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Val Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Cys Arg
100 105 110

Ile Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asp Pro Asn Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Gln Asp Met Ile Pro
165 170 175

Leu Pro Gly Ile Phe Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Glu
180 185 190

Arg Ala Asn Asn Ile Val Lys Gly Ser Lys Lys Glu Gln Ile Glu Lys
195 200 205

Ile Ile Gln Asp Ile Arg Glu Phe Lys Ala Lys Thr Lys Val Glu Lys
210 215 220

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

Val Gly Leu Asn Asp Thr Lys Glu Thr Leu Phe Ala Ser Val Glu Arg
245 250 255

Asn Glu Ser Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Gln Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Phe Ala Ile Glu Lys Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Gly Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Leu Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Arg Lys Glu
435 440 445

Gly Glu Ala Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 970
<211> 510
<212> PRT
<213> Cephalotaxus

<400> 970

Met Phe Ile Glu Ser Phe Arg Val Gln Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Glu Ser Ile Glu Ser Val Tyr Asp Tyr Ala Thr Thr Glu Leu Val
20 25 30

His Glu Asn Thr Asn Gly Arg Tyr Glu Trp Val Val Lys Pro Lys Thr
35 40 45

Val Thr Tyr Asp Phe Arg Thr Asp Thr Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Val Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Cys Arg
100 105 110

Ile Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asp Pro Asn Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Gln Asp Met Ile Pro
165 170 175

Leu Pro Gly Ile Phe Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Glu
180 185 190

Arg Ala Asn Asn Ile Val Lys Gly Ser Lys Lys Glu Gln Ile Glu Lys
195 200 205

Ile Ile Gln Asp Ile Arg Glu Phe Lys Ala Lys Thr Lys Val Glu Lys
210 215 220

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

Val Gly Leu Asn Asp Thr Lys Glu Thr Leu Phe Ala Ser Val Glu Arg
245 250 255

Asn Glu Ser Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Gln Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Met Asp Phe Ala Ile Glu Lys Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Gly Pro Gly Glu His Pro Asp His Val Ile
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Leu Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Arg Lys Glu
435 440 445

Gly Glu Ala Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 971
<211> 510
<212> PRT
<213> Distylium

<400> 971

Met Phe Ile Glu Ser Phe Arg Val Gln Ser Pro Asn Val Lys Tyr Thr

1 5 10 15

Glu Asp Ser Ile Glu Ala Val Tyr Asp Tyr Ala Thr Thr Glu Leu Val
5 20 25 30

His Glu Asn Arg Asn Gly Lys Tyr Glu Trp Val Val Lys Pro Lys Ser
35 40 45
10

Val Lys Tyr Glu Phe Lys Thr Asp Thr Arg Val Pro Lys Leu Gly Val
50 55 60

15

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

20 Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Val Thr Lys Glu Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Cys Arg
25 100 105 110

Ile Gly Ser Tyr Asn Gly Glu Glu Ile His Ala Pro Phe Lys Ser Leu
115 120 125
30

Leu Pro Met Val Asp Pro Asn Glu Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

35

Asn Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Glu

145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Gln Asp Met Leu Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Glu
180 185 190

Arg Ala Asn Asn Ile Ile Lys Gly Ser Lys Lys Glu Gln Val Asp Arg
195 200 205

Ile Ile Gln Asp Ile Arg Glu Phe Lys Ala Ser Thr Lys Val Glu Asn
210 215 220

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

Val Gly Leu Asn Asp Thr Lys Glu Asn Leu Phe Ala Ser Leu Glu Arg
245 250 255

Asn Glu Phe Glu Ile Ser Pro Ser Thr Leu Tyr Ala Leu Ala Cys Val
260 265 270

Gln Glu Asn Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Glu Leu Ala Ile Glu Lys Asn Ser Leu Ile Gly Gly

290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Gly Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Arg Asn Thr Ile Val Leu
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Leu Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Cys Ser Arg Ile Gln Leu Lys Arg Glu

435 440 445

Gly Glu Ser Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 972
<211> 510
<212> PRT
<213> Sciadopitys

<400> 972

Met Phe Ile Glu Arg Phe Arg Val Gln Ser Pro Asn Val Lys Tyr Gly
1 5 10 15

Glu Gly Ser Ile Gln Ser Val Tyr Asp Tyr Ser Thr Thr Glu Leu Val
20 25 30

His Asp Asn Asn Asn Gly Lys Tyr Glu Trp Val Val Arg Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Asn Thr Asp Ser Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Val Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Cys Arg
100 105 110

Ile Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asp Pro Asn Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Asn Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Gln Asp Met Ala Pro
165 170 175

Leu Pro Gly Ile Phe Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Glu
180 185 190

Arg Ala Asn Asn Ile Ile Lys Gly Ser Lys Lys Glu Gln Val Gln Gln
195 200 205

Ile Val Arg Asp Ile Arg Glu Phe Gln Ala Lys Thr Lys Val Glu Lys
210 215 220

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

Val Gly Leu Asn Asp Asn Lys Glu Thr Leu Leu Ala Ser Leu Glu Arg
245 250 255

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

Gln Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Glu Lys Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Leu Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Phe Gly Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Asn Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Leu Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Lys Glu
435 440 445

Gly Glu Ala Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 973
<211> 82
<212> PRT
<213> Sequoia

<400> 973

Met Ser Ser Phe Ser Thr Gln Pro Val Gly Ala Met Asp Ser Val Ser
1 5 10 15

Ser Val Val Ser Met Leu Lys Gly Thr Leu Glu Arg Lys Lys Leu Gly
20 25 30

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

Tyr Val His Asp Glu Asn Ile Tyr Cys Met Asn Gln Asn His Asn Ser
50 55 60

Phe Phe Lys Phe Leu Ser Leu Lys Lys Gly Cys Lys Gln Leu Ser Leu
65 70 75 80

Ser Lys

<210> 974
<211> 510
<212> PRT
<213> Pino marítimo

<400> 974

Met Phe Ile Gln Asn Phe Arg Val Glu Ser Pro Asn Val Lys Tyr Ser
1 5 10 15

Glu Glu Cys Ile Asp Ser Ile Tyr Asp Tyr Gln Thr Thr Glu Leu Val
20 25 30

His Glu Asn Ala Asn Gly Lys Tyr Glu Trp Val Val Lys Pro Lys Thr
35 40 45

Val Arg Tyr Glu Phe Lys Thr Glu Arg Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Val Thr Lys Glu Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Cys Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile His Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asp Pro Asn Ala Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Asn Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Gln Gly Met Asn Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Glu
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Ser Lys Lys Glu Gln Leu Gln Lys
195 200 205

Ile Ile Glu Asp Ile Arg Asp Phe Lys Ser Lys Thr Lys Val Asp Lys
210 215 220

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

Val Gly Leu Asn Asp Thr Lys Glu Thr Leu Leu Ala Ser Leu Glu Arg
245 250 255

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

Gln Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Thr Lys Asn Ser Ile Ile Ala Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Leu Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Cys Thr Arg Ile Gln Leu Lys Lys Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Ser Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Thr Leu Glu Tyr Lys
500 505 510

<210> 975
<211> 512
<212> PRT
<213> Zamia

<400> 975

Met Phe Ile Glu Ser Phe Arg Val Glu Ser Pro Tyr Val Lys Tyr Thr
1 5 10 15

Glu Glu Ser Ile Glu Ser Val Tyr Asn Tyr Glu Thr Thr Glu Val Val
20 25 30

His Ser Arg Asp Ser Arg Thr Gly Lys Tyr Glu Trp Ile Val Lys Pro
35 40 45

Thr Thr Val Lys Tyr Glu Phe His Thr Gln Thr Arg Val Pro Lys Leu
50 55 60

Gly Val Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr
65 70 75 80

Ala Gly Val Ile Ala Asn Arg Glu Gly Met Ser Trp Leu Thr Lys Glu
85 90 95

Gly Ala Arg Arg Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr
100 105 110

Cys Arg Val Gly Ser Phe His Gly Glu Glu Ile Tyr Ala Pro Phe Lys
115 120 125

Ser Leu Leu Pro Leu Val Asp Pro Asn Asp Ile Val Phe Gly Gly Trp

130 135 140

Asp Ile Asn Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val
145 150 155 160

Leu Asp Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Gly Met
165 170 175

Val Pro Leu Pro Gly Ile Tyr Asp Ala Asp Phe Ile Ala Ala Asn Gln
180 185 190

Asp Ser Arg Ala Asn Asn Ile Ile Lys Gly Thr Lys Lys Glu Gln Val
195 200 205

Gln Arg Ile Val Gln Asp Ile Arg Glu Phe Arg Ala Lys Thr Lys Val
210 215 220

Glu Arg Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn
225 230 235 240

Val Leu Ala Gly Leu Asn Asp Thr Glu Glu Asn Leu Leu Ala Ser Leu
245 250 255

Glu Arg Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Leu Ala
260 265 270

Cys Ile Gln Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr

275 280 285

Phe Val Pro Gly Leu Ile Asp Leu Ala Ile Ser Lys Asn Ser Leu Ile
290 295 300

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

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

Tyr Asn His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln
340 345 350

Thr Phe Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met
355 360 365

Val Ser Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His
370 375 380

Val Val Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala
385 390 395 400

Met Asp Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Ser Thr Ile
405 410 415

Val Leu His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Leu Ile

420 425 430

Leu Asp Leu Val Leu Leu Ala Glu Leu Cys Thr Arg Ile Lys Leu Lys
435 440 445

Lys Glu Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile
450 455 460

Leu Ser Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val
465 470 475 480

Val Asn Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg
485 490 495

Ala Cys Val Gly Leu Ala Pro Glu Asn Asn Met Met Leu Glu Tyr Lys
500 505 510

<210> 976
<211> 510
<212> PRT
<213> Pino

<400> 976

Met Phe Ile Gln Ser Phe Arg Val Asp Ser Pro Asn Val Lys Tyr Ser
1 5 10 15

Glu Glu Ser Ile Asp Ser Ile Tyr Asp Tyr Gln Thr Thr Glu Leu Val
20 25 30

His Glu Asn Ala Asn Gly Lys Tyr Glu Trp Val Val Lys Pro Lys Thr
35 40 45

Val Arg Tyr Glu Phe Lys Thr Glu Arg Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Val Thr Lys Glu Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Cys Arg
100 105 110

Ile Gly Ser Phe Asn Gly Glu Glu Ile His Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asp Pro Asn Ala Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Asn Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Gln Gly Met Thr Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Glu
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Ser Lys Lys Glu Gln Leu Gln Lys
195 200 205

Ile Ile Gln Asp Ile Arg Asp Phe Lys Ser Lys Thr Lys Val Asp Lys
210 215 220

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

Val Gly Leu Asn Asp Thr Lys Glu Thr Leu Leu Ala Ser Leu Glu Arg
245 250 255

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

Gln Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Thr Lys Asn Ser Ile Ile Ala Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Leu Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Cys Thr Arg Ile Gln Leu Lys Lys Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Ser Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Thr Leu Glu Tyr Lys
500 505 510

<210> 977
<211> 510
<212> PRT
<213> Podocarpus

<400> 977

Met Phe Ile Glu Ser Phe Arg Val Gln Ser Pro Asn Val Lys Phe Thr
1 5 10 15

Glu Glu Ser Ile Glu Ser Val Tyr Glu Tyr Ser Thr Thr Glu Leu Val
20 25 30

His Glu Asn Lys Asn Gly Lys Phe Glu Trp Ile Val Lys Pro Lys Ser
35 40 45

Val Ile Tyr Glu Phe Lys Thr Asp Arg Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Val Thr Lys Asp Ser Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Cys Arg
100 105 110

Ile Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asp Pro Asn Glu Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

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

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Thr Asp Met Glu Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Glu
180 185 190

Arg Ala Asn Asn Ile Ile Lys Gly Ser Lys Lys Glu Gln Val His Lys
195 200 205

Ile Ile Gln Asp Ile Arg Glu Phe Lys Ala Lys Thr Lys Val Glu Arg
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Glu Val Met
225 230 235 240

Val Gly Leu Asn Asp Thr Lys Glu Asn Leu Leu Ala Ser Leu Glu Arg
245 250 255

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

Glu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Glu Met Ala Ile Glu Lys Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Gly Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Leu Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Cys Thr Arg Ile Gln Leu Lys Lys Glu
435 440 445

Gly Glu Ala Lys Phe His Ser Phe His Pro Val Ala Thr Leu Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Ile Gly Leu Ala Pro Glu Asn Asn Met Met Leu Glu Tyr Lys
500 505 510

<210> 978
<211> 491
<212> PRT
<213> Flaveria

<400> 978

Lys Phe Thr Leu Cys Thr Thr Thr Thr Pro Leu Asn Ser Phe Thr Arg
1 5 10 15

Arg Lys Thr Val Leu Ile Asn Gly Leu Leu Ser Gln Thr Val Lys Tyr
20 25 30

Glu Phe Lys Thr Gln Thr Arg Val Pro Lys Leu Gly Val Met Leu Val
35 40 45

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

Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Glu Lys Val Gln Gln Ala
65 70 75 80

Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg Val Gly Ser
85 90 95

Phe Asn Gly Glu Glu Ile Phe Ala Pro Phe Lys Ser Leu Leu Pro Met
100 105 110

Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile Ser Ser Met
115 120 125

Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp Ile Asp Leu
130 135 140

Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro Leu Pro Gly
145 150 155 160

Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Glu Arg Ala Asp
165 170 175

Asn Val Ile Lys Gly Thr Lys Asn Glu Gln Ile Gln Lys Ile Ile Lys
180 185 190

Asp Ile Arg Glu Phe Lys Glu Ala Asn Lys Val Asp Lys Val Val Val
195 200 205

Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Met Val Gly Leu
210 215 220

Asn Asp Thr Met Glu Ser Leu Phe Ala Ser Leu Asp Lys Asn Glu Ala
225 230 235 240

Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Ile Leu Glu Asn
245 250 255

Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val Pro Gly Val
260 265 270

Ile Asp Leu Ala Ile Lys Arg Asn Ser Leu Ile Gly Gly Asp Asp Phe
275 280 285

Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp Phe Leu Val
290 295 300

Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn His Leu Gly
305 310 315 320

Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe Arg Ser Lys
325 330 335

Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser Ser Asn Ala
340 345 350

Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val Val Ile Lys
355 360 365

Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp Glu Tyr Thr
370 375 380

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

Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp Leu Val Leu
405 410 415

Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu Asp Glu Gly
420 425 430

Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser Tyr Leu Thr
435 440 445

Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn Ala Leu Ala
450 455 460

Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys Val Gly Leu
465 470 475 480

Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
485 490

<210> 979
<211> 510
<212> PRT
<213> Cycas

<400> 979

Met Phe Val Gln Ser Phe Arg Val Glu Ser Asp Asn Val Lys Tyr Ser

1 5 10 15

Glu Asp Ser Ile Glu Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Arg Asn Gly Lys Tyr Glu Trp Val Val Lys Pro Arg Thr
35 40 45

Val Lys Tyr Gln Phe Glu Thr Asp Arg Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Ala
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Val Thr Lys Glu Arg Val
85 90 95

Gln Arg Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Cys Arg
100 105 110

Ile Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asp Pro Asn Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Asn Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp

145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Val Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Ile Ile Gly Gly Thr Lys Lys Glu Gln Val Gln Lys
195 200 205

Ile Val Gln Asp Ile Arg Glu Phe Lys Thr Lys Thr Asn Val Glu Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Phe Ser Asn Val Val
225 230 235 240

Val Gly Leu Asn Asp Thr Glu Glu Asn Leu Leu Ala Ser Val Glu Arg
245 250 255

Asn Glu Ser Glu Ile Ala Pro Ser Thr Leu Tyr Ala Leu Ala Cys Val
260 265 270

Gln Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Val Ser Lys Asn Thr Leu Ile Gly Gly

290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Ser Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Ile
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Arg Asn Thr Ile Val Ile
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Cys Thr Arg Ile Lys Leu Lys Lys Glu

435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Ser Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Ile Gly Leu Ala Pro Glu Asn Asn Met Leu Leu Glu Tyr Lys
500 505 510

<210> 980
<211> 510
<212> PRT
<213> Pino

<400> 980

Met Phe Ile Gln Ser Phe Arg Val Asp Ser Pro Asn Val Asn Tyr Ser
1 5 10 15

Glu Glu Ser Ile Asp Ser Ile Tyr Asp Tyr Gln Thr Thr Glu Leu Val
20 25 30

His Glu Asn Ala Asn Gly Lys Tyr Glu Trp Val Val Lys Pro Lys Thr
35 40 45

Val Arg Tyr Glu Phe Lys Thr Glu Arg Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Val Thr Lys Glu Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Cys Arg
100 105 110

Ile Gly Ser Phe Asn Gly Glu Glu Ile His Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asp Pro Asn Ala Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Asn Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Gln Gly Met Thr Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Glu
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Ser Lys Lys Glu Gln Leu Gln Lys
195 200 205

Ile Ile Gln Asp Ile Arg Asp Phe Lys Ser Lys Thr Lys Val Asp Lys
210 215 220

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

Val Gly Leu Asn Asp Thr Lys Glu Thr Leu Leu Ala Ser Leu Glu Arg
245 250 255

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

Gln Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Thr Lys Asn Ser Ile Ile Ala Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Leu Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Cys Thr Arg Ile Gln Leu Lys Lys Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Ser Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Thr Leu Glu Tyr Lys
500 505 510

<210> 981
<211> 510
<212> PRT
<213> Pícea

<400> 981

Met Phe Ile Gln Ser Phe Arg Val Glu Ser Pro Asn Val Lys Tyr Ser
1 5 10 15

Glu Glu Ser Ile Asp Ser Ile Tyr Asp Tyr Gln Thr Thr Glu Leu Val
20 25 30

His Glu Asn Val Asn Gly Lys Tyr Glu Trp Val Ile Lys Pro Lys Ser
35 40 45

Val Arg Tyr Glu Phe Lys Thr Glu Arg Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Leu Gly Ile Ser Trp Val Thr Lys Glu Lys Ile
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Cys Arg
100 105 110

Ile Gly Ser Phe Lys Gly Glu Glu Ile His Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asp Pro Asn Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Asn Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Gln Gly Met Asn Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Glu
180 185 190

Arg Ala Asn Asn Val Val Lys Gly Ser Lys Lys Glu Gln Val Gln Lys
195 200 205

Ile Ile Gln Asp Ile Arg Asp Phe Lys Ser Lys Thr Lys Val Asp Lys
210 215 220

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

Val Gly Phe Asn Asp Thr Lys Glu Thr Leu Leu Ala Ser Leu Glu Arg
245 250 255

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

Gln Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Thr Lys Asn Ser Ile Ile Ala Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Leu Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Cys Thr Arg Ile Gln Leu Lys Lys Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Ser Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Thr Leu Glu Tyr Lys
500 505 510

<210> 982
<211> 510
<212> PRT
<213> Pícea

<400> 982

Met Phe Ile Gln Ser Phe Arg Val Glu Ser Pro Asn Val Lys Tyr Ser
1 5 10 15

Glu Glu Ser Ile Asp Ser Ile Tyr Asp Tyr Gln Thr Thr Glu Leu Val
20 25 30

His Glu Asn Val Asn Gly Lys Tyr Glu Trp Val Val Lys Pro Lys Ala
35 40 45

Val Arg Tyr Glu Phe Lys Thr Glu Arg Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Val Thr Lys Glu Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Cys Arg
100 105 110

Ile Gly Ser Tyr Lys Gly Glu Glu Ile His Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asp Pro Asn Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Asn Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Gln Gly Met Ser Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Glu
180 185 190

Arg Ala Asn Asn Val Leu Lys Gly Ser Lys Lys Glu Gln Val Gln Lys
195 200 205

Ile Ile Gln Asp Ile Arg Asp Phe Lys Ser Lys Thr Lys Val Asp Lys
210 215 220

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

Val Gly Leu Asn Asp Thr Lys Glu Thr Leu Leu Ala Ser Leu Glu Arg
245 250 255

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

Gln Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Thr Lys Asn Ser Ile Ile Ala Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Leu Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Cys Thr Arg Ile Gln Leu Lys Lys Glu
435 440 445

Gly Glu Glu Lys Phe His Ser Phe His Pro Val Ala Ser Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Thr Leu Glu Tyr Lys
500 505 510

<210> 983
<211> 510
<212> PRT
<213> Pícea

<400> 983

Met Phe Ile Gln Ser Phe Arg Val Glu Ser Pro Asn Val Lys Tyr Ser

1 5 10 15

Glu Glu Ser Ile Asp Ser Ile Tyr Asp Tyr Gln Thr Thr Glu Leu Val
20 25 30

His Glu Asn Val Asn Gly Lys Tyr Glu Trp Val Val Lys Pro Lys Ala
35 40 45

Val Arg Tyr Glu Phe Lys Thr Glu Arg Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Val Thr Lys Glu Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Cys Arg
100 105 110

Ile Gly Ser Tyr Lys Gly Glu Glu Ile His Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asp Pro Asn Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Asn Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp

145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Gln Gly Arg Ser Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Glu
180 185 190

Arg Ala Asn Asn Val Leu Lys Gly Ser Lys Lys Glu Gln Val Gln Lys
195 200 205

Ile Ile Gln Asp Ile Arg Asp Phe Lys Ser Lys Thr Lys Val Asp Lys
210 215 220

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

Val Gly Leu Asn Asp Thr Lys Glu Thr Leu Leu Ala Ser Leu Glu Arg
245 250 255

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

Gln Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Thr Lys Asn Ser Ile Ile Ala Gly

290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Leu Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Cys Thr Arg Ile Gln Leu Lys Lys Glu

435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Ser Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Thr Leu Glu Tyr Lys
500 505 510

<210> 984
<211> 510
<212> PRT
<213> Cedrus

<400> 984

Met Phe Ile Gln Asn Phe Arg Val Glu Ser Pro Asn Val Lys Tyr Ser
1 5 10 15

Glu Asp Ser Ile Asp Ser Ile Tyr Asp Tyr Gln Thr Thr Glu Leu Val
20 25 30

His Glu Asn Val Asn Gly Lys Tyr Glu Trp Val Val Lys Pro Thr Ser
35 40 45

Val Arg Tyr Glu Phe Lys Thr Glu Arg Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Val Thr Lys Glu Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Cys Arg
100 105 110

Ile Gly Ser Phe Lys Gly Glu Glu Ile His Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asp Pro Asn Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Asn Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Gln Gly Met Ala Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Glu
180 185 190

Arg Ala Asn Asn Val Leu Lys Gly Ser Lys Lys Glu Gln Val Gln Lys
195 200 205

Ile Ile Gln Asp Ile Arg Asp Phe Lys Ser Lys Thr Lys Val Asp Lys
210 215 220

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

Val Gly Leu Asn Asp Thr Lys Glu Thr Leu Leu Ala Ser Leu Glu Arg
245 250 255

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

Gln Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Thr Lys Asn Ser Ile Ile Ala Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Ala Ile Leu Tyr Gly Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Leu Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Cys Thr Arg Ile Gln Leu Lys Lys Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Ser Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Leu Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Thr Leu Glu Tyr Lys
500 505 510

<210> 985
<211> 510
<212> PRT
<213> Gnetum

<400> 985

Met Phe Ile Glu Asn Phe Arg Val Glu Ser Pro Asn Val Thr Tyr Thr
1 5 10 15

Glu Glu Ser Ile Glu Ser Val Tyr Gly Tyr Gln Thr Thr Glu Leu Val
20 25 30

His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Arg Pro Lys Glu
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Arg Gln Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Cys Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Val Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Cys Arg
100 105 110

Ile Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Leu Val Asp Pro Asn Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Glu
145 150 155 160

Met Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Gln Gly Met Thr Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Glu
180 185 190

Arg Ala Asn Asn Ile Val Lys Gly Ser Arg Lys Glu Gln Met Leu Lys
195 200 205

Ile Ile Gln Asp Ile Arg Glu Phe Lys Ala Asn Thr Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val
225 230 235 240

Val Gly Leu Asn Asp Thr Lys Glu Asn Leu Leu Ala Ala Leu Asp Arg
245 250 255

Asn Glu Leu Glu Ile Ser Pro Ser Thr Ile Tyr Ala Ile Ala Cys Val
260 265 270

Leu Glu Gly Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Val Glu Lys Asn Ser Leu Ile Gly Gly
290 295 300

Asp Asp Phe Lys Ser Gly Gln Thr Lys Leu Lys Ser Val Leu Val Asp
305 310 315 320

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Gln Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Leu Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Cys Thr Arg Ile Gln Leu Lys Lys Glu
435 440 445

Gly Glu Ala Lys Phe His Ser Phe His Pro Val Ala Ser Leu Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Val Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Thr Leu Glu Tyr Lys
500 505 510

<210> 986
<211> 510
<212> PRT
<213> Abies

<400> 986

Met Phe Ile Gln Ser Phe Arg Val Glu Ser Pro Asn Val Lys Tyr Ser
1 5 10 15

Glu Glu Ser Ile Glu Ser Val Tyr Asp Tyr Gln Thr Thr Glu Leu Val
20 25 30

His Glu Asn Val Ser Gly Lys Tyr Glu Trp Val Val Lys Pro Lys Ser
35 40 45

Val Arg Tyr Glu Phe Lys Thr Asp Arg Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Val Thr Lys Glu Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Cys Arg
100 105 110

Ile Gly Ser Phe Lys Gly Glu Glu Ile His Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Leu Val Asp Pro Asn Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Asn Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Gln Cys Met Ser Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Glu
180 185 190

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

Ile Ile Gln Asp Ile Arg Asp Phe Lys Ser Glu Thr Lys Val Asp Lys
210 215 220

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

Met Gly Leu Asn Asp Thr Lys Glu Thr Leu Leu Ala Ser Leu Glu Arg
245 250 255

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

Gln Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Thr Lys Asn Ser Ile Ile Ala Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Leu Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Cys Thr Arg Ile Gln Leu Lys Lys Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Ser Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Leu Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ser Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Thr Leu Glu Tyr Lys
500 505 510

<210> 987
<211> 508
<212> PRT
<213> Brachypodium

<400> 987

Met Phe Val Glu Gly Phe Lys Val Glu Ser Pro His Val Arg Tyr Gly

1 5 10 15

Ala Gly Glu Ile Glu Ser Glu Tyr Arg Tyr Asp Thr Thr Glu Val Ala
5 20 25 30

Pro Ser Pro Glu Gly Thr Gly Trp Val Val Arg Pro Lys Ser Val Thr
35 40 45
10

Tyr Asn Phe Lys Thr Ser Thr Ala Val Pro Lys Leu Gly Val Met Leu
50 55 60

15

Val Gly Trp Gly Gly Asn Asn Gly Thr Thr Leu Thr Ala Gly Val Ile
65 70 75 80

20 Ala Asn Arg Leu Ala Ile Ser Trp Ala Thr Lys Glu Lys Val Gln Lys
85 90 95

Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg Val Gly
25 100 105 110

Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu Val Pro
115 120 125
30

Met Val Asn Pro Asn Asp Ile Val Phe Gly Gly Trp Asp Ile Ser Ser
130 135 140

35

Leu Asn Leu Ala Asp Ala Met Gly Arg Ala Lys Val Leu Asp Ile Asp

145 150 155 160

Leu Gln Lys Gln Leu Arg Val Tyr Met Glu Ser Met Val Pro Leu Pro
165 170 175

Gly Ile Tyr Asn Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser Arg Ala
180 185 190

Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Glu Gln Ile Ile
195 200 205

Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys Val Val
210 215 220

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

Leu Asn Asp Thr Met Asp Asn Leu Leu Ala Ser Leu Asp Lys Asn Met
245 250 255

Ala Glu Ile Ser Pro Ser Ser Met Tyr Ala Ile Ala Cys Val Thr Glu
260 265 270

Gly Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val Pro Gly
275 280 285

Leu Ile Glu Leu Ala Ile Lys Lys Asn Ser Leu Ile Gly Gly Asp Asp

290 295 300

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

Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Ala Ser Tyr Asn His Leu
325 330 335

Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Val Phe Arg Ser
340 345 350

Lys Glu Ile Ser Lys Ser Gly Val Val Asp Asp Met Val Ala Ser Asn
355 360 365

Gly Ile Leu Tyr Asn Pro Gly Glu His Pro Asp His Val Ile Val Ile
370 375 380

Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp Glu Tyr
385 390 395 400

Thr Ser Glu Ile Phe Met Gly Gly Arg Asn Thr Ile Val Leu His Asn
405 410 415

Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp Leu Val
420 425 430

Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Gln Gly Gln

435 440 445

Glu Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser Tyr Leu
450 455 460

Ser Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn Ala Leu
465 470 475 480

Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys Val Gly
485 490 495

Leu Ala Pro Glu Asn Asn Met Met Leu Glu His Lys
500 505

<210> 988
<211> 510
<212> PRT
<213> Taxus

<400> 988

Met Phe Val Glu Arg Phe Arg Val Gln Ser Pro Asn Val Lys Tyr Asn
1 5 10 15

Glu Glu Ser Ile Glu Ser Val Tyr Asp Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Gln Asn Thr Asn Gly Lys Tyr Glu Trp Val Val Ile Pro Lys Ser
35 40 45

Val Arg Tyr His Phe Asn Thr His Thr Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Val Thr Lys Glu Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Cys Arg
100 105 110

Ile Gly Ser Tyr Asn Gly Glu Glu Ile His Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asp Pro Asn Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asn Leu Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Gln Asp Met Val Pro
165 170 175

Leu Pro Gly Ile Phe Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Glu
180 185 190

Arg Ala Asn Asn Ile Ile Lys Gly Ser Lys Lys Glu Gln Val Gln Gln
195 200 205

Ile Val Gln Asp Ile Thr Glu Phe Lys Val Lys Thr Lys Val Asp Arg
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Met
225 230 235 240

Val Gly Leu Asn Asp Thr Lys Glu Thr Leu Leu Ala Ser Leu Glu Arg
245 250 255

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

Gln Glu Asn Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Glu Phe Ala Ile Glu Lys Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Gly Pro Gly Glu His Pro Asp His Val Ile
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Leu Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Lys Glu
435 440 445

Gly Glu Ala Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Ile Gly Leu Ser Pro Asp Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 989
<211> 220
<212> PRT
<213> Pino

<400> 989

Met Phe Ile Gln Asn Phe Arg Val Glu Ser Pro Asn Val Lys Tyr Ser
1 5 10 15

Glu Glu Cys Ile Asp Ser Ile Tyr Asp Tyr Gln Thr Thr Glu Leu Val
20 25 30

His Glu Asn Ala Asn Gly Lys Tyr Glu Trp Val Val Lys Pro Lys Thr
35 40 45

Val Arg Tyr Glu Phe Lys Thr Glu Arg Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Val Thr Lys Glu Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Cys Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile His Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asp Pro Asn Ala Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Asn Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Gln Gly Met Asn Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Glu
180 185 190

Arg Ala Asn Asn Val Arg Lys Ser Ser Cys Lys Arg Leu Ser Lys Ile
195 200 205

Ser Glu Ile Leu Asn Arg Lys Gln Arg Trp Thr Arg
210 215 220

<210> 990
<211> 472
<212> PRT
<213> Canola

<400> 990

Thr Tyr Gln Trp Val Val Lys Pro Lys Thr Val Lys Tyr Asp Phe Lys
1 5 10 15

Thr Asp Thr Arg Val Pro Lys Leu Gly Val Met Leu Val Gly Trp Gly
20 25 30

Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly Val Ile Ala Asn Lys Glu
35 40 45

Gly Ile Ser Trp Ala Thr Lys Asp Lys Val Gln Gln Ala Asn Tyr Phe
50 55 60

Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg Val Gly Ser Tyr Asn Gly
65 70 75 80

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

Asp Asp Val Val Phe Gly Gly Trp Asp Ile Ser Asp Met Asn Leu Ala
100 105 110

Asp Ala Met Ala Arg Ala Arg Val Leu Asp Ile Asp Leu Gln Lys Gln
115 120 125

Leu Arg Pro Tyr Met Glu His Met Val Pro Leu Pro Gly Ile Tyr Asp
130 135 140

Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser Arg Ala Asn Ser Val Ile
145 150 155 160

Lys Gly Thr Lys Lys Glu Gln Val Asp Gln Ile Ile Lys Asp Met Arg
165 170 175

Glu Phe Lys Glu Lys Asn Lys Val Asp Lys Leu Val Val Leu Trp Thr
180 185 190

Ala Asn Thr Glu Arg Tyr Ser Asp Val Val Val Gly Leu Asn Asp Thr
195 200 205

Met Glu Asn Leu Leu Ala Ser Val Glu Lys Asn Glu Ser Glu Ile Ser
210 215 220

Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val Leu Glu Gly Ile Pro Phe
225 230 235 240

Ile Asn Gly Ser Pro Gln Asn Thr Phe Val Pro Gly Leu Ile Glu Leu
245 250 255

Ala Ile Thr Lys Asn Cys Leu Ile Gly Gly Asp Asp Phe Lys Ser Gly
260 265 270

Gln Thr Lys Met Lys Ser Val Leu Val Asp Phe Leu Val Gly Ala Gly
275 280 285

Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn His Leu Gly Asn Asn Asp
290 295 300

Gly Met Asn Leu Ser Ala Pro Gln Thr Phe Arg Ser Lys Glu Ile Ser
305 310 315 320

Lys Ser Asn Val Val Asp Asp Met Val Ala Ser Asn Gly Ile Leu Phe
325 330 335

Glu Pro Gly Glu His Pro Asp His Val Val Val Ile Lys Tyr Val Pro
340 345 350

Tyr Val Gly Asp Ser Lys Arg Ala Met Asp Glu Tyr Thr Ser Glu Ile
355 360 365

Phe Met Gly Gly Lys Asn Thr Ile Val Met His Asn Thr Cys Glu Asp
370 375 380

Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp Leu Val Leu Leu Ala Glu
385 390 395 400

Leu Ser Thr Arg Ile Gln Phe Lys Ala Glu Gly Glu Gly Lys Phe His
405 410 415

Ser Phe His Pro Val Ala Thr Ile Leu Ser Tyr Leu Thr Lys Ala Pro
420 425 430

Leu Val Pro Pro Gly Thr Pro Val Val Asn Ala Leu Ser Lys Gln Arg
435 440 445

Ala Met Leu Glu Asn Ile Leu Arg Ala Cys Val Gly Leu Ala Pro Glu
450 455 460

Asn Asn Met Ile Leu Glu Tyr Lys
465 470

<210> 991
<211> 265
<212> PRT
<213> Gnetum

<400> 991

Met Phe Ile Glu Asn Phe Arg Val Glu Ser Pro Asn Val Thr Tyr Thr
1 5 10 15

Glu Glu Ser Ile Glu Ser Val Tyr Gly Tyr Gln Thr Thr Glu Leu Val
20 25 30

His Glu Asn Arg Asn Gly Met Tyr Gln Trp Ile Val Arg Pro Lys Glu

35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Arg Lys Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Val Thr Lys Asp Lys Val
85 90 95

Gln Pro Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Cys Arg
100 105 110

Ile Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Leu Val Asp Pro Asn Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Glu
145 150 155 160

Met Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Gln Gly Ile Thr Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Glu

180 185 190

Arg Ala Asn Asn Ile Val Lys Gly Ser Arg Lys Glu Gln Met Leu Lys
195 200 205

Ile Ile Gln Asp Ile Arg Glu Phe Lys Ala Asn Thr Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val
225 230 235 240

Val Gly Leu Asn Asp Thr Lys Glu Asn Leu Leu Ala Glu Thr Asn Trp
245 250 255

Lys Phe Leu Arg Pro Gln Ser Thr Pro
260 265

<210> 992
<211> 510
<212> PRT
<213> Pseudotsuga

<400> 992

Met Phe Ile Gln Ser Phe Arg Val Glu Ser Pro Asn Val Lys Tyr Ser
1 5 10 15

Glu Glu Ser Ile Asp Ser Thr Tyr Asp Tyr Gln Thr Thr Glu Leu Val
20 25 30

His Glu Asn Ala Asn Gly Lys Tyr Glu Trp Val Ile Lys Pro Lys Ser
35 40 45

Val Arg Tyr Glu Phe Lys Thr Glu Arg Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Val Thr Lys Glu Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Cys Arg
100 105 110

Ile Gly Ser Tyr Lys Gly Glu Glu Ile His Ala Pro Phe Lys Ser Leu
115 120 125

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

Asn Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Gln Gly Met Phe Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Glu
180 185 190

Arg Ala Asn Asn Val Leu Lys Gly Ser Lys Lys Glu Gln Leu Glu Lys
195 200 205

Ile Val Gln Asp Ile Arg Asp Phe Lys Ser Lys Thr Lys Val Asp Lys
210 215 220

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

Val Gly Leu Asn Asp Thr Lys Glu Thr Leu Leu Ala Ser Leu Glu Arg
245 250 255

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

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Thr Lys Asn Ser Ile Ile Ala Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Ile
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Leu Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Cys Thr Arg Ile Gln Leu Lys Lys Glu
435 440 445

Gly Glu Ala Lys Phe His Ser Phe His Pro Val Ala Ser Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Leu Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Thr Leu Glu Tyr Lys
500 505 510

<210> 993
<211> 509
<212> PRT
<213> Arroz

<400> 993

Met Phe Val Glu Gly Phe Arg Val Glu Ser Pro Arg Val Arg Tyr Gly
1 5 10 15

Asp Gly Glu Ile Glu Ser Glu Tyr Arg Tyr Asp Thr Thr Glu Val Val
20 25 30

Ala Pro Pro Ser Pro Glu Lys Gly Trp Val Val Arg Pro Lys Ser Val
35 40 45

Thr Tyr His Phe Lys Thr Thr Thr Thr Val Pro Lys Leu Gly Val Met
50 55 60

Leu Val Gly Trp Gly Gly Asn Asn Gly Thr Thr Leu Thr Ala Gly Val
65 70 75 80

Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Glu Lys Val His
85 90 95

Lys Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ser Ser Thr Ile Arg Val
100 105 110

Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu Val
115 120 125

Pro Met Val Asn Pro Asn Asp Ile Val Phe Gly Gly Trp Asp Ile Ser
130 135 140

Ser Met Asn Leu Ala Asp Ala Met Thr Arg Ala Arg Val Leu Asp Ile
145 150 155 160

Asp Leu Gln Lys Gln Leu Arg His His Met Glu Ser Met Val Pro Leu
165 170 175

Pro Gly Val Tyr Asn Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser Arg
180 185 190

Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Glu Gln Val
195 200 205

Lys Lys Asp Ile Arg Glu Phe Lys Glu Lys Ser Lys Val Asp Lys Val
210 215 220

Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val Ala
225 230 235 240

Gly Met Asn Asp Thr Met Asp Asn Leu Leu Ala Ser Leu Asp Lys Asp
245 250 255

Glu Pro Glu Met Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val Met
260 265 270

Glu Gly Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val Pro
275 280 285

Gly Leu Ile Glu Leu Ala Ile Lys Lys Asn Ser Val Ile Gly Gly Asp
290 295 300

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

Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Ala Ser Tyr Asn His
325 330 335

Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe Arg
340 345 350

Ser Lys Glu Ile Ser Lys Ser Gly Val Val Asp Asp Met Val Ser Ser
355 360 365

Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Ile Val
370 375 380

Ile Lys Tyr Ile Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp Glu
385 390 395 400

Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Leu His
405 410 415

Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp Leu
420 425 430

Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu Asp
435 440 445

Gln Asp Lys Tyr His Ser Phe His Pro Val Ala Thr Ile Leu Ser Tyr
450 455 460

Leu Ser Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn Ala
465 470 475 480

Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys Val
485 490 495

Gly Leu Ala Pro Glu Asn Asn Met Met Leu Glu Tyr Lys
500 505

<210> 994
<211> 509
<212> PRT
<213> Mijo menor

<400> 994

Met Phe Val Glu Gly Phe Arg Val Glu Ser Pro Arg Val Arg Tyr Gly
1 5 10 15

Ala Gly Glu Ile Glu Ser Glu Tyr Arg Tyr Asp Thr Thr Glu Val Val
20 25 30

Pro Pro Gly Asp Gly Gly Ala Gly Trp Val Val Arg Pro Lys Ser Val
35 40 45

Thr Tyr Asn Phe Lys Thr Ser Thr Ser Val Pro Lys Leu Gly Val Met
50 55 60

Leu Val Gly Trp Gly Gly Asn Asn Gly Thr Thr Leu Thr Ala Gly Val
65 70 75 80

Ile Ala Asn Arg Glu Gly Ile Ser Trp Glu Thr Lys Glu Lys Val His
85 90 95

Lys Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg Val
100 105 110

Gly Ser His Asn Gly Glu Glu Val Tyr Ala Pro Phe Lys Ser Leu Val
115 120 125

Pro Met Val Asp Pro Asn Ser Ile Val Phe Gly Gly Trp Asp Ile Ser
130 135 140

Asn Leu Ser Met Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp Ile
145 150 155 160

Asn Leu Gln Lys Gln Leu Arg Pro Tyr Met Gln Ser Met Val Pro Leu
165 170 175

Pro Gly Ile Phe Asn Pro Asp Phe Val Ala Ala Asn Gln Gly Ala Arg
180 185 190

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

Lys Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys Val
210 215 220

Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val Thr
225 230 235 240

Gly Leu Asn Asp Thr Met Asp Asn Leu Met Ala Ser Leu Glu Lys Asn
245 250 255

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

Glu Gly Val Pro Phe Val Asn Gly Ser Pro Gln Asn Thr Phe Val Pro
275 280 285

Gly Leu Ile Glu Leu Ala Ile Lys Lys Asn Ser Leu Ile Gly Gly Asp
290 295 300

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

Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Ala Ser Tyr Asn His
325 330 335

Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Val Phe Arg
340 345 350

Ser Lys Glu Ile Ser Lys Ser Ser Val Val Asp Asp Met Val Ala Ser
355 360 365

Asn Pro Ile Leu Tyr Ser Pro Gly Glu His Pro Asp His Val Ile Val
370 375 380

Ile Lys Tyr Ile Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp Glu
385 390 395 400

Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Leu His
405 410 415

Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp Leu
420 425 430

Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu Gly
435 440 445

Gln Asp Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser Tyr
450 455 460

Leu Ser Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn Ala
465 470 475 480

Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys Val
485 490 495

Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu His Lys
500 505

<210> 995
<211> 509
<212> PRT
<213> Maíz

<400> 995

Met Phe Ala Glu Ser Phe Arg Val Glu Ser Pro Arg Val Arg Tyr Gly
1 5 10 15

Asp Gly Glu Ile Gln Ser Glu Tyr Arg Tyr Asp Thr Thr Glu Val Val
20 25 30

Pro Pro Gly Asn Ser Gly Ala Gly Trp Val Val Arg Pro Lys Ser Val
35 40 45

Thr Tyr Asn Phe Lys Thr Ser Thr Asn Val Pro Lys Leu Gly Val Met
50 55 60

Leu Val Gly Trp Gly Gly Asn Asn Gly Thr Thr Leu Thr Ala Gly Val
65 70 75 80

Ile Ala Asn Arg Glu Gly Ile Ser Trp Glu Thr Lys Glu Lys Val His
85 90 95

Lys Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg Val
100 105 110

Gly Ser His Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu Val
115 120 125

Pro Met Val Asn Pro Asn Thr Ile Val Phe Gly Gly Trp Asp Ile Ser

130 135 140

Asn Leu Asn Met Ala Asp Ala Met Ala Arg Ala Gln Val Leu Asp Ile
145 150 155 160

His Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Gln Pro Leu
165 170 175

Ala Gly Ile Phe Asn Pro Asp Phe Val Ala Ala Asn Gln Gly Ala Arg
180 185 190

Ala Asn Asn Ile Ile Lys Gly Thr Lys Lys Glu Gln Val Glu Gln Ile
195 200 205

Arg Lys Asp Ile Arg Glu Phe Lys Glu Lys Thr Lys Val Asp Lys Val
210 215 220

Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val Ala
225 230 235 240

Gly Leu Asn Asp Thr Met Asp Asn Leu Leu Ala Ser Leu Asp Lys Asn
245 250 255

Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val Phe
260 265 270

Glu Gly Val Pro Phe Val Asn Gly Ser Pro Gln Asn Thr Phe Val Pro

275 280 285

Gly Leu Met Glu Leu Ala Ile Lys Lys Asn Ser Val Ile Gly Gly Asp
290 295 300

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

Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Ala Ser Tyr Asn His
325 330 335

Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Val Phe Arg
340 345 350

Ser Lys Glu Ile Ser Lys Ser Ser Val Val Asp Asp Met Val Ala Ser
355 360 365

Asn Pro Ile Leu Tyr Lys Pro Asp Glu His Pro Asp His Val Ile Val
370 375 380

Ile Lys Tyr Ile Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp Glu
385 390 395 400

Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Leu His
405 410 415

Asn Thr Cys Glu Asp Ser Leu Leu Ala Ser Pro Ile Ile Leu Asp Leu

420 425 430

Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu Gly
435 440 445

Gln Asp Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser Tyr
450 455 460

Leu Ser Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn Ala
465 470 475 480

Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys Ile
485 490 495

Gly Leu Ala Pro Glu Asn Asn Met Met Leu Glu His Lys
500 505

<210> 996
<211> 510
<212> PRT
<213> Zamia

<220>
<221> misc_feature
<222> (214)..(214)
<223> Xaa puede ser cualquier aminoácido de origen natural

<220>
<221> misc_feature

<222> (260)..(260)
<223> Xaa puede ser cualquier aminoácido de origen natural

<400> 996

Met Phe Val Glu Ser Phe Arg Val Glu Ser Pro Asn Val Lys Tyr Ser
1 5 10 15

Glu Glu Ser Ile Glu Ser Val Tyr Asn Tyr Glu Thr Thr Glu Val Val
20 25 30

His Gln Cys Lys Asn Gly Lys Tyr Glu Trp Ile Val Lys Pro Thr Thr
35 40 45

Val Lys Tyr Gln Phe Asn Thr Asp Arg Arg Val Pro Thr Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Thr Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Leu Thr Lys Glu Gly Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Cys Arg
100 105 110

Ile Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Arg Ser Leu
115 120 125

Leu Pro Met Val Asp Pro Asn Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Asn Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Val Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Gly Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Asp Ser
180 185 190

Arg Ala Asn Asn Ile Ile Gly Gly Thr Lys Lys Glu Gln Val Gln Lys
195 200 205

Ile Val Gln Asp Ile Xaa Glu Phe Lys Ala Lys Thr Lys Val Glu Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ser
225 230 235 240

Val Gly Leu Asn Asp Thr Glu Glu Asn Leu Leu Ala Ser Leu Glu Arg
245 250 255

Asn Glu Ser Xaa Ile Ser Pro Ser Thr Leu Tyr Ala Leu Ala Cys Val
260 265 270

Gln Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Ser Lys Asn Ser Leu Ile Ala Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Leu Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Thr Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Gly Ile Leu Tyr Gly Pro Gly Glu His Pro Asp His Val Ile
370 375 380

Val Ile Lys Tyr Ile Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Ile Leu Leu Ala Glu Leu Cys Ser Arg Ile Lys Leu Lys Lys Glu
435 440 445

Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Ser Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Ile Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Ile Gly Leu Ala Pro Glu Asn Asn Met Leu Leu Glu Tyr Lys
500 505 510

<210> 997
<211> 446
<212> PRT
<213> Papa

<400> 997

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Ala Leu Thr Gly Gly
1 5 10 15

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
20 25 30

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
35 40 45

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Ile
50 55 60

Leu Pro Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp Asp Ile
65 70 75 80

Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
85 90 95

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
100 105 110

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
115 120 125

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

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Asn Asn Lys Val Asp Lys
145 150 155 160

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Ser Val Ala
165 170 175

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Phe Ala Ser Val Asp Arg
180 185 190

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Ile
195 200 205

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
210 215 220

Pro Gly Leu Ile Asp Leu Ala Ile Lys Arg Asn Thr Leu Ile Gly Gly
225 230 235 240

Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp
245 250 255

Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn
260 265 270

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
275 280 285

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
290 295 300

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
305 310 315 320

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
325 330 335

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Arg Asn Thr Ile Val Leu
340 345 350

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
355 360 365

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

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

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
405 410 415

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
420 425 430

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
435 440 445

<210> 998
<211> 509
<212> PRT
<213> Mijo

<400> 998

Met Phe Val Glu Gly Phe Arg Val Asp Ser Pro Arg Val Arg Tyr Gly
1 5 10 15

Ala Gly Glu Ile Glu Ser Glu Tyr Arg Tyr Asp Thr Thr Glu Val Val
20 25 30

Pro Pro Ala Asp Gly Gly Ala Gly Trp Val Val Arg Pro Met Ser Val
35 40 45

Thr Tyr Asn Phe Lys Thr Ser Thr Thr Val Pro Lys Leu Gly Val Met
50 55 60

Leu Val Gly Trp Gly Gly Asn Asn Gly Thr Thr Leu Thr Ala Gly Val
65 70 75 80

Ile Ala Asn Arg Glu Gly Ile Ser Trp Glu Thr Lys Glu Lys Val His
85 90 95

Lys Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg Val
100 105 110

Gly Ser His Asn Gly Glu Glu Val Tyr Ala Pro Phe Lys Ser Leu Val

115 120 125

Pro Met Val Asp Pro Asn Ser Ile Val Phe Gly Gly Trp Asp Ile Ser
130 135 140

Asn Leu Ser Met Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp Ile
145 150 155 160

Asn Leu Gln Lys Gln Leu Lys Pro Tyr Met Gln Ser Met Val Pro Leu
165 170 175

Pro Gly Val Phe Asn Pro Asp Phe Val Ala Ala Asn Gln Gly Ala Arg
180 185 190

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

Lys Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys Val
210 215 220

Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val Ala
225 230 235 240

Gly Leu Asn Asp Thr Met Asp Asn Leu Met Ala Ser Leu Glu Lys Asn
245 250 255

Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val Ser

260 265 270

Glu Gly Val Pro Phe Val Asn Gly Ser Pro Gln Asn Thr Phe Val Pro
275 280 285

Gly Leu Ile Glu Leu Ala Ile Lys Lys Asn Ser Leu Ile Gly Gly Asp
290 295 300

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

Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Ala Ser Tyr Asn His
325 330 335

Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Val Phe Arg
340 345 350

Ser Lys Glu Ile Ser Lys Ser Ser Val Val Asp Asp Met Val Ala Ser
355 360 365

Asn Pro Ile Leu Tyr Ser Pro Gly Glu His Pro Asp His Val Ile Val
370 375 380

Ile Lys Tyr Ile Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp Glu
385 390 395 400

Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Leu His

405 410 415

Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp Leu
420 425 430

Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu Gly
435 440 445

Gln Asp Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser Tyr
450 455 460

Leu Ser Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn Ala
465 470 475 480

Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys Val
485 490 495

Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu His Lys
500 505

<210> 999
<211> 212
<212> PRT
<213> Cleome gynandra

<400> 999

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Asn Glu Ile His Ser Val Tyr Asn Tyr Glu Thr Thr Glu Val Val
20 25 30

His Glu Asn Ile Asn Gly Val Tyr Gln Trp Ile Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Val His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Lys Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp Asp Ile
130 135 140

Asn Asp Met Asn Leu Ala Asp Ala Met Glu Gly Pro Arg Phe Leu Thr
145 150 155 160

Leu Ile Cys Arg Ser Asn Ser Asp Leu Thr Trp Arg Thr Trp Ser His
165 170 175

Ser Gln Gly Ser Thr Ile Leu Ile Ser Ser Gln Arg Ile Lys Ile His
180 185 190

Val Pro Ile Thr Ser Ser Lys Ala Pro Arg Arg Asn Lys Leu Ile Arg
195 200 205

Ser Leu Lys Thr
210

<210> 1000
<211> 449
<212> PRT
<213> Trébol

<400> 1000

Leu Gly Val Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu
1 5 10 15

Thr Gly Gly Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys
20 25 30

Asp Asn Ile Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser
35 40 45

Ala Ile Arg Val Gly Ser Phe Gln Gly Glu Glu Ile His Ala Pro Phe
50 55 60

Lys Ser Leu Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly
65 70 75 80

Trp Asp Ile Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Arg
85 90 95

Val Phe Asp Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser
100 105 110

Met Val Pro Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn
115 120 125

Gln Gly Glu Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Arg Glu Gln
130 135 140

Ile Asn Gln Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Ala Asn Lys
145 150 155 160

Val Asp Arg Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser
165 170 175

Asn Leu Val Val Gly Leu Asn Asp Thr Thr Glu Asn Leu Phe Ala Ala
180 185 190

Val Asp Arg Asn Glu Ser Glu Ile Ser Pro Ser Thr Leu Phe Gly Ile
195 200 205

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

Thr Phe Val Pro Gly Leu Ile Asp Leu Ala Ile Lys Asn Asn Ser Leu
225 230 235 240

Ile Gly Gly Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val
245 250 255

Leu Val Asp Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val
260 265 270

Ser Tyr Asn His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro
275 280 285

Gln Thr Phe Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp
290 295 300

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

His Val Val Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg
325 330 335

Ala Met Asp Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr
340 345 350

Ile Val Leu His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile
355 360 365

Ile Leu Asp Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe
370 375 380

Lys Ser Glu Ala Glu Asn Lys Phe His Thr Phe His Pro Val Ala Thr
385 390 395 400

Ile Leu Ser Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro
405 410 415

Val Val Asn Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met
420 425 430

Arg Ala Cys Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr
435 440 445

Lys

<210> 1001
<211> 510
<212> PRT

<213> Pteridium

<400> 1001

Met Phe Ile Glu Ser Phe Arg Ile Glu Ser Pro Asn Val Glu Tyr Thr
1 5 10 15

Glu Asp Tyr Ile Gln Ser Ser Tyr Glu Tyr Ser Thr Thr Glu Leu Leu
20 25 30

His Glu Lys Arg Gly Gly Gln Tyr Gln Trp Val Val Lys Pro Thr Ser
35 40 45

Val His Tyr Gln Phe Lys Thr Ser Arg Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ala Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Val Thr Lys Glu Gly Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Cys Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asp Pro Asn Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

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

Met Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Glu Ile Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ser Asn Gln Gly Ala
180 185 190

Arg Ala Asn Asn Leu Ile Lys Gly Thr Lys Lys Gln Gln Met Glu Gln
195 200 205

Ile Val Ser Asp Ile Arg Glu Phe Lys Ala Lys Ser Met Val Asp Lys
210 215 220

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

Val Gly Leu Asn Asp Thr Lys Glu Asn Leu Phe Lys Ser Leu Glu Arg
245 250 255

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

Gln Glu Lys Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Val Ile Glu Tyr Ala Val Ser Gln Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Gly
355 360 365

Ser Asn Ala Ile Leu Tyr Lys Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Arg Asn Thr Ile Val Leu
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Leu Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Leu Thr Arg Ile Glu Leu Lys Lys Glu
435 440 445

Gly Glu Asp Lys Phe His Ser Leu His Pro Val Ala Ala Leu Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Ile Asn
465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Phe Arg Ala Cys
485 490 495

Ile Gly Leu Ala Pro Glu Asn Asn Met Leu Met Glu Tyr Lys
500 505 510

<210> 1002
<211> 461
<212> PRT
<213> Palma aceitera

<400> 1002

Asn Thr Leu Gln Asp Arg His Pro Tyr Pro Gln Ala Arg Cys Asn Ala
1 5 10 15

Cys Gly Asp Gly Val Gly Thr Met Asp Pro Pro Ser Pro Leu Val Leu

20 25 30

Leu Pro Thr Glu Lys Gly Ser Pro Gly Ala Thr Lys Asp Lys Val Gln
35 40 45

Arg Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg Val
50 55 60

Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu Leu
65 70 75 80

Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile Ser
85 90 95

Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp Ile
100 105 110

Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro Leu
115 120 125

Ala Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser Arg
130 135 140

Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Gln Gln Ile
145 150 155 160

Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Met Lys Val Asp Lys Val

165 170 175

Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Leu Val
180 185 190

Gly Val Asn Asp Thr Met Asp Asn Leu Leu Ala Ser Leu Glu Lys Asn
195 200 205

Gln Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val Leu
210 215 220

Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val Pro
225 230 235 240

Ser Leu Ile Asp Leu Ala Ile Gln Lys Asn Ser Leu Ile Gly Gly Asp
245 250 255

Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp Phe
260 265 270

Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn His
275 280 285

Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe Arg
290 295 300

Ser Lys Glu Ile Ser Lys Ser Ser Val Val Asp Asp Met Val Ser Ser

305 310 315 320

Asn Gly Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Ile Val
325 330 335

Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp Glu
340 345 350

Tyr Thr Ser Glu Ile Phe Met Gly Gly Arg Ser Thr Ile Val Leu His
355 360 365

Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp Leu
370 375 380

Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu Glu
385 390 395 400

Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser Tyr
405 410 415

Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn Ala
420 425 430

Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys Ile
435 440 445

Gly Leu Ala Pro Glu Asn Asn Met Met Leu Glu His Lys

450 455 460

<210> 1003
<211> 586
<212> PRT
<213> Zostera

<400> 1003

Met Ala Met Glu Met Val Ala Thr Ser Ala Val Ser Leu Arg Ala His
1 5 10 15

Arg Ser Asn Ser Phe Leu Ser Asn Asp Ile Lys Thr Thr Arg Gly Leu
20 25 30

Phe Pro Pro Ser Asn Leu Thr Arg Arg Arg Leu Val Met Thr Leu Asp
35 40 45

Val Lys Gln Gly Asp Asn Met Val Glu Leu Lys Ser Asn Gln Ser Gly
50 55 60

Thr Gln Ile Pro Ile Asp Gln Lys Ala Pro Thr Phe Val Glu Asn Phe
65 70 75 80

Arg Val Asp Ser Pro Asp Val Lys Tyr Gly Glu Asn Glu Ile Glu Thr
85 90 95

Glu Tyr Lys Tyr Asp Thr Thr Glu Leu Val Tyr Glu Asn Arg Asn Gly
100 105 110

Ser Asn Ser Lys Gln Trp Tyr Val Lys Pro Lys Ser Val Val Tyr Asn
115 120 125

Phe Lys Thr Ser Thr Arg Val Pro Lys Leu Gly Val Met Leu Val Gly
130 135 140

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

Arg Glu Ser Met Ser Trp Pro Thr Lys Glu Lys Met Leu His Ala Asn
165 170 175

Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Val Arg Val Gly Ser Tyr
180 185 190

Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu Leu Pro Met Val
195 200 205

Asp Pro Asn Asp Val Val Phe Gly Gly Trp Asp Ile Asn Gly Met Asn
210 215 220

Leu Ala Asp Ala Met Asp Arg Ala Lys Val Leu Asp Tyr Glu Leu Gln
225 230 235 240

Arg Gln Leu Lys Pro Ile Met Glu Ser Met Val Pro Leu Pro Gly Ile
245 250 255

Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser Arg Ala Asp Asn
260 265 270

Val Ile Lys Gly Thr Lys Lys Glu Gln Leu Arg Gln Ile Ile Asn Asp
275 280 285

Ile Arg Asp Phe Lys Asp Lys Thr Lys Val Asp Lys Val Val Val Leu
290 295 300

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

Asp Thr Ser Asp Asn Leu Leu Ala Ala Leu Asp Arg Asn Glu Ser Glu
325 330 335

Ile Ser Pro Ser Thr Ile Tyr Ala Met Ala Cys Ile Leu Glu Lys Ile
340 345 350

Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val Pro Gly Leu Ile
355 360 365

Glu Leu Ala Ile Lys Asn Asn Thr Met Ile Gly Gly Asp Asp Phe Lys
370 375 380

Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp Phe Leu Val Gly
385 390 395 400

Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn His Leu Gly Asn
405 410 415

Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe Arg Ser Lys Glu
420 425 430

Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala Ser Asn Pro Ile
435 440 445

Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val Val Ile Lys Tyr
450 455 460

Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp Glu Tyr Ser Ser
465 470 475 480

Glu Leu Phe Met Gly Gly Lys Ser Thr Ile Ile Leu His Asn Thr Cys
485 490 495

Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp Leu Val Leu Leu
500 505 510

Ala Glu Met Ser Thr Arg Ile Gln Leu Lys Ala Glu Gly Glu Glu Asn
515 520 525

Phe His Ser Phe His Pro Ile Ala Thr Ile Leu Ser Tyr Leu Ser Lys
530 535 540

Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn Ala Leu Ser Lys
545 550 555 560

Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys Ile Gly Leu Ala
565 570 575

Pro Glu Asn Asn Met Leu Leu Glu His Lys
580 585

<210> 1004
<211> 476
<212> PRT
<213> Centeno

<400> 1004

Met Phe Ile Glu Ser Phe Arg Val Glu Ser Pro Asn Val Arg Tyr Gly
1 5 10 15

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

His Glu Ser His Asp Gly Ala Ser Lys Trp Val Val Arg Pro Lys Ser
35 40 45

Val Asn Tyr His Phe Lys Thr Asn Thr Asn Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Met Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

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

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Ile Thr Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Leu Lys Gly Thr Lys Lys Glu Gln Met Glu Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ser
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Val Asp Lys
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Met Glu Gly Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Asn Asn Cys Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Asp Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Cys Arg Leu Ala Arg Val
465 470 475

<210> 1005
<211> 469
<212> PRT

<213> Centeno

<400> 1005

Met Phe Ile Glu Ser Phe Arg Val Glu Ser Pro Asn Val Arg Tyr Gly
1 5 10 15

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

His Glu Ser His Asp Gly Ala Ser Lys Trp Val Val Arg Pro Lys Ser
35 40 45

Val Asn Tyr His Phe Lys Thr Asn Thr Asn Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Met Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

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

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Ile Thr Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Leu Lys Gly Thr Lys Lys Glu Gln Met Glu Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ser
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Val Asp Lys
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Met Glu Gly Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Asn Asn Cys Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala Glu
435 440 445

Gly Glu Asp Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala
465

<210> 1006
<211> 461
<212> PRT
<213> Canola

<400> 1006

Lys Tyr Glu Phe Lys Thr Asp Thr His Val Pro Lys Leu Gly Val Met
1 5 10 15

Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly Val
20 25 30

Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Glu Lys Val Gln
35 40 45

Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg Val

50 55 60

Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu Leu
65 70 75 80

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

Asp Met Asn Leu Ala Asp Ala Met Gly Arg Ala Lys Val Leu Asp Ile
100 105 110

Asp Leu Gln Lys Gln Leu Arg Pro Phe Met Glu His Met Val Pro Leu
115 120 125

Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser Arg
130 135 140

Ala Asn His Leu Ile Lys Gly Thr Lys Lys Glu Gln Leu Glu Gln Val
145 150 155 160

Ile Lys Asp Ile Arg Asp Phe Lys Glu Lys Asn Lys Val Asp Lys Val
165 170 175

Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val Ala
180 185 190

Gly Leu Asn Asp Thr Thr Glu Asn Leu Met Ser Ser Leu Asp Lys Asn

195 200 205

Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val Leu
210 215 220

Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val Pro
225 230 235 240

Gly Leu Ile Glu Leu Ala Ile Lys Arg Asn Ser Leu Ile Gly Gly Asp
245 250 255

Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp Phe
260 265 270

Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn His
275 280 285

Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe Arg
290 295 300

Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ala Ser
305 310 315 320

Asn Gly Ile Leu Phe Asp Ser Gly Glu His Pro Asp His Val Val Val
325 330 335

Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp Glu

340 345 350

Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Met His
355 360 365

Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp Leu
370 375 380

Val Leu Leu Ala Glu Leu Thr Thr Arg Ile Glu Leu Lys Ala Asp Asn
385 390 395 400

Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Leu Leu Ser Tyr
405 410 415

Leu Ser Lys Ala Pro Leu Gly Pro Thr Trp His Ala Ser Cys Glu Arg
420 425 430

Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys Val
435 440 445

Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
450 455 460

<210> 1007
<211> 479
<212> PRT
<213> Distylium

<400> 1007

Met Phe Ile Glu Ser Phe Arg Val Gln Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Glu Thr Ile Glu Ser Val Tyr Asp Tyr Ala Thr Thr Glu Leu Val
20 25 30

His Glu Asn Arg Asn Gly Lys Tyr Glu Trp Val Val Lys Pro Lys Cys
35 40 45

Val Lys Tyr Glu Phe Lys Thr Ala Arg Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Val Thr Lys Asp Lys Ile
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Cys Arg
100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile His Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Glu Pro Asn Asp Val Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asn Leu Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Gln Asp Met Met Pro
165 170 175

Leu Pro Gly Ile Phe Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Glu
180 185 190

Arg Ala Asn His Ile Ile Lys Gly Ser Lys Lys Glu Gln Val Asp Lys
195 200 205

Ile Ile Gln Asp Ile Arg Glu Phe Gln Ala Asn Thr Lys Val Glu Lys
210 215 220

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

Val Gly Leu Asn Asp Thr Lys Glu Asn Leu Leu Ala Ser Leu Asn Lys
245 250 255

Asn Lys Ser Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Ile
260 265 270

Gln Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Glu Leu Ala Ile Glu Lys Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Gly Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Gln Asn Thr Ile Val Met
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Leu Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Lys Glu
435 440 445

Gly Glu Ala Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Asp Pro Ser Trp Trp Pro Pro Arg His Thr Ser
465 470 475

<210> 1008
<211> 452
<212> PRT
<213> Utricularia

<400> 1008

Leu Pro Lys Phe Gly Val Leu Leu Val Gly Trp Gly Gly Asn Asn Gly
1 5 10 15

Ser Thr Leu Thr Ala Gly Val Ile Ala Asn Arg Glu Gly Ile Ser Trp
20 25 30

Ala Thr Lys Asp Lys Ile Gln Pro Ala Asn Tyr Phe Gly Ser Leu Thr
35 40 45

Gln Ala Ser Thr Ile Arg Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr
50 55 60

Ala Pro Phe Lys Ser Leu Val Pro Met Val Asn Pro Asp Glu Ile Val
65 70 75 80

Phe Gly Gly Trp Asp Ile Ser Asn Met Asn Leu Ala Asp Ser Met Ala
85 90 95

Arg Ala Lys Val Leu Asp Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr
100 105 110

Met Glu Gln Met Val Pro Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile
115 120 125

Ala Ala Asn Gln Glu Ser Arg Ala Asn Asn Val Ile Gly Gly Thr Lys
130 135 140

Lys Glu Gln Val Asp Arg Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu
145 150 155 160

Lys Asn Gln Leu Asp Lys Val Val Val Leu Trp Thr Ala Asn Thr Glu
165 170 175

Arg Tyr Ser Ser Ile Val Ala Gly Leu Asn Asp Thr Met Glu Asn Leu
180 185 190

Leu Ala Ser Val Glu Lys Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu
195 200 205

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

Pro Gln Asn Thr Phe Val Pro Gly Leu Ile Glu Leu Ala Ile Lys Arg
225 230 235 240

Asn Ser Leu Ile Gly Gly Asp Asp Phe Lys Ser Gly Gln Thr Lys Met
245 250 255

Lys Ser Val Leu Val Asp Phe Leu Val Gly Ala Gly Ile Lys Pro Thr
260 265 270

Ser Ile Val Ser Tyr Asn His Leu Gly Asn Asn Asp Gly Met Asn Leu
275 280 285

Ser Ala Pro Gln Thr Phe Arg Ser Lys Glu Ile Ser Lys Ser Asn Val
290 295 300

Val Asp Asp Met Val Ala Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu
305 310 315 320

His Pro Asp His Val Val Val Ile Lys Tyr Val Pro Tyr Val Gly Asp
325 330 335

Ser Lys Arg Ala Met Asp Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly
340 345 350

Lys Ser Thr Ile Val Leu His Asn Thr Cys Glu Asp Ser Leu Leu Ala
355 360 365

Ala Pro Ile Ile Leu Asp Leu Val Leu Leu Ala Glu Leu Ser Thr Arg
370 375 380

Ile Gln Leu Lys Ala Glu Gly Glu Gly Lys Phe His Ser Phe His Pro
385 390 395 400

Val Ala Thr Ile Leu Ser Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro
405 410 415

Gly Thr Pro Val Val Asn Ala Leu Ser Lys Gln Arg Ala Met Leu Glu
420 425 430

Asn Ile Leu Arg Ala Cys Val Gly Leu Ala Pro Glu Asn Asn Met Ile
435 440 445

Leu Glu Tyr Lys
450

<210> 1009
<211> 136
<212> PRT
<213> Centeno

<400> 1009

Met Phe Ile Glu Ser Phe Arg Val Glu Ser Pro Asn Val Arg Tyr Gly
1 5 10 15

Gly Gly Gly Asp Arg Val Gly Val Pro Leu Arg His His Gly Ala Gly
20 25 30

Ala Arg Glu Pro Arg Arg Arg Ile Gln Val Gly Arg Pro Pro Gln Val
35 40 45

Arg Gln Leu Pro Leu Gln Asp Gln His Gln Arg Pro Gln Ala Arg Gly
50 55 60

Asp Ala Arg Gly Val Gly Arg Gln Gln Trp Leu His Thr His Gly Trp
65 70 75 80

Gly His Arg Gln Arg Gly Glu Gly Ile Ser Val Gly Asp Gln Gly Gln
85 90 95

Gly Ala Ala Ser Gln Leu Leu Trp Val Pro His Pro Gly Leu His His
100 105 110

Gln Gly Arg Glu Leu Gln Arg Arg Gly Asp Leu Cys Ala Leu Gln Glu
115 120 125

Pro Pro Ala His Gly Glu Pro Arg
130 135

<210> 1010
<211> 511
<212> PRT
<213> Selagineláceas

<400> 1010

Met Phe Ile Glu Ser Phe Arg Val Glu Ser Pro Asn Val Lys Tyr Ser
1 5 10 15

Glu Glu His Ile Ser Ser Val Tyr Asp Tyr Asn Thr Thr Asp Leu Val
20 25 30

His Glu Lys Asn Arg Glu Gly Lys Tyr Glu Trp Val Val Lys Pro Ser
35 40 45

Thr Val Thr Tyr Glu Phe Gln Thr Gln Arg Lys Val Pro Lys Leu Gly
50 55 60

Ile Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala
65 70 75 80

Gly Ile Ile Ala Asn Arg Glu Gly Ile Ser Trp Val Thr Lys Asp Gly
85 90 95

Val Gln Arg Pro Asn Tyr Phe Gly Ser Val Thr Gln Ala Ser Thr Cys
100 105 110

Arg Ile Gly Ser Phe Arg Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser

115 120 125

Leu Leu Pro Met Val Asn Pro Asp Asp Val Val Leu Gly Gly Trp Asp
130 135 140

Ile Asn Asn Met Asn Leu Ala Asp Ala Met Glu Arg Ala Lys Val Leu
145 150 155 160

Asp Met Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Asp Lys Met Val
165 170 175

Pro Leu Pro Gly Val Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly
180 185 190

Ser Arg Ala Asn Asn Ile Phe Lys Gly Ser Lys Lys Glu Lys Met Asp
195 200 205

Lys Ile Ile Glu Asp Ile Arg His Phe Lys Ser Gln Thr Lys Val Asp
210 215 220

Lys Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asp Val
225 230 235 240

Ile Val Gly Leu Asn Asp Thr Lys Glu Asn Leu Phe Ala Ser Leu Glu
245 250 255

Arg Asp Glu Pro Glu Ile Ser Pro Ser Thr Ile Tyr Ala Leu Ala Cys

260 265 270

Ile Gln Glu Gly Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe
275 280 285

Val Pro Gly Val Ile Asp Phe Ala Val Glu Lys Gly Thr Leu Ile Gly
290 295 300

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

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

Asn His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr
340 345 350

Phe Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val
355 360 365

Ser Ser Asn Ala Ile Leu Phe Lys Pro Gly Glu His Pro Asp His Val
370 375 380

Ile Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met
385 390 395 400

Asp Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Arg Ser Thr Ile Ala

405 410 415

Met His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Leu Ile Leu
420 425 430

Asp Leu Val Leu Leu Ala Glu Leu Cys Ser Arg Ile Gln Leu Lys Arg
435 440 445

Glu Gly Glu Glu Lys Phe His Ser Phe His Pro Val Ala Ala Leu Leu
450 455 460

Ser Tyr Met Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Ile
465 470 475 480

Asn Ala Leu Ser Lys Gln Arg Ala Cys Leu Glu Asn Val Leu Arg Ala
485 490 495

Cys Ile Gly Leu Ala Pro Glu Asn Asn Met Leu Leu Glu Tyr Lys
500 505 510

<210> 1011
<211> 415
<212> PRT
<213> Momordica

<400> 1011

Met Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly
1 5 10 15

Gly Ile Ile Ala Asn Arg Glu Glu Ile Ser Trp Ala Thr Lys Asp Lys
20 25 30

Val Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile
35 40 45

Arg Val Gly Ser Thr Asp Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser
50 55 60

Leu Leu Pro Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp Asp
65 70 75 80

Ile Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu
85 90 95

Asp Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val
100 105 110

Pro Leu Pro Gly Ile Phe Asp Pro Asp Phe Val Ala Ala Asn Gln Gly
115 120 125

Ser Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Leu Gln
130 135 140

Gln Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Ser Lys Val Asp
145 150 155 160

Lys Ile Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val
165 170 175

Ile Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Val Asp
180 185 190

Lys Asn Glu Ser Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys
195 200 205

Val Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe
210 215 220

Val Pro Gly Leu Ile Asp Leu Ala Ile His Arg Asn Ser Leu Ile Gly
225 230 235 240

Gly Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val
245 250 255

Asp Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr
260 265 270

Asn His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr
275 280 285

Phe Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val
290 295 300

Ser Ser Asn Gly Ile Leu Phe Glu Pro Gly Glu His Pro Asp His Val
305 310 315 320

Val Val Ile Lys Tyr Val Pro Tyr Val Ala Asp Ser Lys Arg Ala Met
325 330 335

Asp Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Ser Thr Ile Val
340 345 350

Met His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu
355 360 365

Asp Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ala
370 375 380

Glu Gly Arg Glu Ser Phe Thr Leu Ser Ile Leu Trp Leu Pro Ser Ser
385 390 395 400

Val Thr Leu Gln Arg Leu Leu Leu Tyr Arg Gln Ala His Gln Trp
405 410 415

<210> 1012
<211> 519
<212> PRT
<213> Sorgo

<400> 1012

Met Phe Val Glu Ser Phe Arg Val Asp Ser Pro Leu Val Gln Tyr Gly
1 5 10 15

Asp Gly Glu Ile Gln Ser Glu Tyr Arg Tyr Asp Thr Thr Glu Val Val
20 25 30

Pro Pro Gly Asn Gly Gly Gly Ala Gly Trp Met Val Arg Pro Lys Ser
35 40 45

Val Thr Tyr Asn Phe Lys Thr Ser Thr Asn Val Pro Lys Leu Gly Cys
50 55 60

Ile Val Ser Asn Asp Gly Cys Arg Val Met Leu Val Gly Trp Gly Gly
65 70 75 80

Asn Asn Gly Thr Thr Leu Thr Ala Gly Val Ile Ala Asn Arg Glu Gly
85 90 95

Ile Ser Trp Glu Thr Lys Glu Lys Val His Lys Ala Asn Tyr Phe Gly
100 105 110

Ser Leu Thr Gln Ala Ser Thr Ile Arg Val Gly Ser His Asn Gly Glu
115 120 125

Glu Val Tyr Ala Pro Phe Lys Ser Leu Val Pro Met Val Asp Pro Asn
130 135 140

Ser Ile Val Phe Gly Gly Trp Asp Ile Ser Asn Leu Asn Met Ala Asp
145 150 155 160

Ala Met Ala Arg Ala Lys Val Leu Asp Ile His Leu Gln Lys Gln Leu
165 170 175

Arg Pro Tyr Met Glu Ser Met Leu Pro Leu Ala Gly Ile Phe Asn Pro
180 185 190

Asp Phe Val Ala Ala Asn Gln Gly Ala Arg Ala Asn Asn Ile Ile Lys
195 200 205

Gly Thr Lys Lys Glu Gln Val Glu Gln Ile Lys Lys Asp Ile Arg Glu
210 215 220

Phe Lys Glu Lys Thr Lys Val Asp Lys Ile Val Val Leu Trp Thr Ala
225 230 235 240

Asn Thr Glu Arg Tyr Ser Asn Val Val Ser Gly Leu Asn Asp Thr Met
245 250 255

Asp Asn Leu Leu Ala Ser Leu Glu Lys Asn Glu Ala Glu Ile Ser Pro
260 265 270

Ser Thr Leu Tyr Ala Ile Ala Cys Val Phe Glu Gly Val Pro Phe Val
275 280 285

Asn Gly Ser Pro Gln Asn Thr Phe Val Pro Gly Leu Met Glu Leu Ala
290 295 300

Ile Lys Lys Asn Ser Val Ile Gly Gly Asp Asp Phe Lys Ser Gly Gln
305 310 315 320

Thr Lys Met Lys Ser Val Leu Val Asp Phe Leu Val Gly Ala Gly Ile
325 330 335

Lys Pro Thr Ser Ile Ala Ser Tyr Asn His Leu Gly Asn Asn Asp Gly
340 345 350

Met Asn Leu Ser Ala Pro Gln Val Phe Arg Ser Lys Glu Ile Ser Lys
355 360 365

Ser Ser Val Val Asp Asp Met Val Ala Ser Asn Pro Ile Leu Tyr Lys
370 375 380

Leu Asn Glu His Pro Asp His Val Ile Val Ile Lys Tyr Ile Pro Tyr
385 390 395 400

Val Gly Asp Ser Lys Arg Ala Met Asp Glu Tyr Thr Ser Glu Ile Phe
405 410 415

Met Gly Gly Lys Asn Thr Ile Val Leu His Asn Thr Cys Glu Asp Ser
420 425 430

Leu Leu Ala Ala Pro Ile Ile Leu Asp Leu Val Leu Leu Ala Glu Leu
435 440 445

Ser Thr Arg Ile Gln Leu Lys Ala Glu Gly Gln Asp Lys Phe His Ser
450 455 460

Phe His Pro Val Ala Thr Ile Leu Ser Tyr Leu Ser Lys Ala Pro Leu
465 470 475 480

Val Pro Pro Gly Thr Pro Val Val Asn Ala Leu Ala Lys Gln Arg Ala
485 490 495

Met Leu Glu Asn Ile Leu Arg Ala Cys Ile Gly Leu Ala Pro Glu Asn
500 505 510

Asn Met Met Leu Glu His Lys
515

<210> 1013
<211> 451
<212> PRT
<213> Amaranthus

<400> 1013

Pro Lys Leu Gly Val Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser
1 5 10 15

Thr Leu Thr Gly Gly Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala
20 25 30

Thr Lys Asp Lys Val Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln
35 40 45

Ala Ser Ser Ile Arg Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala
50 55 60

Pro Phe Lys Ser Leu Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe
65 70 75 80

Gly Gly Trp Asp Ile Ser Asp Leu Asn Leu Ala Asp Ala Met Thr Arg
85 90 95

Ala Lys Val Leu Asp Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met
100 105 110

Glu His Met Ile Pro Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala
115 120 125

Ala Asn Gln Asp Ser Arg Ala Asn Asn Ile Ile Lys Gly Thr Lys Lys
130 135 140

Glu Gln Ile Glu Gln Val Ile Lys Asp Met Arg Glu Phe Lys Glu Lys
145 150 155 160

Asn Lys Val Asp Lys Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg
165 170 175

Tyr Ser Asp Val Val Val Gly Leu Asn Asp Thr Met Glu Asn Leu Met
180 185 190

Ala Ala Val Glu Arg Asn Glu Ser Glu Ile Ser Pro Ser Thr Leu Tyr
195 200 205

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

Gln Asn Thr Phe Val Pro Gly Leu Ile Glu Leu Ala Ile Lys His Asn
225 230 235 240

Ser Leu Ile Gly Gly Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys
245 250 255

Ser Val Leu Val Asp Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser
260 265 270

Ile Val Ser Tyr Asn His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser
275 280 285

Ala Pro Gln Thr Phe Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val
290 295 300

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

Pro Asp His Val Val Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser
325 330 335

Lys Arg Ala Met Asp Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys
340 345 350

Ser Thr Ile Val Leu His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala
355 360 365

Pro Ile Ile Leu Asp Leu Val Leu Leu Ala Glu Leu Ser Ser Arg Ile
370 375 380

Gln Leu Lys Ala Glu Thr Glu Asp Lys Phe His Ser Phe His Pro Val
385 390 395 400

Ala Thr Ile Leu Ser Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly
405 410 415

Thr Pro Val Val Asn Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn
420 425 430

Ile Met Arg Ala Cys Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu
435 440 445

Glu Tyr Lys
450

<210> 1014
<211> 511
<212> PRT
<213> Selaginelláceas

<400> 1014

Met Phe Ile Glu Ser Phe Arg Val Glu Ser Pro Asn Val Lys Tyr Ser
1 5 10 15

Glu Glu His Ile Ser Ser Val Tyr Asp Tyr Asn Thr Thr Asp Leu Val
20 25 30

His Glu Lys Asn Arg Glu Gly Lys Tyr Glu Trp Val Val Lys Pro Ser
35 40 45

Thr Val Thr Tyr Glu Ile Gln Thr Gln Arg Lys Val Pro Lys Leu Gly
50 55 60

Ile Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala
65 70 75 80

Gly Ile Ile Ala Asn Arg Glu Gly Ile Ser Trp Val Thr Lys Asp Gly
85 90 95

Val Gln Arg Pro Asn Tyr Phe Gly Ser Val Thr Gln Ala Ser Thr Cys

100 105 110

Arg Ile Gly Ser Phe Arg Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser
115 120 125

Leu Leu Pro Met Val Asn Pro Asp Asp Val Val Leu Gly Gly Trp Asp
130 135 140

Ile Asn Asn Met Asn Leu Ala Asp Ala Met Glu Arg Ala Lys Val Leu
145 150 155 160

Asp Met Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Asp Lys Met Val
165 170 175

Pro Leu Pro Gly Val Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly
180 185 190

Ser Arg Ala Asn Asn Ile Phe Lys Gly Ser Lys Lys Glu Lys Met Asp
195 200 205

Lys Ile Ile Glu Asp Ile Arg His Phe Lys Ser Gln Thr Lys Val Asp
210 215 220

Lys Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asp Val
225 230 235 240

Ile Val Gly Leu Asn Asp Thr Lys Glu Asn Leu Phe Ala Ser Leu Glu

245 250 255

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

Ile Gln Glu Gly Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe
275 280 285

Val Pro Gly Val Ile Asp Phe Ala Val Glu Lys Gly Thr Leu Ile Gly
290 295 300

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

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

Asn His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr
340 345 350

Phe Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val
355 360 365

Ser Ser Asn Ala Ile Leu Phe Lys Pro Gly Glu His Pro Asp His Val
370 375 380

Ile Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met

385 390 395 400

Asp Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Arg Ser Thr Ile Ala
405 410 415

Met His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Leu Ile Leu
420 425 430

Asp Leu Val Leu Leu Ala Glu Leu Cys Ser Arg Ile Gln Leu Lys Arg
435 440 445

Glu Gly Glu Glu Lys Phe His Ser Phe His Pro Val Ala Ala Leu Leu
450 455 460

Ser Tyr Met Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Ile
465 470 475 480

Asn Ala Leu Ser Lys Gln Arg Ala Cys Leu Glu Asn Val Leu Arg Ala
485 490 495

Cys Ile Gly Leu Ala Pro Glu Asn Asn Met Leu Leu Glu Tyr Lys
500 505 510

<210> 1015
<211> 478
<212> PRT
<213> Sandía

<400> 1015

Met Phe Ile Asp Ser Phe Lys Val Glu Ser Pro Asn Val Thr Tyr Ser
1 5 10 15

Asp His Glu Ile His Ser Ile Tyr Asn Tyr Asp Thr Thr Glu Leu Leu
20 25 30

His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser
35 40 45

Val Gln Tyr Gln Phe Lys Thr Asp Ile Arg Val Pro Lys Leu Gly Met
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Ile Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ser Ile Arg
100 105 110

Val Gly Ser Ile Asp Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Leu Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Phe Asp Pro Asp Phe Val Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Gln Gly Thr Lys Lys Glu Gln Leu Gln Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Ser Lys Val Asp Lys
210 215 220

Ile Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ile
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Val Asp Lys
245 250 255

Asn Glu Ser Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile His Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Gly Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ala Glu
435 440 445

Gly Glu Val Ser Phe Thr Leu Ser Thr Leu Trp Pro Pro Ser Ser Val
450 455 460

Thr Leu Gln Arg Leu Leu Leu Tyr Arg Gln Ala Arg Leu Trp
465 470 475

<210> 1016
<211> 535
<212> PRT
<213> Soja

<400> 1016

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

Thr Ile Thr Arg Leu Ile Tyr Thr Val Gly Lys Thr Glu Gln Trp Lys
20 25 30

Ala Pro Ile Leu Thr Glu Leu Asp Ile Asn Asn Ile Ser His Lys Leu
35 40 45

His Asp Asp Pro Glu Ile Ile Gln Met Ala Ser Arg Asp Tyr Gly His
50 55 60

Ile Val His Glu Phe Pro Leu Ala Val Phe Arg Pro Ser Ser Ile Asp
65 70 75 80

Asp Ile Ala Thr Leu Ile Lys Ser Ser Tyr Asn Ser Phe Ala Pro Phe
85 90 95

Gly Ile Ala Ala Arg Gly Gln Gly His Ser Thr His Gly Gln Ala Met
100 105 110

Ala Arg Asp Gly Val Val Val Asp Met Ala Asn Leu Arg Lys Gln Arg
115 120 125

Asn Gly Val Ala Ile Ser Val Ser Lys Asp Pro Leu Met Gly His Tyr
130 135 140

Ala Asp Val Gly Gly Glu Gln Leu Trp Ile Asp Val Leu His Thr Thr
145 150 155 160

Leu Lys His Gly Leu Ala Pro Val Ser Trp Thr Asp Tyr Leu Tyr Leu
165 170 175

Thr Val Gly Gly Thr Leu Ser Asn Ala Gly Ile Ser Gly Gln Ser Phe
180 185 190

Arg Tyr Gly Pro Gln Ile Ser Asn Val His Glu Met Asp Val Ile Thr
195 200 205

Gly Lys Gly Glu Phe Val Thr Cys Ser Ser Gln Lys Asn Leu Glu Leu
210 215 220

Phe His Ala Val Leu Gly Gly Leu Gly Gln Phe Gly Val Ile Ala Arg
225 230 235 240

Ala Arg Ile Ala Leu Glu Pro Ala Pro Lys Arg Val Lys Trp Val Arg
245 250 255

Leu Leu Tyr Ser Asp Phe Phe Ala Phe Thr Lys Asp Gln Glu Arg Leu
260 265 270

Ile Ser Ile Asn Gly Arg Lys Gln Lys Asn Ala Leu Asp Phe Leu Glu
275 280 285

Gly Met Leu Leu Met Asn Gln Gly Pro Ile Asn Asn Trp Arg Ser Ser
290 295 300

Phe Phe Pro Leu Ser Asp His Pro Arg Ile Ser Ser Leu Ile Thr Glu
305 310 315 320

His Ser Ile Leu Tyr Cys Leu Glu Val Ala Lys Tyr Tyr Asp Glu Gln
325 330 335

Thr Glu Ile Asn Val Asp Lys Glu Ile Gln Val Leu Leu Gln Gly Leu
340 345 350

Ala Tyr Ile Pro Gly Phe Tyr Tyr Glu Lys Asn Val Ser Tyr Val Glu
355 360 365

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

Leu Trp Asp Val Pro His Pro Trp Leu Asn Leu Phe Ile Pro Lys Ser
385 390 395 400

Gln Ile Leu Asp Phe Asn Ser Arg Val Phe Lys Asp Ile Val Leu Lys
405 410 415

Arg Asn Ile Ser Ser Gly Pro Val Leu Val Tyr Pro Thr Asn Arg Asn
420 425 430

Lys Trp Asp Asp Arg Met Ser Ala Ser Ile Pro Asp Glu Glu Val Phe
435 440 445

Tyr Thr Val Gly Phe Leu His Ser Ser Gly Phe Asp Thr Trp Lys Ala
450 455 460

Tyr Asp Ala Gln Asn Ser Glu Ile Leu Glu Phe Cys Arg Asp Ala Gly
465 470 475 480

Ile Lys Val Lys Gln Tyr Leu Pro Asn His Ser Thr Gln Glu Asp Trp
485 490 495

Thr Asn His Phe Gly Ala Lys Trp Ile Lys Phe Leu Glu Arg Lys His
500 505 510

Gln Phe Asp Pro Arg Met Ile Leu Ser Pro Gly Gln Lys Ile Phe His
515 520 525

Lys Gln Leu Gln Pro Ala Phe
530 535

<210> 1017
<211> 535
<212> PRT
<213> Poroto

<400> 1017

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

Thr Ile Thr Arg Leu Ile Tyr Thr Glu Gly Lys Thr Glu Gln Trp Lys
20 25 30

Gly Leu Ile Leu Pro Asp Leu Asp Phe Glu Asn Ile Phe His Lys Leu
35 40 45

His Asp Asp Pro Glu Thr Ile Gln Met Ala Ser Ser Asp Tyr Gly His
50 55 60

Ile Val His Glu Leu Pro Ala Ala Val Phe His Pro Ser Ser Ile Glu
65 70 75 80

Asp Ile Ala Thr Leu Ile Lys Ser Ser Tyr Asn Ser Leu Ala Pro Phe
85 90 95

His Ile Ala Ala Arg Gly Gln Gly His Ser His His Gly Gln Ala Met
100 105 110

Ala Arg Asp Gly Val Val Val Asp Met Ala Thr Leu Arg Lys Gln Arg
115 120 125

Asn Gly Val Ser Ile Ser Val Ser Lys Asp Pro Leu Ile Gly His Tyr
130 135 140

Ala Asp Val Gly Gly Glu Gln Leu Trp Ile Asp Val Leu His Ala Ser
145 150 155 160

Leu Glu His Gly Leu Ala Pro Val Ser Trp Thr Asp Tyr Leu Tyr Leu
165 170 175

Thr Val Gly Gly Thr Leu Ser Asn Ala Gly Ile Ser Gly Gln Ser Phe
180 185 190

Arg Tyr Gly Pro Gln Ile Ser Asn Val His Glu Met Asp Val Ile Thr
195 200 205

Gly Lys Gly Glu Phe Val Thr Cys Ser Thr Gln Lys Asn Leu Glu Leu
210 215 220

Phe Asn Ala Val Leu Gly Gly Phe Gly Gln Phe Gly Val Ile Ala Arg
225 230 235 240

Ala Arg Ile Ala Leu Glu Thr Ala Pro Lys Arg Val Lys Trp Val Arg
245 250 255

Leu Leu Tyr Ser Asp Phe Ser Ala Phe Thr Lys Asp Gln Glu Arg Leu
260 265 270

Ile Ser Ile Asn Gly Arg Lys Gln Lys Asn Ala Leu Asp Phe Leu Glu
275 280 285

Gly Met Leu Leu Met Asn Gln Gly Pro Ile Asn Asn Trp Arg Ser Ser
290 295 300

Phe Phe Pro Leu Ser Asp His Pro Arg Ile Ala Ser Leu Ile Thr Glu
305 310 315 320

His Gly Ile Leu Tyr Cys Leu Glu Val Ala Lys Tyr Tyr Asp Asp Gln
325 330 335

Thr Glu Lys Asn Val Asp Lys Glu Ile His Val Leu Leu Gln Gly Leu
340 345 350

Ala Tyr Ile Pro Gly Phe Tyr Tyr Glu Lys Asn Val Ser Tyr Val Glu
355 360 365

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

Leu Trp Glu Val Pro His Pro Trp Leu Asn Leu Phe Leu Pro Lys Ser
385 390 395 400

Gln Ile Leu Asp Phe Asn Ser Gly Val Phe Met Asp Ile Ile Leu Lys
405 410 415

Arg Asn Ile Ser Ser Gly Pro Val Leu Val Tyr Pro Met Asn Arg Asn
420 425 430

Lys Trp Asp Asp Arg Met Ser Ala Ser Ile Pro Asp Glu Asp Val Phe
435 440 445

Tyr Thr Val Gly Phe Leu His Ser Ser Gly Phe Asp Ser Trp Lys Ala
450 455 460

His Asp Ala Gln Asn Arg Glu Ile Leu Glu Phe Cys Arg Asp Ala Gly
465 470 475 480

Ile Lys Val Lys Gln Tyr Leu Pro Asn His Ser Thr Gln Glu Asp Trp
485 490 495

Thr Asn His Phe Gly Thr Lys Trp Leu Lys Phe Leu Glu Arg Lys His
500 505 510

Gln Phe Asp Pro Arg Met Ile Leu Ser Pro Gly Gln Lys Ile Phe His
515 520 525

Lys Gln Leu Gln Pro Ala Phe
530 535

<210> 1018
<211> 536
<212> PRT
<213> Guandú

<400> 1018

Met Ala Leu Asn His Pro Leu Ser Thr Tyr Phe Ile Leu Leu Leu Ile
1 5 10 15

Thr Ile Thr Arg Leu Ile Ser Ile Val Gly Lys Thr Glu Gln Trp Lys
20 25 30

Lys Ala Pro Ile Leu Gln Glu Leu Asp Ile Asp Asn Ile Ser Leu Lys
35 40 45

Phe His Asp Asp Pro Glu Thr Ile Gln Ile Ala Ser Arg Asp Tyr Gly
50 55 60

Asn Ile Val His Glu Phe Pro Arg Ser Val Phe Arg Pro Ser Ser Ile

65 70 75 80

Asp Asp Ile Val Thr Leu Ile Lys Ser Ser Tyr Asn Ser Pro Ser Pro
85 90 95

Phe His Ile Ala Ala Arg Gly Gln Gly His Ser Thr Asn Gly Gln Ala
100 105 110

Met Ala Arg Glu Gly Val Val Val Asp Met Ala Thr Leu Arg Lys Gln
115 120 125

Arg Asn Gly Val Ala Ile Asn Val Ser Lys Asp Pro Leu Ile Gly His
130 135 140

Tyr Ala Asp Val Gly Gly Glu Gln Leu Trp Ile Asp Val Leu His Ser
145 150 155 160

Thr Leu Glu His Gly Leu Ala Pro Val Ser Trp Thr Asp Tyr Leu Tyr
165 170 175

Leu Thr Val Gly Gly Thr Leu Ser Asn Ala Gly Ile Ser Gly Gln Ser
180 185 190

Phe Arg Tyr Gly Pro Gln Ile Ser Asn Val His Glu Met Asp Val Ile
195 200 205

Thr Gly Lys Gly Glu Phe Val Thr Cys Ser Trp Gln Lys Asn Leu Glu

210 215 220

Leu Phe His Ala Val Leu Gly Gly Leu Gly Gln Phe Gly Val Ile Ala
225 230 235 240

Arg Ala Arg Ile Ala Leu Glu Pro Ala Pro Lys Arg Val Lys Trp Val
245 250 255

Arg Leu Leu Tyr Ser Asp Phe Ser Ala Phe Thr Lys Asp Gln Glu Arg
260 265 270

Leu Ile Ser Ile Asn Gly Arg Lys Gln Lys Thr Ala Leu Asp Phe Leu
275 280 285

Glu Gly Ile Leu Leu Met Asn Gln Gly Pro Ile Asn Asn Trp Arg Ser
290 295 300

Ser Phe Phe Pro Ile Ser Asp His Pro Arg Ile Ala Ser Leu Ile Thr
305 310 315 320

Gln His Ser Ile Ile Tyr Cys Leu Glu Val Ala Lys Tyr Tyr Asp Asp
325 330 335

Gln Thr Glu Lys Asn Val Asp Lys Glu Ile Lys Val Leu Leu Gln Gly
340 345 350

Leu Val Tyr Ile Pro Gly Phe Tyr Tyr Glu Lys Asn Val Ser Tyr Val

355 360 365

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

Gly Leu Trp Asp Val Pro His Pro Trp Leu Asn Phe Phe Ile Pro Lys
385 390 395 400

Ser Gln Ile Leu Asp Phe Asp Ser Gly Val Phe Arg Asp Ile Val Leu
405 410 415

Lys Arg Asn Ile Ser Ser Gly Pro Val Leu Val Tyr Pro Met Asn Arg
420 425 430

Asn Lys Trp Asp Asp Arg Met Ser Ala Ser Ile Pro Glu Glu Asp Val
435 440 445

Phe Tyr Thr Val Gly Phe Leu His Ser Ser Gly Phe Asp Asn Trp Lys
450 455 460

Glu Tyr Asp Ala Gln Asn Arg Glu Ile Leu Glu Phe Cys Ser Asp Ala
465 470 475 480

Gly Ile Glu Val Lys Gln Tyr Leu Pro Asn His Thr Thr Gln Glu Asp
485 490 495

Trp Ser Asn His Phe Gly Ala Lys Trp Val Thr Phe Leu Glu Arg Lys

500 505 510

Arg Gln Phe Asp Pro Arg Met Ile Leu Ser Pro Gly Gln Lys Ile Phe
515 520 525

Asp Lys Gln Leu Gln Gln Ala Phe
530 535

<210> 1019
<211> 419
<212> PRT
<213> Chícharo salvaje

<400> 1019

Met Gly Ile Pro Trp Asp Asp Val Val Val Ile Gln Gln Gly Lys Asp
1 5 10 15

Leu Asn Glu Pro Cys Ile Val Thr Val Asn Cys Pro Asp Lys Ala Gly
20 25 30

Leu Gly Cys Asp Leu Cys Arg Ile Ile Leu Glu Phe Gly Leu Arg Ile
35 40 45

Thr Arg Ala Asp Ile Ser Thr Asp Gly Arg Trp Cys Tyr Ile Val Phe
50 55 60

Trp Val Leu Pro Asn Pro Ala Ser Ile Lys Val Asp Trp Glu Ser Leu
65 70 75 80

Lys Thr Arg Leu Leu Ser Val Cys Pro Ser Cys Leu Phe Ser Tyr His
85 90 95

Phe Asn Gln Leu Ser Thr Ser Pro Ser Pro Pro Leu Ile Tyr Leu Leu
100 105 110

Lys Val Trp Cys Val Asp Gln Lys Gly Leu Leu His Asp Ile Asn Glu
115 120 125

Ile Leu Cys Asn Leu Glu Leu Ile Ile Gln Arg Val Lys Ala Met Pro
130 135 140

Thr Pro Asp Gly Arg Val Leu Asp Met Phe Phe Ile Thr Asp Gly Met
145 150 155 160

Glu Leu Leu His Thr Lys Lys Arg Gln Asp Tyr Val Cys Glu Ser Leu
165 170 175

Lys Asp Ala Leu Gly Glu Arg Cys Ile Ser Ser Glu Leu Gln Leu Ala
180 185 190

Gly Pro Glu Tyr Gly His Leu Gln Gly Phe Ser Ser Leu Pro Pro Ala
195 200 205

Phe Ala Glu Glu Leu Phe Ser Ser Glu Leu Leu Asp Lys Val Ser Leu
210 215 220

His Pro Leu Ser Gln Asp Met Lys Thr Leu Lys Thr Pro Thr Val Thr
225 230 235 240

Val Asp Asn Ser Leu Ser Pro Val His Thr Leu Leu Gln Ile Gln Cys
245 250 255

Val Asp Gln Lys Gly Leu Cys Tyr Asp Ile Met Arg Ile Ser Lys Asp
260 265 270

Ser Asp Ile Lys Val Ala Phe Gly Arg Phe Ser Ser Ser Val Glu Gly
275 280 285

Phe Arg Asn Ile Asp Leu Phe Val Gln Gln Asn Asp Gly Lys Lys Ile
290 295 300

Ile Asp Pro Asp Ser Gln Lys Thr Leu Cys Ser Cys Leu Lys Glu Glu
305 310 315 320

Met Leu His Pro Leu Arg Val Ile Ile Ala Ser Arg Gly Pro Asp Thr
325 330 335

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

Arg Val Phe Tyr Asp Val Thr Leu Ala Leu Lys Ala Leu Gly Val Cys
355 360 365

Ile Phe Ser Ala Glu Val Val Arg His Ser Thr Gln Glu Arg Gln Trp
370 375 380

Glu Val Tyr Arg Phe Leu Leu Glu Glu Asn Arg Asn Phe Pro Leu Thr
385 390 395 400

Arg Ser Gln Thr Arg Ser Gln Ile Val Asp Lys Val Arg Arg Thr Leu
405 410 415

Met Gly Trp

<210> 1020
<211> 419
<212> PRT
<213> Poroto

<400> 1020

Met Gly Ile Pro Trp Asp Asp Gly Val Val Ile Gln Gln Gly Lys Asp
1 5 10 15

Ala Asn Glu Pro Cys Ile Val Thr Val Asn Cys Pro Asp Lys Ala Gly
20 25 30

Leu Gly Cys Asp Leu Cys Arg Ile Ile Leu Glu Phe Gly Leu Arg Ile
35 40 45

Thr Arg Ala Asp Ile Ser Thr Asp Gly Arg Trp Cys Tyr Ile Val Tyr
50 55 60

Trp Val Leu Pro His Pro Ala Ser Val Lys Val Asp Trp Glu Ser Leu
65 70 75 80

Lys Thr Arg Leu Leu Ser Ala Cys Pro Ser Cys Leu Phe Ser Tyr Cys
85 90 95

Phe Asn Gln Leu Ser Thr Ser Pro Ser Pro Pro Pro Ile Tyr Leu Leu
100 105 110

Lys Val Trp Cys Val Asp Lys Lys Gly Leu Leu His Asp Ile Asn Glu
115 120 125

Ile Leu Cys Asn Leu Glu Leu Ile Ile Gln Arg Val Lys Ala Met Pro
130 135 140

Thr Pro Asp Gly Arg Val Leu Glu Met Leu Phe Ile Thr Asp Gly Met
145 150 155 160

Glu Leu Leu His Thr Lys Lys Arg Gln Asp His Val Ser Glu Phe Leu
165 170 175

Met Asp Ala Leu Gly Glu Arg Cys Ile Ser Ser Glu Leu Gln Leu Ala
180 185 190

Gly Pro Glu Tyr Gly His Leu Gln Gly Phe Ser Ser Leu Pro Pro Ala
195 200 205

Phe Ala Glu Glu Leu Phe Ser Ser Glu Leu Leu Asp Lys Val Ser Leu
210 215 220

His Pro Leu Ser Gln Asp Met Lys Thr Leu Lys Thr Pro Thr Val Thr
225 230 235 240

Val Asp Asn Ser Leu Ser Pro Val His Thr Leu Leu Gln Ile Gln Cys
245 250 255

Val Asp Gln Lys Gly Leu Cys Tyr Asp Ile Met Arg Ile Ser Lys Asp
260 265 270

Ser Asp Ile Lys Val Ala Phe Gly Arg Phe Ser Ser Ser Val Glu Gly
275 280 285

Phe Arg Asn Ile Asp Leu Phe Val Gln Gln Asn Asp Gly Lys Lys Ile
290 295 300

Ile Asp Leu Asp Ser Gln Lys Thr Leu Cys Ser Cys Leu Lys Glu Glu
305 310 315 320

Met Leu His Pro Leu Arg Val Ile Ile Val Ser Arg Gly Pro Asp Thr
325 330 335

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

Arg Val Phe Tyr Asp Val Thr Leu Ala Leu Lys Ala Leu Gly Ile Cys
355 360 365

Ile Phe Ser Ala Glu Val Val Arg His Ser Thr Gln Glu Arg Gln Trp
370 375 380

Glu Val Tyr Arg Phe Leu Leu Glu Glu Asn Arg Asn Phe Pro Leu Thr
385 390 395 400

Arg Ser Gln Thr Arg Ser Gln Ile Val Asp Lys Val Arg Arg Thr Leu
405 410 415

Met Gly Trp

<210> 1021
<211> 418
<212> PRT
<213> Guandú

<400> 1021

Met Gly Ile Pro Trp Asp Asp Val Val Val Ile Gln Gln Gly Lys Asp
1 5 10 15

Pro Gly Asp Pro Cys Ile Val Thr Val Asn Cys Pro Asp Lys Ala Gly
20 25 30

Leu Gly Cys Asp Leu Cys Gln Ile Ile Leu Glu Phe Gly Leu Arg Ile
35 40 45

Thr Arg Ala Asp Ile Ser Thr Asp Gly Arg Trp Cys Tyr Ile Val Tyr
50 55 60

Trp Val Val Pro His Pro Ala Ser Leu Lys Val Asp Trp Glu Ser Leu
65 70 75 80

Lys Ile Arg Leu Leu Ser Ala Cys Pro Ser Cys Leu Phe Ser Tyr Tyr
85 90 95

Phe Lys Asn Ser Thr Cys Pro Ser Pro Pro Pro Val Tyr Leu Leu Lys
100 105 110

Val Trp Cys Val Asp Gln Lys Gly Leu Leu His Asp Ile Asn Glu Ile
115 120 125

Leu Cys Asn Leu Gln Leu Ile Ile Gln Arg Val Lys Ala Met Pro Thr
130 135 140

Pro Asp Gly Arg Val Leu Asp Met Phe Phe Ile Thr Asp Gly Met Glu
145 150 155 160

Leu Leu His Thr Lys Lys Arg Gln Asp Tyr Val Cys Glu Tyr Leu Lys
165 170 175

Glu Ala Leu Gly Glu Arg Cys Ile Ser Ser Glu Leu Gln Leu Ala Gly
180 185 190

Pro Glu Tyr Gly His Leu Gln Gly Phe Ser Ser Leu Pro Pro Ala Phe
195 200 205

Ala Glu Glu Leu Phe Ser Ser Glu Leu Leu Asp Lys Val Ser Leu His
210 215 220

Pro Leu Ser Gln Asp Met Arg Thr Leu Lys Thr Pro Thr Val Ile Val
225 230 235 240

Asp Asn Ser Leu Ser Gln Ala His Thr Leu Leu Gln Ile Gln Cys Val
245 250 255

Asp Gln Lys Gly Leu Cys Tyr Asp Ile Met Arg Ile Ser Lys Asp Ser
260 265 270

Asp Ile Lys Val Ala Phe Gly Arg Phe Ser Ser Ser Val Lys Gly Phe
275 280 285

Arg Asn Ile Asp Leu Phe Val Gln Gln Lys Asp Gly Lys Lys Ile Ile
290 295 300

Asp Pro Glu Ser Gln Lys Thr Leu Cys Ser Ser Leu Lys Glu Glu Met
305 310 315 320

Leu His Pro Leu Arg Val Ile Ile Val Asn Arg Gly Pro Asp Thr Glu
325 330 335

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

Val Phe Tyr Asp Val Thr Ser Ala Leu Lys Ala Leu Gly Val Phe Ile
355 360 365

Phe Ser Ala Glu Val Val Arg His Ser Thr Gln Glu Arg Gln Trp Glu
370 375 380

Val Tyr Arg Phe Leu Leu Glu Glu Ser Arg Glu Phe Pro Leu Thr Arg
385 390 395 400

Ser Gln Ala Arg Ser Gln Ile Val Asp Lys Val Arg Arg Thr Leu Met
405 410 415

Gly Trp

<210> 1022
<211> 419
<212> PRT
<213> Lotus

<400> 1022

Met Gly Ile Pro Phe Glu Asp Leu Val Val Ile Arg Glu Gly Lys Asn
1 5 10 15

Leu Asp Glu Pro Ser Val Val Thr Val Asn Cys Pro Asp Lys Ala Gly
20 25 30

Leu Gly Cys Asp Leu Cys Arg Ile Ile Leu Glu Phe Gly Leu Arg Val
35 40 45

Thr Arg Ala Asp Val Ser Thr Asp Gly Arg Trp Cys Tyr Ile Val Tyr
50 55 60

Trp Val Val Pro His Pro Ala Ser Leu Lys Val Asp Trp Glu Ser Leu
65 70 75 80

Lys Thr Arg Leu Leu Ser Ala Cys Pro Ser Cys Leu Phe Ser Tyr Tyr
85 90 95

Phe Asn Gln Gln Ser Thr Thr Pro Ser Pro Pro Pro Ile Tyr Val Leu
100 105 110

Lys Val Trp Cys Val Asp Gln Lys Gly Leu Leu His Asp Ile Asn Glu
115 120 125

Ile Leu Cys Asn Leu Gln Leu Ile Ile Gln Arg Val Lys Ala Met Pro

130 135 140

Thr Pro Asp Gly Arg Val Leu Asp Leu Phe Phe Ile Thr Asp Gly Met
145 150 155 160

Glu Leu Leu His Thr Lys Lys Arg Gln Asp Tyr Val Cys Glu Tyr Leu
165 170 175

Met Asp Ala Leu Gly Glu Arg Cys Ile Ser Ser Glu Leu Gln Leu Ala
180 185 190

Gly Pro Glu Tyr Gly Gln Ile Gln Gly Phe Ser Ser Leu Pro Pro Ala
195 200 205

Phe Ser Glu Glu Leu Phe Gly Ser Glu Leu Leu Asp Lys Val Tyr Met
210 215 220

His Pro Leu Ser Lys Asp Met Thr Thr Leu Lys Lys Pro Thr Val Met
225 230 235 240

Val Asp Asn Ser Leu Ser Pro Val His Thr Leu Leu Gln Ile Gln Cys
245 250 255

Val Asp Gln Lys Gly Leu Cys Tyr Asp Ile Met Arg Ile Ser Lys Asp
260 265 270

Ser Asp Ile Lys Val Ala Tyr Ala Arg Phe Ser Ser Ser Val Lys Gly

275 280 285

Phe Gln Asn Ile Asp Leu Phe Val Gln Gln Asn Asp Gly Lys Lys Ile
290 295 300

Ile Asp Pro Glu Leu Gln Lys Thr Leu Cys Ser Cys Leu Lys Glu Glu
305 310 315 320

Met Leu His Pro Leu Arg Val Ile Ile Val Asn Arg Gly Pro Asp Thr
325 330 335

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

Arg Val Phe Tyr Asp Val Thr Leu Ala Leu Lys Ala Leu Gly Val Phe
355 360 365

Val Phe Ser Ala Glu Val Val Arg His Ser Thr Gln Glu Arg Gln Trp
370 375 380

Glu Val Tyr Arg Phe Leu Leu Asp Glu Ser His Gly Phe Pro Leu Thr
385 390 395 400

Ser Ser Lys Ala Arg Ser Gln Ile Val Asp Lys Val Arg Arg Thr Leu
405 410 415

Met Gly Trp

<210> 1023
<211> 420
<212> PRT
<213> Maní

<400> 1023

Met Gly Ile Pro Trp Asp Asp Val Val Val Ile Gln His Gly Lys Asp
1 5 10 15

Lys Asn Asp Pro Thr Val Val Thr Val Asn Cys Pro Asp Lys Ala Gly
20 25 30

Leu Gly Cys Asp Leu Cys Arg Ile Thr Leu Glu Phe Gly Leu Arg Ile
35 40 45

Lys Lys Ala Asp Ile Ser Thr Asp Gly Arg Trp Cys Tyr Ile Val Phe
50 55 60

Trp Val Val Pro Asn Pro Ser Ser Leu Thr Val Asp Trp Gly Ser Leu
65 70 75 80

Lys Thr Arg Leu Leu Ser Ala Cys Pro Ser Cys Leu Leu Thr Tyr His
85 90 95

Leu Asn Gln Gln Leu Thr Thr Ser Pro Ser Pro Pro Pro Ile Tyr Leu
100 105 110

Leu Lys Val Trp Leu Ile Asp Gln Lys Gly Leu Leu His Asp Ile Asn
115 120 125

Glu Ile Leu Cys Asn Leu Glu Leu Leu Ile Gln Arg Val Lys Val Met
130 135 140

Pro Thr Pro Asp Gly Arg Ala Leu Asp Met Phe Phe Ile Asn Asp Gly
145 150 155 160

Met Glu Leu Leu His Thr Lys Lys Arg Gln Asp Tyr Val Cys Glu Phe
165 170 175

Leu Lys Asp Ala Leu Gly Asp Arg Cys Ile Ser Thr Glu Leu Gln Leu
180 185 190

Ala Gly Pro Glu Tyr Gly Gln Leu Gln Gly Ile Ser Ser Leu Pro Pro
195 200 205

Ala Phe Ala Glu Glu Leu Phe Ser Ser Glu Leu Leu Asp Lys Gly Ser
210 215 220

Leu His Pro Leu Ser Gln Asp Met Ala Pro Leu Lys Lys Pro Thr Val
225 230 235 240

Met Val Asp Asn Ser Leu Ser Pro Ala His Thr Leu Leu Gln Ile Glu
245 250 255

Cys Val Asp Gln Lys Gly Leu Cys Tyr Asp Ile Met Arg Ile Ser Lys
260 265 270

Asp Ser Asp Ile Lys Val Ala His Gly Arg Phe Ser Ser Ser Ala Lys
275 280 285

Gly Phe Arg Ser Ile Asp Leu Leu Val Gln Gln Lys Asp Gly Lys Lys
290 295 300

Ile Ile Asp Pro Glu Ser Gln Lys Thr Leu Cys Ser Cys Leu Lys Glu
305 310 315 320

Glu Met Leu His Pro Leu Arg Val Ile Ile Val Asn Arg Gly Pro Asp
325 330 335

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

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

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

Trp Glu Val Tyr Arg Phe Leu Leu Asp Glu Ser Arg Asp Phe Pro Leu
385 390 395 400

Thr Ser Ser Lys Ala Arg Ser Gln Ile Val Asp Lys Val Arg Arg Thr
405 410 415

Leu Met Gly Trp
420

<210> 1024
<211> 418
<212> PRT
<213> Medicago

<400> 1024

Met Gly Ile Pro Ser Asp Asp Leu Val Val Ile Gln His Ala Lys Asn
1 5 10 15

Ala Asn Glu Pro Thr Ile Val Thr Val Asn Cys Pro Asp Lys Ala Gly
20 25 30

Leu Gly Cys Asp Leu Cys Arg Ile Ile Leu Glu Phe Gly Leu Arg Ile
35 40 45

Thr Arg Ala Asp Ile Ser Thr Asp Gly Arg Trp Cys Phe Ile Val Phe
50 55 60

Trp Val Ile Pro His Pro Ala Ser Leu Lys Ile Asp Trp Glu Asn Leu
65 70 75 80

Lys Thr Arg Leu Leu Ser Pro Cys Pro Ser Cys Leu Phe Ser Tyr Asn
85 90 95

Phe Asn Gln Arg Asn Pro Ser Pro Pro Pro Ile Tyr Leu Leu Lys Val
100 105 110

Trp Ile Ile Asp Gln Lys Gly Leu Leu His Asp Ile Asn Glu Ile Leu
115 120 125

Cys Asn Leu Gln Leu Thr Ile Gln Arg Val Lys Val Met Pro Thr Pro
130 135 140

Asp Gly Arg Ala Leu Asp Leu Phe Phe Ile Thr Asp Glu Met Glu Leu
145 150 155 160

Phe His Thr Lys Glu Arg Arg Asp Asp Val Cys Gln Tyr Leu Ser Glu
165 170 175

Ala Leu Gly Glu Arg Cys Ile Ser Ser Glu Leu Gln Leu Ala Gly Pro
180 185 190

Glu Tyr Gly His Leu Gln Gly Phe Ser Ser Leu Pro Pro Ala Tyr Ser
195 200 205

Glu Glu Leu Phe Gly Pro Glu Leu Val Asp Lys Val Ser Leu His Pro
210 215 220

Leu Ser Gln Asp Met Thr Thr Leu Lys Thr Pro Thr Val Thr Val Asp
225 230 235 240

Asn Ser Leu Ser Ser Val His Thr Leu Leu Gln Ile Gln Cys Val Asp
245 250 255

Gln Lys Ser Leu Cys Tyr Asp Leu Met Arg Ile Ser Lys Asp Ser Asp
260 265 270

Ile Lys Val Ala Tyr Gly Arg Phe Asn Ser Ser Ala Lys Gly Phe Gln
275 280 285

Asn Ile Asp Leu Phe Val Gln Gln Lys Glu Asp Gly Gln Lys Ile Ile
290 295 300

Asp Pro Glu Arg Leu Lys Thr Leu Cys Thr Cys Leu Lys Glu Glu Met
305 310 315 320

Leu His Pro Leu Arg Val Ile Ile Val Asn Arg Gly Pro Asp Ile Glu
325 330 335

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

Val Phe Tyr Asp Val Thr Leu Ala Leu Lys Ala Leu Gly Val Phe Ile
355 360 365

Phe Ser Ala Glu Val Val Arg His Ser Thr Gln Glu Arg Gln Trp Glu
370 375 380

Val Tyr Arg Phe Leu Leu Asp Glu Ser Arg Asp Phe Pro Leu Asn Ser
385 390 395 400

Ser Lys Ala Arg Ser Gln Ile Val Asp Lys Val Arg Arg Thr Leu Met
405 410 415

Gly Trp

<210> 1025
<211> 559
<212> PRT
<213> Soja

<400> 1025

Met Asp Ser Trp Val Arg Met Leu Phe Leu Ile Ala Cys Ile Val Pro
1 5 10 15

Ala Leu Val Glu Cys Lys Val Arg His Tyr Lys Phe Asn Val Val Leu
20 25 30

Lys Asn Thr Thr Arg Leu Cys Ser Ser Lys Pro Ile Val Thr Val Asn
35 40 45

Gly Lys Phe Pro Gly Pro Thr Leu Tyr Ala Arg Glu Asp Asp Thr Val
50 55 60

Leu Val Lys Val Asn Asn Leu Val Asn His Asn Val Thr Ile His Trp
65 70 75 80

His Gly Val Arg Gln Leu Arg Thr Gly Trp Ala Asp Gly Pro Ala Tyr
85 90 95

Ile Thr Gln Cys Pro Ile Leu Ser Gly Gln Ser Tyr Leu Tyr Asn Phe
100 105 110

Thr Leu Thr Gly Gln Arg Gly Thr Leu Leu Trp His Ala His Val Asn
115 120 125

Trp Leu Arg Ser Thr Leu His Gly Ala Ile Val Ile Leu Pro Lys Arg
130 135 140

Gly Val Pro Tyr Pro Phe Pro Lys Pro Asp Lys Glu Leu Val Val Ile
145 150 155 160

Leu Gly Glu Trp Trp Lys Ser Asp Thr Glu Asp Val Ile Asn Glu Ala
165 170 175

Leu Lys Ser Gly Leu Ala Pro Asn Val Ser Asp Ala His Thr Ile Asn
180 185 190

Gly Leu Pro Gly Ile Val Ser Val Ala Asn Cys Ser Thr Gln Asp Val
195 200 205

Tyr Lys Leu Pro Val Glu Ser Gly Lys Thr Tyr Leu Leu Arg Ile Ile
210 215 220

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

Phe Thr Val Val Glu Val Asp Ala Ser Tyr Val Lys Pro Phe Lys Thr
245 250 255

Asp Thr Leu Ser Ile Ala Pro Gly Gln Thr Thr Asn Ala Leu Leu Thr
260 265 270

Ala Asp Gln Asn Ser Gly Lys Tyr Thr Ile Val Ala Ser Thr Phe Met
275 280 285

Asp Ser Pro Val Val Ala Val Asp Asn Leu Thr Ala Thr Ala Thr Leu
290 295 300

His Tyr Thr Gly Thr Leu Ala Thr Thr Pro Thr Leu Leu Thr Thr Pro
305 310 315 320

Pro Pro Arg Asn Ala Thr Gln Val Ala Asn Asn Phe Thr Asn Ser Leu
325 330 335

Lys Ser Leu Asn Ser Lys Lys Tyr Pro Ala Lys Val Pro Gln Lys Val
340 345 350

Asp His Ser Leu Leu Leu Thr Val Gly Leu Gly Ile Asn Pro Cys Pro
355 360 365

Ser Cys Thr Ala Gly Asn Gly Ser Arg Val Val Ala Ala Val Asn Asn
370 375 380

Val Thr Phe Val Met Pro Thr Thr Ala Leu Leu Gln Ala His Tyr Phe
385 390 395 400

Asn Ile Lys Gly Val Phe Thr Thr Asp Phe Pro Gly Asn Pro Ser His
405 410 415

Val Tyr Asn Tyr Thr Ala Thr Pro Pro Ala Ala Ala Trp Gln Thr Thr
420 425 430

Asn Gly Thr Lys Ala Tyr Arg Leu Ala Phe Asn Ser Thr Val Gln Val
435 440 445

Val Leu Gln Asp Thr Gly Val Ile Ala Pro Glu Ser His Pro Val His
450 455 460

Leu His Gly Phe Asn Phe Phe Val Val Gly Ser Gly Val Gly Asn Tyr
465 470 475 480

Asp Pro Lys Thr Asp Gln Asn Asn Phe Asn Leu Ala Asp Pro Val Glu
485 490 495

Arg Asn Thr Ile Gly Val Pro Thr Gly Gly Trp Val Ala Phe Arg Phe
500 505 510

Arg Ala Asp Asn Pro Val Trp Phe Leu His Cys His Phe Glu Val His
515 520 525

Thr Thr Trp Gly Leu Lys Met Ala Phe Leu Val Asp Asn Gly Lys Gly
530 535 540

Pro Asn Glu Ser Leu Leu Pro Pro Pro Lys Asp Leu Pro Lys Cys
545 550 555

<210> 1026
<211> 560
<212> PRT
<213> Poroto

<400> 1026

Met Asp Ser Trp Val Arg Val Leu Leu Phe Ile Ala Cys Ile Val Pro
1 5 10 15

Ala Leu Val Glu Cys Lys Val Arg His Tyr Lys Phe Asn Val Val Leu
20 25 30

Lys Asn Thr Thr Arg Leu Cys Ser Ser Lys Pro Ile Val Thr Val Asn

35 40 45

Gly Lys Phe Pro Gly Pro Thr Leu Tyr Ala Arg Glu Asp Asp Thr Val
50 55 60

Leu Val Lys Val Arg Asn Leu Val Asn His Asn Val Thr Ile His Trp
65 70 75 80

His Gly Val Arg Gln Ile Arg Thr Gly Trp Ala Asp Gly Pro Ala Tyr
85 90 95

Ile Thr Gln Cys Pro Ile Leu Pro Gly Gln Ser Tyr Leu Tyr Asn Phe
100 105 110

Thr Leu Thr Gly Gln Arg Gly Thr Leu Leu Trp His Ala His Val Asn
115 120 125

Trp Leu Arg Ser Thr Leu His Gly Ala Ile Val Ile Leu Pro Lys His
130 135 140

Gly Val Pro Tyr Pro Phe Pro Lys Pro Val Lys Glu Leu Val Val Ile
145 150 155 160

Leu Gly Glu Trp Trp Lys Ser Asp Thr Glu Asp Val Ile Asn Glu Ala
165 170 175

Leu Lys Ser Gly Leu Ala Pro Asn Val Ser Asp Ala His Thr Ile Asn

180 185 190

Gly Leu Pro Gly Ile Val Phe Val Ala Asn Cys Ser Thr Gln Asp Val
195 200 205

Tyr Lys Leu Pro Val Glu Ser Gly Lys Thr Tyr Leu Leu Arg Ile Ile
210 215 220

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

Phe Thr Val Val Glu Val Asp Ala Ser Tyr Val Lys Pro Phe Lys Thr
245 250 255

Asp Thr Leu Leu Ile Ala Pro Gly Gln Thr Thr Asn Ala Leu Leu Thr
260 265 270

Thr Asp Gln Asn Ser Gly Lys Tyr Thr Ile Val Ala Ser Thr Phe Met
275 280 285

Asp Ser Pro Val Val Ala Val Asp Asn Leu Thr Ala Thr Ala Thr Leu
290 295 300

His Tyr Thr Gly Thr Leu Ala Thr Thr Pro Thr Val Leu Ile Thr Pro
305 310 315 320

Pro Pro Arg Asn Ala Thr Gln Val Ala Asn Asn Phe Thr Lys Ser Leu

325 330 335

Lys Ser Leu Asn Ser Lys Lys Tyr Pro Ala Asn Val Pro Leu Thr Val
340 345 350

Asp His Ser Leu Leu Phe Thr Val Gly Leu Gly Ile Asn Pro Cys Pro
355 360 365

Ser Cys Thr Ala Gly Asn Gly Ser Arg Val Val Ala Ala Val Asn Asn
370 375 380

Val Thr Phe Val Met Pro Thr Thr Ala Leu Leu Gln Ala His Tyr Phe
385 390 395 400

Asn Thr Gln Gly Val Phe Thr Thr Asp Phe Pro Gly Asn Pro Pro Gln
405 410 415

Val Tyr Asn Tyr Thr Ala Thr Pro Arg Ala Ala Ser Ser Gln Thr Thr
420 425 430

Asn Gly Thr Lys Val Tyr Arg Leu Ala Phe Asn Ser Thr Val Gln Val
435 440 445

Val Leu Gln Asp Thr Gly Val Ile Ala Leu Glu Ser His Pro Ile His
450 455 460

Leu His Gly Phe Asn Phe Phe Val Val Gly Ser Gly Val Gly Asn Tyr

465 470 475 480

Asp Pro Lys Thr Asp Gly Ser Asn Phe Asn Leu Val Asp Pro Val Glu
485 490 495

Arg Asn Thr Ile Gly Val Pro Thr Gly Gly Trp Ile Ala Leu Arg Phe
500 505 510

Arg Ala Asp Asn Pro Gly Val Trp Phe Leu His Cys His Phe Glu Val
515 520 525

His Thr Thr Trp Gly Leu Lys Met Ala Phe Leu Val Asp Asn Gly Lys
530 535 540

Gly Pro Asn Glu Ser Leu Ile Ala Pro Pro Asn Asp Leu Pro Lys Cys
545 550 555 560

<210> 1027
<211> 560
<212> PRT
<213> Guandú

<400> 1027

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

Ala Leu Val Glu Cys Lys Val Arg His Tyr Lys Phe His Val Val Leu
20 25 30

Lys Asn Thr Thr Arg Leu Cys Ser Ser Lys Ala Ile Val Thr Val Asn
35 40 45

Gly Lys Phe Pro Gly Pro Thr Leu Tyr Ala Arg Glu Asp Asp Thr Val
50 55 60

Leu Val Lys Val Arg Asn Leu Val Asn His Asn Val Thr Ile His Trp
65 70 75 80

His Gly Ile Arg Gln Leu Arg Thr Gly Trp Ala Asp Gly Pro Ala Tyr
85 90 95

Ile Thr Gln Cys Pro Ile Leu Pro Gly Gln Ser Tyr Leu Tyr Asn Phe
100 105 110

Thr Ile Thr Gly Gln Arg Gly Thr Leu Leu Trp His Ala His Val Asn
115 120 125

Trp Leu Arg Ser Thr Leu His Gly Ala Ile Val Ile Leu Pro Lys Arg
130 135 140

Gly Val Pro Tyr Pro Phe Pro Lys Pro Asp Lys Glu Leu Val Val Ile
145 150 155 160

Leu Gly Glu Trp Trp Lys Ser Asp Thr Glu Asp Val Ile Asn Glu Ala
165 170 175

Leu Lys Ser Gly Leu Ala Pro Asn Val Ser Asp Ala His Thr Ile Asn
180 185 190

Gly Leu Pro Gly Ile Val Ser Val Ala Asn Cys Ser Thr Gln Asp Val
195 200 205

Tyr Lys Leu Pro Val Glu Ser Gly Lys Thr Tyr Leu Leu Arg Ile Ile
210 215 220

Asn Ala Ala Leu Asn Glu Glu Leu Phe Phe Lys Ile Ala Gly His Ser
225 230 235 240

Leu Thr Val Ile Glu Val Asp Ala Ser Tyr Val Lys Pro Phe Lys Thr
245 250 255

Asp Thr Leu Leu Ile Ala Pro Gly Gln Thr Thr Asn Ala Leu Leu Thr
260 265 270

Ala Asp Gln Asn Ser Gly Lys Tyr Ile Ile Val Ala Ser Thr Phe Met
275 280 285

Asp Ala Ser Val Val Ala Ile Asp Asn Leu Thr Ala Thr Ala Thr Leu
290 295 300

His Tyr Thr Gly Thr Leu Ala Ser Thr Pro Thr Ile Leu Thr Thr Pro
305 310 315 320

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

Lys Ser Leu Asn Ser Lys Lys Tyr Pro Ala Asn Val Pro Leu Thr Val
340 345 350

Asp His Ser Leu Leu Phe Thr Val Gly Leu Gly Ile Asn Pro Cys Pro
355 360 365

Ser Cys Thr Ala Gly Asn Gly Ser Arg Ala Val Ala Ala Val Asn Asn
370 375 380

Val Thr Phe Val Met Pro Thr Thr Ala Leu Leu Gln Ala His Tyr Phe
385 390 395 400

Asn Ile Lys Gly Val Phe Thr Thr Asp Phe Pro Gly Asn Pro Ala His
405 410 415

Val Tyr Asn Tyr Thr Ala Thr Pro Ala Thr Ala Ser Ser Gln Thr Lys
420 425 430

Asn Gly Thr Lys Val Tyr Arg Leu Lys Phe Asn Ser Thr Val Gln Val
435 440 445

Val Leu Gln Asp Thr Gly Val Ile Ala Pro Glu Ser His Pro Val His
450 455 460

Leu His Gly Phe Asn Phe Phe Ala Val Gly Ser Gly Val Gly Asn Tyr
465 470 475 480

Asp Pro Lys Thr Gly Pro Asn Asn Phe Asn Leu Val Asp Pro Val Glu
485 490 495

Arg Asn Thr Ile Gly Val Pro Thr Gly Gly Trp Val Ala Ile Arg Phe
500 505 510

Arg Ala Asp Asn Pro Gly Val Trp Phe Leu His Cys His Phe Glu Val
515 520 525

His Thr Thr Trp Gly Leu Lys Met Ala Phe Leu Val Asp Asn Gly Glu
530 535 540

Gly Pro Asn Glu Ser Leu Ile Pro Pro Pro Lys Asp Leu Pro Lys Cys
545 550 555 560

<210> 1028
<211> 557
<212> PRT
<213> Guandú

<400> 1028

Met Asp Ser His Trp Val Arg Ile Ile Leu Leu Ile Ala Cys Ile Leu
1 5 10 15

Pro Ala Leu Val Glu Cys Arg Val Arg His Tyr Lys Phe His Val Val
20 25 30

Ala Lys Lys Thr Thr Arg Leu Cys Ser Ser Lys Ser Ile Val Thr Ile
35 40 45

Asn Gly Lys Phe Pro Gly Pro Thr Leu Tyr Ala Arg Glu Asp Asp Thr
50 55 60

Val Leu Val Lys Val Ile Asn Gln Val Asn His Asn Val Thr Ile His
65 70 75 80

Trp His Gly Val Arg Gln Leu Arg Thr Gly Trp Ala Asp Gly Pro Ala
85 90 95

Tyr Val Thr Gln Cys Pro Ile Gln Pro Gly Gln Thr Tyr Val Tyr Asn
100 105 110

Phe Thr Leu Thr Gly Gln Arg Gly Thr Leu Leu Trp His Ala His Val
115 120 125

Asn Trp Leu Arg Ser Thr Leu His Gly Ala Leu Val Ile Leu Pro Lys
130 135 140

Arg Gly Val Pro Tyr Pro Phe Pro Lys Pro Asp Asp Glu Leu Val Val
145 150 155 160

Val Leu Gly Glu Trp Trp Lys Ser Asp Thr Glu Ala Val Ile Asn Glu
165 170 175

Ala Leu Lys Ser Gly Leu Ala Pro Asn Val Ser Asp Ala His Thr Ile
180 185 190

Asn Gly Leu Pro Gly Thr Val Thr Asn Cys Ser Thr Gln Asp Val Tyr
195 200 205

Asn Leu Pro Val Glu Ser Gly Lys Thr Tyr Leu Val Arg Ile Ile Asn
210 215 220

Ala Ala Leu Asn Glu Glu Leu Phe Phe Lys Ile Ala Gly His Lys Leu
225 230 235 240

Thr Val Val Glu Val Asp Ala Thr Tyr Val Lys Pro Phe Lys Ile Glu
245 250 255

Thr Ile Val Ile Ala Pro Gly Gln Thr Thr Asn Val Leu Leu Thr Ala
260 265 270

Asp Gln Lys Ser Gly Lys Tyr Leu Val Ala Ala Ser Pro Phe Met Asp
275 280 285

Ala Pro Val Ala Val Asp Asn Leu Thr Ala Thr Ala Thr Leu His Tyr
290 295 300

Thr Gly Thr Leu Ala Thr Thr Pro Thr Ile Leu Thr Thr Pro Pro Gln
305 310 315 320

Lys Asn Ala Thr Gln Val Ala Asn Asn Phe Ile Asn Ser Leu Lys Gly
325 330 335

Leu Asn Ser Lys Lys Tyr Pro Val Asn Val Pro Leu Thr Val Asp His
340 345 350

Ser Leu Phe Phe Thr Val Gly Leu Gly Ile Asn Pro Cys Pro Ser Cys
355 360 365

Lys Ala Gly Asn Gly Ser Arg Val Val Ala Ala Val Asn Asn Val Thr
370 375 380

Phe Val Met Pro Thr Ile Ala Leu Leu Gln Ala His Tyr Phe Asn Ile
385 390 395 400

Gly Gly Val Phe Thr Thr Asp Phe Pro Ala Lys Pro Pro His Val Phe
405 410 415

Asn Tyr Ser Gly Thr Gly Pro Ala Asn Leu Asn Thr Thr Ser Gly Thr
420 425 430

Lys Leu Tyr Arg Leu Pro Phe Asn Ala Thr Val Gln Val Val Leu Gln
435 440 445

Asp Thr Gly Ile Ile Ala Pro Glu Asn His Pro Val His Leu His Gly
450 455 460

Phe Asn Phe Phe Ile Val Gly Arg Gly Val Gly Asn Tyr Asn Pro Asn
465 470 475 480

Thr Asp Pro Lys Asn Phe Asn Leu Ala Asp Pro Val Glu Arg Asn Thr
485 490 495

Val Gly Val Pro Ala Gly Gly Trp Thr Ala Ile Arg Phe Arg Ala Asp
500 505 510

Asn Pro Gly Val Trp Phe Met His Cys His Leu Glu Val His Thr Thr
515 520 525

Trp Gly Leu Lys Met Ala Phe Leu Val Asp Asn Gly Lys Gly Pro Lys
530 535 540

Gln Ser Val Ile Pro Pro Pro Asn Asp Leu Pro Lys Cys
545 550 555

<210> 1029
<211> 557
<212> PRT
<213> Soja

<400> 1029

Met Asp Ser His Trp Val Arg Met Val Leu Leu Ile Ala Cys Ile Leu
1 5 10 15

Pro Ala Leu Val Glu Cys Arg Val Arg His Tyr Lys Phe His Val Val
20 25 30

Ser Lys Gln Thr Asn Arg Leu Cys Ser Ser Lys Ser Ile Val Thr Ile
35 40 45

Asn Gly Lys Phe Pro Gly Pro Thr Leu Tyr Ala Arg Glu Asp Asp Thr
50 55 60

Val Leu Val Lys Val Ile Asn Gln Val Asn His Asn Val Thr Ile His
65 70 75 80

Trp His Gly Val Arg Gln Leu Arg Thr Gly Trp Ala Asp Gly Pro Ala
85 90 95

Tyr Val Thr Gln Cys Pro Ile Gln Pro Gly Gln Thr Tyr Leu Tyr Asn
100 105 110

Phe Thr Leu Thr Gly Gln Arg Gly Thr Leu Leu Tyr His Ala His Val
115 120 125

Asn Trp Leu Arg Ser Thr Leu His Gly Ala Leu Val Ile Leu Pro Lys
130 135 140

Arg Gly Val Pro Tyr Pro Phe Pro Lys Pro Asp Asp Glu Leu Val Val
145 150 155 160

Val Leu Gly Glu Trp Trp Lys Ser Asp Thr Glu Ala Ile Ile Asn Glu
165 170 175

Ala Leu Lys Ser Gly Leu Ala Pro Asn Val Ser Asp Ala His Thr Ile
180 185 190

Asn Gly Leu Pro Gly Ala Val Thr Asn Cys Ser Thr Gln Asp Val Tyr
195 200 205

Asn Leu Pro Val Glu Ser Gly Lys Thr Tyr Leu Leu Arg Ile Ile Asn
210 215 220

Ala Ala Leu Asn Glu Glu Leu Phe Phe Lys Ile Ala Gly His Lys Leu
225 230 235 240

Thr Val Val Glu Val Asp Ala Thr Tyr Val Lys Pro Phe Lys Ile Glu
245 250 255

Thr Ile Leu Ile Ala Pro Gly Gln Thr Thr Asn Val Leu Leu Asn Ala
260 265 270

Asp Gln Lys Phe Gly Lys Tyr Leu Val Ala Ala Ser Pro Phe Met Asp
275 280 285

Ala Pro Ile Ala Val Asp Asn Leu Thr Ala Thr Ala Thr Leu His Tyr
290 295 300

Thr Gly Thr Leu Ala Ala Thr Pro Thr Ile Leu Thr Thr Pro Pro Pro
305 310 315 320

Lys Asn Ser Thr Gln Ile Ala Asn Asn Phe Ile Ser Ser Leu Arg Gly
325 330 335

Leu Asn Ser Lys Lys Tyr Pro Val Asn Val Pro Leu Thr Val Asp His
340 345 350

Ser Leu Phe Phe Thr Val Gly Leu Gly Ile Ser Pro Cys Pro Ser Cys
355 360 365

Lys Ala Ala Asn Gly Ser Arg Val Val Ala Ala Ile Asn Asn Val Thr
370 375 380

Phe Ile Met Pro Thr Ile Ala Leu Leu Gln Ala His Tyr Phe Asn Ile
385 390 395 400

Lys Gly Val Phe Thr Thr Asp Phe Pro Ala Asn Pro Pro His Leu Phe
405 410 415

Asn Tyr Ser Gly Pro Gly Pro Ala Asn Leu Asn Thr Glu Thr Gly Thr
420 425 430

Lys Val Tyr Arg Val Pro Phe Asn Ala Thr Val Gln Val Val Leu Gln
435 440 445

Asp Thr Gly Ile Ile Ala Pro Glu Asn His Pro Val His Leu His Gly
450 455 460

Phe Asn Phe Phe Val Val Gly Arg Gly Val Gly Asn Phe Asn Pro Lys
465 470 475 480

Ile Asp Pro Lys Asn Phe Asn Leu Val Asp Pro Val Glu Arg Asn Thr
485 490 495

Ile Gly Val Pro Ala Gly Gly Trp Thr Ala Phe Arg Phe Arg Ala Asp
500 505 510

Asn Pro Gly Val Trp Phe Met His Cys His Leu Glu Val His Thr Thr
515 520 525

Trp Gly Leu Lys Met Ala Phe Leu Val Asp Asn Gly Lys Gly Pro Lys
530 535 540

Gln Ser Val Ile Pro Pro Pro Lys Asp Leu Pro Lys Cys
545 550 555

<210> 1030
<211> 557
<212> PRT
<213> Soja

<400> 1030

Met Tyr Ser His Trp Val Arg Leu Met Leu Leu Ile Ala Cys Ile Leu
1 5 10 15

Pro Ala Leu Val Glu Cys Arg Glu Arg His Tyr Lys Phe His Val Val
20 25 30

Ser Lys Gln Thr Asn Arg Leu Cys Ser Ser Lys Ser Ile Val Thr Ile
35 40 45

Asn Gly Lys Phe Pro Gly Pro Thr Leu Tyr Ala Arg Glu Asp Asp Thr
50 55 60

Val Leu Val Lys Val Ile Asn Gln Val Asn His Asn Val Thr Ile His
65 70 75 80

Trp His Gly Val Arg Gln Leu Arg Thr Gly Trp Ala Asp Gly Pro Ala
85 90 95

Tyr Val Thr Gln Cys Pro Ile Gln Pro Gly Gln Thr Tyr Val Tyr Asn
100 105 110

Phe Thr Leu Thr Gly Gln Arg Gly Thr Leu Leu Tyr His Ala His Val
115 120 125

Asn Trp Leu Arg Ser Thr Leu Tyr Gly Ala Leu Val Ile Leu Pro Lys

130 135 140

Arg Gly Val Pro Tyr Pro Phe Pro Lys Pro Asp Asp Glu Leu Val Val
145 150 155 160

Val Leu Gly Glu Trp Trp Lys Ser Asp Thr Glu Ala Val Ile Asn Glu
165 170 175

Ala Leu Lys Ser Gly Leu Ala Pro Asn Val Ser Asp Ala His Thr Ile
180 185 190

Asn Gly Leu Pro Gly Thr Val Thr Asn Cys Ser Thr Gln Asp Val Tyr
195 200 205

Asn Leu Pro Val Glu Ser Gly Lys Thr Tyr Leu Leu Arg Ile Val Asn
210 215 220

Ala Ala Leu Asn Glu Glu Leu Phe Phe Lys Ile Ala Gly His Lys Leu
225 230 235 240

Thr Val Val Glu Val Asp Ala Thr Tyr Val Lys Pro Phe Lys Ile Glu
245 250 255

Thr Ile Val Ile Ala Pro Gly Gln Thr Thr Asn Val Leu Leu Asn Ala
260 265 270

Asn Gln Lys Ser Gly Lys Tyr Leu Val Ala Ala Ser Pro Phe Met Asp

275 280 285

Ala Pro Val Ala Val Asp Asn Leu Thr Ala Thr Ala Thr Leu His Tyr
290 295 300

Thr Gly Thr Leu Ala Ala Thr Pro Thr Ile Leu Thr Thr Pro Pro Pro
305 310 315 320

Lys Asn Ala Thr Gln Ile Ala Asn Asn Phe Ile Ser Ser Leu Arg Gly
325 330 335

Leu Asn Ser Lys Lys Tyr Pro Val Asn Val Pro Leu Thr Val Asp His
340 345 350

Ser Leu Ile Phe Thr Val Gly Leu Gly Ile Asn Pro Cys Pro Ser Cys
355 360 365

Lys Ala Ala Asn Gly Ser Arg Val Val Ala Ala Ile Asn Asn Val Thr
370 375 380

Phe Ile Met Pro Thr Ile Ala Leu Leu Gln Ala His Tyr Phe Asn Ile
385 390 395 400

Lys Gly Val Phe Thr Thr Asp Phe Pro Ala Asn Pro Pro His Val Phe
405 410 415

Asn Tyr Ser Gly Pro Gly Pro Ala Asn Leu Asn Thr Glu Thr Gly Thr

420 425 430

Lys Val Tyr Arg Leu Pro Phe Asn Ala Thr Val Gln Val Val Leu Gln
435 440 445

Asp Thr Gly Ile Ile Ala Pro Glu Asn His Pro Val His Leu His Gly
450 455 460

Phe Asn Phe Phe Val Val Gly Arg Gly Val Gly Asn Phe Asn Pro Lys
465 470 475 480

Ile Asp Pro Lys Asn Phe Asn Leu Val Asp Pro Val Glu Arg Asn Thr
485 490 495

Ile Gly Val Pro Ala Gly Gly Trp Thr Ala Phe Arg Phe Arg Ala Asp
500 505 510

Asn Pro Gly Val Trp Phe Met His Cys His Leu Glu Val His Thr Thr
515 520 525

Trp Gly Leu Lys Met Ala Phe Leu Val Asp Asn Gly Lys Gly Pro Lys
530 535 540

Gln Ser Val Ile Pro Pro Pro Lys Asp Leu Pro Lys Cys
545 550 555

<210> 1031

<211> 557
<212> PRT
<213> Medicago

<400> 1031

Met Val Ser Trp Ile Arg Val Leu Leu Leu Ile Cys Cys Ile Phe Pro
1 5 10 15

Ala Leu Val Glu Cys Lys Val Arg His Tyr Lys Phe His Val Val Ala
20 25 30

Lys Asn Thr Ser Arg Leu Cys Ser Ser Lys Ala Ile Val Thr Val Asn
35 40 45

Gly Lys Phe Pro Gly Pro Thr Leu Tyr Ala Arg Glu Asp Asp Thr Val
50 55 60

Ile Val Lys Val Arg Asn Gln Val Asn Asn Asn Ile Thr Ile His Trp
65 70 75 80

His Gly Ile Arg Gln Leu Arg Thr Gly Trp Ala Asp Gly Pro Ala Tyr
85 90 95

Ile Thr Gln Cys Pro Ile Gln Pro Gly His Ser Tyr Thr Tyr Asn Phe
100 105 110

Thr Ile Thr Gly Gln Arg Gly Thr Leu Leu Trp His Ala His Val Asn
115 120 125

Trp Leu Arg Ser Thr Val His Gly Ala Ile Val Ile Leu Pro Lys Lys
130 135 140

Gly Val Pro Tyr Pro Phe Pro Lys Pro Asp Asp Glu Leu Val Leu Val
145 150 155 160

Leu Gly Glu Trp Trp Lys Ser Asp Thr Glu Ala Val Ile Asn Glu Ala
165 170 175

Leu Lys Ser Gly Leu Ala Pro Asn Val Ser Asp Ala His Thr Ile Asn
180 185 190

Gly Leu Pro Gly Thr Val Ala Asn Cys Ser Thr Gln Asp Val Tyr Lys
195 200 205

Leu Pro Val Glu Ser Gly Lys Thr Tyr Leu Leu Arg Ile Ile Asn Ala
210 215 220

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

Val Val Glu Val Asp Ala Thr Tyr Thr Lys Pro Phe Gln Ile Glu Thr
245 250 255

Ile Val Ile Ala Pro Gly Gln Thr Thr Asn Val Leu Leu Lys Ala Asn
260 265 270

Gln Lys Ser Gly Lys Tyr Leu Val Ala Ala Ser Pro Phe Met Asp Ala
275 280 285

Pro Val Ala Val Asp Asn Leu Thr Ala Thr Ala Thr Leu His Tyr Ser
290 295 300

Gly Thr Thr Leu Thr Asn Thr Pro Thr Phe Leu Thr Thr Pro Pro Pro
305 310 315 320

Thr Asn Ala Thr Gln Ile Ala Asn Asn Phe Leu Asn Ser Leu Lys Gly
325 330 335

Leu Asn Ser Lys Lys Tyr Pro Val Asn Val Pro Leu Lys Ile Asp His
340 345 350

Ser Leu Phe Phe Thr Val Gly Leu Gly Val Asn Pro Cys Pro Ser Cys
355 360 365

Lys Ala Gly Asn Gly Ser Arg Val Val Ala Ala Ile Asn Asn Val Thr
370 375 380

Phe Val Met Pro Thr Thr Ala Leu Leu Gln Ala His Tyr Phe Asn Ile
385 390 395 400

Lys Asn Val Phe Thr Ala Asp Phe Pro Pro Asn Pro Pro His Ile Tyr
405 410 415

Asn Phe Thr Gly Ala Gly Pro Lys Asn Leu Asn Thr Thr Ser Gly Thr
420 425 430

Lys Leu Tyr Lys Leu Ser Phe Asn Asp Thr Val Gln Leu Val Met Gln
435 440 445

Asp Thr Gly Ile Ile Ala Pro Glu Ser His Pro Val His Leu His Gly
450 455 460

Phe Asn Phe Phe Val Val Gly Arg Gly Val Gly Asn Tyr Asp Ser Lys
465 470 475 480

Asn Asp Ser Lys Lys Phe Asn Leu Val Asp Pro Val Glu Arg Asn Thr
485 490 495

Val Gly Val Pro Ala Gly Gly Trp Val Ala Ile Arg Phe Arg Ala Asp
500 505 510

Asn Pro Gly Val Trp Phe Met His Cys His Leu Glu Val His Thr Thr
515 520 525

Trp Gly Leu Lys Met Ala Phe Leu Val Asp Asn Gly Lys Gly Pro Lys
530 535 540

Gln Ser Val Ile Ala Pro Pro Lys Asp Leu Pro Lys Cys
545 550 555

<210> 1032
<211> 274
<212> PRT
<213> Chícharo salvaje

<400> 1032

Met Asp Ser Ala Leu Arg Thr Val Gly Val Lys Tyr Glu Cys Leu Leu
1 5 10 15

Phe Asp Met Asp Asp Thr Leu Tyr Pro Leu Ser Ile Gly Leu Asn Leu
20 25 30

Phe Cys Arg Lys Asn Ile Gln Glu Tyr Met Leu Glu His Leu His Ile
35 40 45

Glu Glu Asp Glu Val Pro Lys Met Cys Leu Asp Leu Tyr Arg Glu Tyr
50 55 60

Gly Thr Thr Met Ala Gly Leu Lys Val Leu Gly Tyr Glu Phe Asp Asn
65 70 75 80

Asp Glu Phe His Ala Tyr Val His Gly Arg Leu Pro Tyr Glu Lys Leu
85 90 95

Lys Pro Asp Pro Val Leu Arg Asn Leu Leu Leu Ser Met Pro Gln Arg
100 105 110

Lys Ile Ile Phe Thr Asn Ala Asp His Ala His Ala Val Lys Val Leu
115 120 125

Asn Arg Met Gly Leu Glu Asp Cys Phe Glu Gly Ile Ile Cys Phe Glu
130 135 140

Thr Leu Asn Pro His Lys Gln Ile Asn Cys Met Asp Leu Pro Asn Asp
145 150 155 160

Asp Asn Val Leu Thr Asp Leu Thr Glu Asn Gly Cys Phe Asn Ser Gln
165 170 175

Thr His Ile Leu Cys Lys Pro Ser Val Glu Ala Phe Glu Ala Ala Ile
180 185 190

Arg Ile Ala Asn Val Asp Pro Lys Lys Thr Ile Phe Phe Asp Asp Ser
195 200 205

Val Arg Asn Val Ala Ser Ala Lys Val Ala Gly Leu His Thr Val Ile
210 215 220

Leu Gly His Ser Asp Leu Val Pro Gly Ala Asp His Ala Leu Asn Ser
225 230 235 240

Ile His Asn Ile Lys Glu Ala Leu Pro Glu Ile Trp Glu Ile Glu Glu
245 250 255

Gly Asn Gln Gln Gln Lys Ile Gln Pro Pro Ala Val Glu Thr Met Val
260 265 270

Leu Ala

<210> 1033
<211> 271
<212> PRT
<213> Guandú

<400> 1033

Met Asp Thr Asp His Arg Ala Gly Gly Val Lys Tyr Glu Cys Leu Leu
1 5 10 15

Phe Asp Met Asp Asp Thr Leu Tyr Pro Leu Ser Leu Gly Leu Asn Leu
20 25 30

Phe Cys Arg Gln Asn Ile Gln Glu Tyr Met Leu Glu His Leu His Ile
35 40 45

Glu Glu Ser Glu Val Pro Lys Met Cys Leu Asp Leu Tyr Arg Glu Tyr
50 55 60

Gly Thr Thr Met Ala Gly Leu Lys Leu Leu Gly Tyr Glu Phe Asp Asn
65 70 75 80

Asp Glu Phe His Ala Tyr Val His Gly Arg Leu Pro Tyr Glu Lys Leu
85 90 95

Lys Pro Asp Pro Val Leu Arg Asn Leu Leu Leu Ser Met Pro Gln Arg
100 105 110

Lys Ile Ile Phe Thr Asn Ala Asp His Ala His Ala Val Gln Val Leu
115 120 125

Asn Arg Leu Gly Leu Glu Asp Cys Phe Glu Gly Ile Ile Cys Phe Glu
130 135 140

Thr Leu Asn Pro Leu Lys Gln Ile Asn Val Pro Asp Asn Asp His Val
145 150 155 160

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

Leu Cys Lys Pro Ser Val Glu Ala Phe Glu Ala Ala Ile Arg Ile Ala
180 185 190

Asn Val Asp Pro Asn Lys Thr Ile Phe Phe Asp Asp Ser Val Arg Asn
195 200 205

Val Glu Ser Ala Lys Leu Ala Gly Leu His Thr Val Leu Val Gly His
210 215 220

Ser Asp Leu Val Pro Gly Ala Asp His Ala Leu Asn Ser Ile His Asn
225 230 235 240

Ile Lys Glu Ala Leu Pro Glu Ile Trp Glu Ile Glu Glu Ala Asn Gln
245 250 255

Gln Gln Lys Met Gln Pro Pro Ala Val Glu Thr Met Val Gln Ala
260 265 270

<210> 1034
<211> 272
<212> PRT
<213> Poroto

<400> 1034

Met Asp Thr Ala Leu Arg Asn Ala Gly Val Lys Tyr Glu Cys Leu Leu
1 5 10 15

Phe Asp Met Asp Asp Thr Leu Tyr Pro Leu Ser Ile Gly Leu Asn Leu
20 25 30

Phe Cys Arg Lys Asn Ile Gln Glu Tyr Met Leu Glu His Leu His Ile
35 40 45

Glu Glu Asn Glu Val Pro Lys Met Cys Leu Asp Leu Tyr Arg Glu Tyr
50 55 60

Gly Thr Thr Met Ala Gly Leu Lys Val Leu Gly Tyr Glu Phe Asp Asn

65 70 75 80

Asp Glu Phe His Ala Tyr Val His Gly Arg Leu Pro Tyr Glu Lys Leu
85 90 95

Lys Pro Asp Pro Val Leu Arg Asn Leu Leu Ile Ser Met Pro Gln Arg
100 105 110

Lys Ile Ile Phe Thr Asn Ala Asp His Ala His Ala Val Lys Val Leu
115 120 125

Asn Arg Met Gly Leu Glu Asp Cys Phe Glu Gly Ile Ile Cys Phe Glu
130 135 140

Thr Leu Asn Pro His Lys Gln Tyr Met Asp Leu Pro Asn Asp Asn His
145 150 155 160

Val Leu Thr Asp Ile Ala Glu Ser Gly Cys Phe Asn Ser His Thr Arg
165 170 175

Ile Leu Cys Lys Pro Ser Val Glu Ala Phe Glu Ala Ala Ile Arg Thr
180 185 190

Ser Asn Val Asp Pro Lys Lys Thr Ile Phe Phe Asp Asp Ser Val Arg
195 200 205

Asn Val Ala Ser Ala Lys Val Ala Gly Leu His Thr Val Ile Leu Gly

210 215 220

His Ser Asp Leu Val Pro Gly Ala Asp His Ala Leu Asn Ser Ile His
225 230 235 240

Asn Ile Lys Glu Ala Leu Pro Glu Ile Trp Glu Ile Glu Glu Ser Asn
245 250 255

Gln Gln Gln Lys Ile Gln Pro Pro Ala Val Glu Thr Met Val Leu Ala
260 265 270

<210> 1035
<211> 265
<212> PRT
<213> Lotus

<400> 1035

Met Asp Ala His Arg Ile Asp Gly Val Lys Tyr Glu Cys Leu Leu Phe
1 5 10 15

Asp Ile Asp Asp Thr Leu Tyr Pro Leu Ser Leu Gly Leu Asn Leu Ala
20 25 30

Cys Arg Lys Asn Ile Gln Glu Tyr Met Leu Glu His Leu His Ile Glu
35 40 45

Glu Ser Glu Val Pro Lys Met Cys Leu Asp Leu Tyr Ile Glu His Gly
50 55 60

Thr Thr Met Ala Gly Leu Lys Ala Leu Gly Tyr Glu Phe Asp Asn Asp
65 70 75 80

Glu Phe His Ala Tyr Val His Gly Arg Leu Pro Tyr Glu Lys Leu Lys
85 90 95

Pro Asp Ser Val Leu Arg Asn Leu Leu Leu Ser Met Pro Gln Arg Lys
100 105 110

Ile Ile Phe Thr Asn Ser Asp His Lys His Ala Val Glu Val Leu Asn
115 120 125

Arg Leu Gly Leu Glu Asp Cys Phe Glu Gly Ile Ile Cys Phe Glu Thr
130 135 140

Leu Asn Pro Pro Asn Ile Asp Val Ser Asp Asp Asn His Val Thr Glu
145 150 155 160

Ser Gly Arg Phe Asn Ser His Thr Gln Ile Leu Cys Lys Pro Ser Val
165 170 175

Glu Ala Phe Glu Ala Ala Ile Arg Ile Ala Asn Val Asp Pro Lys Lys
180 185 190

Thr Ile Phe Phe Asp Asp Ser Thr Arg Asn Ile Ala Ser Ala Lys Val
195 200 205

Ala Gly Leu His Thr Val Met Val Gly Arg Ser Asp Leu Val Pro Gly
210 215 220

Ala Asn His Ala Leu Asn Ser Ile His Asn Ile Arg Glu Ala Leu Pro
225 230 235 240

Glu Ile Trp Glu Val Glu Glu Asp Ser Gln Gln Gln Met Ile Gln Ser
245 250 255

Leu Ala Val Glu Ala Ile Val Leu Ala
260 265

<210> 1036
<211> 529
<212> PRT
<213> Soja

<400> 1036

Met Glu Ala Ser Pro Ser Thr Leu Asp Trp Arg Gly Arg Pro Ser Asn
1 5 10 15

Pro Ala Lys His Gly Gly Met Ile Pro Ala Ala Phe Val Leu Gly Leu
20 25 30

Gln Ala Phe Glu Ile Met Ala Ile Ala Ala Val Gly Asn Asn Leu Ile
35 40 45

Thr Tyr Val Ala Asn Asp Met His Phe Pro Leu Ser Lys Ala Ala Asn
50 55 60

Leu Val Thr Asn Phe Val Gly Thr Ile Phe Leu Leu Ser Leu Leu Gly
65 70 75 80

Gly Tyr Leu Ser Asp Ser Tyr Leu Gly Ser Phe Trp Thr Met Leu Leu
85 90 95

Phe Gly Phe Val Glu Leu Ser Gly Phe Ile Leu Leu Ser Val Gln Ala
100 105 110

His Val Pro Gln Leu Lys Pro Pro Pro Cys Asn Val Asn Asp Gly Glu
115 120 125

Gln Cys Val Glu Ala Lys Gly Met Lys Ala Met Ile Phe Phe Val Ala
130 135 140

Leu Tyr Leu Val Ala Leu Gly Ser Gly Cys Val Lys Pro Asn Met Leu
145 150 155 160

Ala Tyr Gly Gly Asp Gln Phe Glu Gln Asn Asp Pro Lys Gln Leu Lys
165 170 175

Lys Leu Ser Thr Tyr Phe Asn Ala Ala Tyr Phe Ala Phe Ser Val Gly
180 185 190

Gln Leu Val Ser Leu Thr Ile Leu Val Trp Val Gln Thr His Ser Gly
195 200 205

Met Asp Val Gly Phe Gly Val Ser Ala Ala Val Met Ala Met Gly Leu
210 215 220

Ile Ser Leu Ile Cys Gly Thr Leu Tyr Tyr Arg Asn Lys Pro Pro Gln
225 230 235 240

Gly Ser Ile Leu Thr Pro Val Ala Gln Val Leu Val Ala Ala Phe Ser
245 250 255

Lys Arg Asn Leu Pro Ser Ser Pro Ser Ser Met Ile Arg Val Glu Gln
260 265 270

Val Glu Gln Val Lys Ile Leu Leu Ser Val Ile Pro Ile Phe Ser Cys
275 280 285

Thr Ile Val Phe Asn Thr Ile Leu Ala Gln Leu Gln Thr Phe Ser Val
290 295 300

Gln Gln Gly Arg Ala Met Asp Thr His Leu Thr Lys Ser Phe Asn Ile
305 310 315 320

Pro Pro Ala Ser Leu Gln Ser Ile Pro Tyr Ile Leu Leu Ile Phe Leu
325 330 335

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

Gly His Glu Ser Gly Ile Ser Pro Leu Arg Arg Ile Gly Phe Gly Leu
355 360 365

Phe Leu Ala Thr Phe Ser Met Val Ala Ala Ala Leu Leu Glu Lys Lys
370 375 380

Arg Arg Asp Ala Ala Val Asn His His Lys Val Leu Ser Ile Phe Trp
385 390 395 400

Ile Thr Pro Gln Tyr Leu Ile Phe Gly Leu Ser Glu Met Phe Thr Ala
405 410 415

Ile Gly Leu Leu Glu Phe Phe Tyr Lys Gln Ser Leu Lys Gly Met Gln
420 425 430

Ala Phe Phe Thr Ala Ile Thr Tyr Cys Ser Tyr Ser Phe Gly Phe Tyr
435 440 445

Leu Ser Thr Leu Leu Val Ser Leu Val Asn Lys Ile Thr Ser Thr Ser
450 455 460

Ser Ser Ser Ala Ala Gly Trp Leu His Asn Asn Asp Leu Asn Gln Asp
465 470 475 480

Arg Leu Asp Leu Phe Tyr Trp Leu Leu Ala Val Leu Ser Phe Leu Asn
485 490 495

Phe Leu Asn Tyr Leu Phe Cys Tyr Cys Lys Glu Leu Tyr Arg Ser Lys
500 505 510

Cys Arg Ile Asp Arg Val Ala Ser Ile Tyr Asn Ile Leu Gln Leu Gln
515 520 525

Ala

<210> 1037
<211> 567
<212> PRT
<213> Soja

<400> 1037

Met Glu Thr Asp Lys Gly Glu Ala Gln Ala Gln Asp Trp Arg Gly Arg
1 5 10 15

Pro Ser Asn Pro Ala Lys His Gly Gly Met Ile Pro Ala Ala Phe Val
20 25 30

Leu Gly Leu Gln Ala Phe Glu Ile Met Ala Ile Ala Ala Val Gly Asn
35 40 45

Asn Leu Ile Thr Tyr Val Thr Ser Glu Met His Phe Pro Leu Ser Lys
50 55 60

Ala Ala Asn Leu Val Thr Asn Phe Val Gly Thr Ile Phe Leu Leu Ala
65 70 75 80

Leu Leu Gly Gly Tyr Leu Ser Asp Ser Tyr Leu Gly Ser Phe Trp Thr
85 90 95

Met Leu Ile Phe Gly Phe Val Glu Leu Ser Gly Phe Ile Leu Leu Ser
100 105 110

Val Gln Ala His Val Pro Gln Leu Lys Pro Pro Pro Cys Asn Ile Asn
115 120 125

Asp Leu Gly Glu Gln Cys Ser Glu Ala Lys Gly Met Lys Ala Met Ile
130 135 140

Phe Phe Val Ala Leu Tyr Leu Val Ala Leu Gly Ser Gly Cys Val Lys
145 150 155 160

Pro Asn Met Val Ala Tyr Gly Gly Asp Gln Phe Asp Gln Asp Asn Pro
165 170 175

Lys Gln Leu Lys Lys Leu Ser Thr Tyr Phe Asn Ala Ala Tyr Phe Ala
180 185 190

Phe Ser Leu Gly Glu Leu Val Ser Leu Thr Ile Leu Val Trp Val Gln
195 200 205

Thr His Ser Gly Met Asp Val Gly Phe Gly Val Ser Ala Ala Val Met
210 215 220

Ala Met Gly Leu Ile Ser Leu Ile Cys Gly Thr Leu Tyr Tyr Arg Asn
225 230 235 240

Lys Pro Pro Gln Gly Ser Ile Leu Thr Pro Ile Ala Gln Val Leu Val
245 250 255

Ala Ala Ile Phe Lys Arg Asn Leu Leu Leu Pro Ser Asn Pro Gln Met
260 265 270

Leu His Gly Thr Gln Asn Asn Leu Ile His Thr Asp Lys Phe Arg Phe
275 280 285

Leu Asp Lys Ala Cys Ile Arg Val Glu Gln Glu Gly Asn Gln Glu Ser
290 295 300

Ala Trp Arg Leu Cys Ser Val Ala Gln Val Glu Gln Val Lys Ile Leu
305 310 315 320

Leu Ser Val Ile Pro Ile Phe Ser Cys Thr Ile Val Phe Asn Thr Ile
325 330 335

Leu Ala Gln Leu Gln Thr Phe Ser Val Gln Gln Gly Arg Ala Met Asp
340 345 350

Thr His Leu Thr Lys Ser Phe Asn Ile Pro Pro Ala Ser Leu Gln Ser
355 360 365

Ile Pro Tyr Ile Leu Leu Ile Val Leu Val Pro Leu Tyr Asp Thr Phe
370 375 380

Phe Val Pro Phe Ala Arg Lys Phe Thr Gly His Glu Ser Gly Ile Pro
385 390 395 400

Pro Leu Arg Arg Ile Gly Phe Gly Leu Phe Leu Ala Thr Phe Ser Met
405 410 415

Val Ala Ala Ala Leu Leu Glu Lys Lys Arg Arg Asp Glu Ala Val Asn
420 425 430

His Asp Lys Val Leu Ser Ile Phe Trp Ile Thr Pro Gln Tyr Leu Ile
435 440 445

Phe Gly Leu Ser Glu Met Phe Thr Ala Ile Gly Leu Leu Glu Phe Phe
450 455 460

Tyr Lys Gln Ser Leu Lys Gly Met Gln Ala Phe Leu Thr Ala Ile Thr
465 470 475 480

Tyr Cys Ser Tyr Ser Phe Gly Phe Tyr Leu Ser Thr Leu Leu Val Ser
485 490 495

Leu Val Asn Lys Ile Thr Ser Thr Ser Ser Ser Ala Ala Gly Trp Leu
500 505 510

His Asn Asn Asn Leu Asn Gln Asp Arg Leu Asp Leu Phe Tyr Trp Leu
515 520 525

Leu Ala Val Leu Ser Phe Leu Asn Phe Leu Asn Tyr Leu Phe Trp Ser
530 535 540

Arg Arg Tyr Ser His Ala Pro Ser Ala Leu Pro Pro Pro Asn Thr Lys
545 550 555 560

Glu His His His Asn Ile Pro
565

<210> 1038
<211> 584
<212> PRT
<213> Poroto

<400> 1038

Met Glu Thr Thr Lys Val Ser Glu Asn Glu Asp Glu Leu His His Ser
1 5 10 15

Gln Pro Gln Ser Ser Thr Leu Asp Trp Arg Gly Arg Pro Ser Asp Pro

20 25 30

Ala Lys His Gly Gly Val Leu Pro Ala Ala Phe Ile Leu Gly Leu Gln
35 40 45

Ala Phe Glu Ile Met Ala Ile Ala Ala Val Gly Asn Asn Leu Ile Thr
50 55 60

Tyr Val Thr Asn Asp Met His Phe Ser Leu Ser Lys Ala Ala Asn Val
65 70 75 80

Val Thr Asn Phe Val Gly Thr Ile Phe Leu Leu Ala Leu Leu Gly Gly
85 90 95

Tyr Leu Ser Asp Ser Tyr Leu Gly Ser Phe Trp Thr Met Leu Ile Phe
100 105 110

Gly Phe Leu Glu Leu Ser Gly Phe Ile Leu Leu Ser Val Gln Ala His
115 120 125

Val Pro Gln Leu Lys Pro Ala Pro Cys Asn Val Leu Thr Asp Gly Glu
130 135 140

His Cys Ala Glu Ala Lys Gly Phe Lys Ala Val Ile Phe Phe Val Ala
145 150 155 160

Leu Tyr Leu Val Ala Leu Gly Ser Gly Cys Val Lys Pro Asn Met Leu

165 170 175

Ala Tyr Gly Gly Asp Gln Phe Glu Gln Asp Asn Pro Lys Gln Ser Lys
180 185 190

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

Glu Leu Val Ser Leu Thr Ile Leu Val Trp Val Gln Thr His Ser Gly
210 215 220

Met Asp Val Gly Phe Gly Val Ser Ala Ala Val Met Ala Met Gly Leu
225 230 235 240

Ile Ser Leu Ile Cys Gly Thr Leu Tyr Tyr Arg Asn Lys Pro Pro Gln
245 250 255

Gly Ser Ile Leu Thr Pro Ile Ala Gln Val Leu Val Ala Ala Ile Ser
260 265 270

Lys Arg Asn Leu Val Leu Pro Ser Asn Pro Gln Met Leu His Gly Ser
275 280 285

Gln Asn Asn Thr Gly Leu Leu Leu Ser Asp Lys Leu Gly Phe Leu Asp
290 295 300

Lys Ala Cys Ile Arg Val Gln Glu Gly Glu Asn Arg Lys Glu Ser Ala

305 310 315 320

Trp Arg Leu Cys Ser Val Glu Gln Val Glu Gln Val Lys Ile Leu Leu
325 330 335

Ser Val Ile Pro Ile Phe Ser Cys Thr Ile Val Phe Asn Thr Ile Leu
340 345 350

Ala Gln Leu Gln Thr Phe Ser Val Gln Gln Gly Arg Ala Met Asp Ser
355 360 365

His Leu Thr Lys Ser Phe Asn Ile Pro Pro Ala Ser Leu Gln Ser Ile
370 375 380

Pro Tyr Ile Leu Leu Ile Val Leu Val Pro Leu Tyr Asp Thr Phe Phe
385 390 395 400

Val Pro Phe Ala Arg Lys Ile Thr Gly His Glu Ser Gly Ile Ser Pro
405 410 415

Leu Arg Arg Ile Gly Phe Gly Leu Phe Leu Ala Thr Phe Ser Met Val
420 425 430

Ala Ala Ala Val Met Glu Lys Lys Arg Arg Asp Ala Ala Val Asn Leu
435 440 445

Asn Gln Thr Leu Ser Ile Phe Trp Ile Thr Pro Gln Phe Leu Ile Phe

450 455 460

Gly Leu Ser Glu Met Phe Thr Ala Ile Gly Leu Leu Glu Phe Phe Tyr
465 470 475 480

Lys Gln Ser Leu Lys Gly Met Gln Ala Phe Leu Thr Ala Ile Thr Tyr
485 490 495

Cys Ser Tyr Ser Phe Gly Phe Tyr Phe Ser Thr Val Leu Val Ser Leu
500 505 510

Val Asn Lys Ile Thr Ser Thr Ser Ser Thr Gly Gly Trp Leu His Tyr
515 520 525

Asn Asn Leu Asn Gln Asp Arg Leu Asp Leu Phe Tyr Trp Leu Leu Ala
530 535 540

Val Leu Ser Phe Leu Asn Phe Leu Asn Tyr Leu Phe Trp Ser Lys Arg
545 550 555 560

Tyr His Ala Pro Ser Pro Tyr Gln Pro Asn Ala Lys Glu Ile Asn Pro
565 570 575

Tyr Val Gly Asp Asp Asn Ile Pro
580

<210> 1039

<211> 579
<212> PRT
<213> Guandú

<400> 1039

Met Glu Ile Asp Lys Gly Asp His Gln Asp Gln Glu Glu Ser Ser Ser
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Leu Thr Leu Asp Trp Arg Gly Arg Pro Ser Asn Pro Ala Lys His Gly
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Gly Met Val Pro Ala Ala Phe Val Leu Gly Leu Gln Ala Phe Glu Ile
35 40 45

Met Ala Ile Ala Ala Val Gly Asn Asn Leu Ile Thr Tyr Val Thr Asn
50 55 60

His Met His Phe Pro Leu Ser Lys Ala Ala Asn Val Val Thr Asn Phe
65 70 75 80

Val Gly Thr Ile Phe Leu Leu Ala Leu Leu Gly Gly Tyr Leu Ser Asp
85 90 95

Ser Phe Leu Gly Ser Phe Trp Thr Met Leu Ile Phe Ala Phe Val Glu
100 105 110

Leu Ser Gly Phe Ile Leu Leu Ser Val Gln Ala His Val Pro Gln Leu
115 120 125

Lys Pro Pro Pro Cys Asn Asp Gly Glu His Cys Val Glu Ala Lys Gly
130 135 140

Phe Lys Ala Met Ile Phe Phe Val Ala Leu Tyr Leu Val Ala Leu Gly
145 150 155 160

Ser Gly Cys Val Lys Pro Asn Met Val Ala Tyr Gly Gly Asp Gln Phe
165 170 175

Asp Gln Asp Asn Pro Lys Gln Leu Lys Lys Leu Ser Thr Tyr Phe Asn
180 185 190

Ala Ala Tyr Phe Ala Phe Ser Leu Gly Glu Leu Ile Ser Leu Thr Ile
195 200 205

Leu Val Trp Val Gln Thr His Ser Gly Met Asp Val Gly Phe Gly Val
210 215 220

Ser Ala Ala Val Met Ala Met Gly Leu Ile Ser Leu Ile Cys Gly Thr
225 230 235 240

Leu Tyr Tyr Arg Asn Lys Pro Pro Gln Gly Ser Ile Leu Thr Pro Ile
245 250 255

Ala Gln Val Leu Val Ala Ala Ile Ser Lys Arg Lys Leu Val Cys Pro
260 265 270

Ser Asn Pro Gln Met Leu Tyr Gly Ser Gln Asn Asn Ala Ala Leu Pro
275 280 285

His Thr Asp Lys Leu Arg Phe Leu Asp Lys Ala Cys Ile Arg Val Gln
290 295 300

Glu Gly Thr Asn Thr Lys Glu Ser Pro Trp Arg Leu Cys Ser Val Thr
305 310 315 320

Gln Val Glu Lys Val Lys Ile Leu Val Ser Val Ile Pro Ile Phe Ser
325 330 335

Cys Thr Ile Val Phe Asn Thr Ile Leu Ala Gln Leu Gln Thr Phe Ser
340 345 350

Val Gln Gln Gly Arg Ala Met Asp Thr Arg Leu Thr Lys Ser Phe Ser
355 360 365

Ile Pro Pro Ala Ser Leu Gln Ser Ile Pro Tyr Ile Leu Leu Ile Phe
370 375 380

Leu Val Pro Leu Tyr Asp Thr Phe Phe Val Pro Phe Ala Arg Lys Ile
385 390 395 400

Thr Gly His Glu Ser Gly Ile Ser Pro Leu Arg Arg Ile Gly Phe Gly
405 410 415

Leu Phe Leu Ala Thr Phe Ser Met Val Ala Ala Ala Ile Met Glu Lys
420 425 430

Lys Arg Arg Asp Ala Ala Val Asn His Asn Glu Thr Leu Ser Ile Phe
435 440 445

Trp Ile Thr Pro Gln Phe Leu Ile Phe Gly Leu Ser Glu Met Phe Thr
450 455 460

Ala Ile Gly Leu Leu Glu Phe Phe Tyr Lys Gln Ser Leu Lys Gly Met
465 470 475 480

Gln Ala Phe Phe Thr Ala Ile Thr Tyr Cys Ser Tyr Ser Phe Gly Phe
485 490 495

Tyr Leu Ser Thr Val Leu Val Ser Leu Val Asn Lys Ile Thr Ser Thr
500 505 510

Ser Ser Ser Gly Gly Trp Leu His Tyr Asn Asn Leu Asn Gln Asp Arg
515 520 525

Leu Asp Leu Phe Tyr Trp Met Leu Ala Val Leu Ser Phe Phe Asn Phe
530 535 540

Leu Ser Tyr Val Phe Cys Ser Thr Arg Tyr Ser His Ala Pro Ser Ser
545 550 555 560

Leu Pro Gln Pro Asn Ser Lys Glu Ile Asn Pro Tyr Ser Gly Asp Asp
565 570 575

Asn Ile Pro

<210> 1040
<211> 334
<212> PRT
<213> Soja

<400> 1040

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Arg Leu Leu Ala Ile Ser Thr Val Lys Ser Leu Lys Ile Lys Leu Leu
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Leu Phe Cys Cys Val Ala Phe Thr Leu Leu Ala Phe Ser Thr Ser Ala
35 40 45

Ser Ser Phe Val Leu Trp Ile Asn Asn Gln Thr Pro Pro Pro Pro Pro
50 55 60

Pro Arg Phe Pro Asp Ser Gly Lys Gly Tyr Ser Ile Val Met Asn Thr
65 70 75 80

Trp Lys Arg Tyr Asp Leu Leu Lys Gln Ser Ile Lys His Tyr Ser Ser
85 90 95

Cys Pro Arg Leu Glu Ser Val His Ile Val Trp Ser Glu Pro Asp Pro
100 105 110

Pro Ser Asp Ile Leu Leu Lys Phe Leu His His Val Val Lys Ser Lys
115 120 125

Ser Lys Asp Gly Arg Tyr Val Lys Leu Arg Phe Asp Ile Asn Lys Glu
130 135 140

Asp Ser Leu Asn Asn Arg Phe Lys Glu Ile Lys Asp Leu Glu Thr Asp
145 150 155 160

Ala Val Phe Ser Ile Asp Asp Asp Val Ile Phe Pro Cys Ser Thr Val
165 170 175

Glu Phe Ala Phe Asp Val Trp Gln Ser Ala Pro Asp Thr Met Val Gly
180 185 190

Phe Val Pro Arg Val His Trp Val Asp Ser Leu Glu Gly Asn Asp Ser
195 200 205

Lys Phe Ile Tyr Gly Gly Trp Trp Ser Val Trp Trp Thr Gly Thr Tyr
210 215 220

Ser Met Val Leu Ser Lys Ala Ala Phe Phe His Lys Lys Tyr Phe Asn
225 230 235 240

Ile Tyr Thr Asn Glu Met Pro Ser Ser Ile Arg Glu Tyr Val Thr Lys
245 250 255

Asn Arg Asn Cys Glu Asp Ile Ala Met Ser Phe Leu Val Ala Asn Ala
260 265 270

Thr Gly Ala Pro Pro Ile Trp Val Lys Gly Lys Ile Leu Glu Ile Gly
275 280 285

Ser Thr Gly Ile Ser Ser Leu Gly Gly His Ser Glu Arg Arg Thr Glu
290 295 300

Cys Val Asn Arg Phe Val Ala Ala Tyr Gly Arg Met Pro Leu Val Ser
305 310 315 320

Thr Ser Val Lys Ala Val Asp Ser Arg Asn Ile Trp Phe Trp
325 330

<210> 1041
<211> 329
<212> PRT
<213> Guandú

<400> 1041

Met Arg Gly Ser Cys Trp Asn Arg Arg Thr Glu Gln Arg Phe Arg His
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Leu Ala Ile Ser Thr Val Lys Ser Val Lys Ile Lys Ile Leu Leu Cys
20 25 30

Cys Cys Val Ala Phe Thr Leu Leu Ala Phe Ser Thr Ser Ala Ser Ser
35 40 45

Phe Ile Leu Trp Asn Asn Gln Thr Pro Pro Pro Pro Arg Phe Leu Asp
50 55 60

Ser Arg Lys Gly Tyr Ser Ile Val Met Asn Thr Trp Lys Arg Tyr Asp
65 70 75 80

Leu Leu Lys Gln Ser Ile Lys His Tyr Ser Ser Cys Pro Arg Leu Glu
85 90 95

Ser Val His Ile Val Trp Ser Glu Pro Asp Pro Pro Ser Asp Val Leu
100 105 110

Leu Lys Tyr Leu His His Val Val Lys Ser Lys Ser Lys Asp Gly Arg
115 120 125

Leu Val Lys Leu Lys Phe Asp Ile Asn Lys Glu Asp Ser Leu Asn Asn
130 135 140

Arg Phe Lys Glu Ile Lys Asp Leu Glu Thr Asp Ala Val Phe Ser Ile
145 150 155 160

Asp Asp Asp Val Ile Phe Pro Cys Ser Ser Val Glu Phe Ala Phe Asp
165 170 175

Val Trp Gln Ser Ala Pro Asp Thr Met Val Gly Phe Val Pro Arg Val
180 185 190

His Trp Met Asp Ser Leu Glu Gly Asn Ser Asn Lys Phe Ile Tyr Gly
195 200 205

Gly Trp Trp Ser Val Trp Trp Thr Gly Thr Tyr Ser Met Val Leu Ser
210 215 220

Lys Ala Ala Phe Phe His Lys Lys Tyr Phe Asn Ile Tyr Thr Lys Glu
225 230 235 240

Met Pro Ser Ser Ile Arg Glu Tyr Val Thr Lys Asn Arg Asn Cys Glu
245 250 255

Asp Ile Ala Met Ser Phe Leu Val Ala Asn Ala Thr Gly Ala Pro Pro
260 265 270

Ile Trp Val Lys Gly Lys Ile Phe Glu Ile Gly Ser Thr Gly Ile Ser
275 280 285

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

Ala Ala Val Tyr Gly Gly Met Pro Leu Val Ser Thr Ser Val Lys Ala
305 310 315 320

Val Asp Ser Arg Asn Ile Trp Phe Trp
325

<210> 1042
<211> 331
<212> PRT
<213> Poroto

<400> 1042

Met Arg Gly Ser Cys Cys Gly Trp Asn Arg Arg Thr Glu Gln Arg Phe
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Arg Leu Leu Ala Ile Ser Thr Val Lys Ser Val Lys Ile Lys Leu Leu
20 25 30

Leu Cys Cys Cys Val Ala Leu Thr Leu Leu Ala Phe Ser Thr Ser Ala
35 40 45

Ser Ser Phe Val Leu Trp Asn Asn Gln Thr Pro Leu Pro Pro Leu Leu
50 55 60

Ser Asp Ser Arg Arg Gly Tyr Ser Ile Val Met Asn Thr Trp Lys Arg

65 70 75 80

Tyr Asp Leu Leu Lys Gln Ser Ile Lys His Tyr Ser Ser Cys Pro Arg
85 90 95

Leu Glu Ser Val His Ile Val Trp Ser Glu Pro Asn Pro Pro Ser Asp
100 105 110

Ile Leu Leu Lys Phe Leu His His Val Val Lys Ser Lys Pro Lys Asp
115 120 125

Gly Arg Gln Val Lys Leu Arg Phe Asp Ile Asn Lys Glu Asp Ser Leu
130 135 140

Asn Asn Arg Phe Lys Glu Ile Lys Asp Leu Glu Thr Asp Ala Val Phe
145 150 155 160

Ser Ile Asp Asp Asp Val Ile Phe Pro Cys Ser Ser Val Glu Phe Ala
165 170 175

Phe Asp Val Trp Gln Ser Ala Pro Asp Thr Met Val Gly Phe Val Pro
180 185 190

Arg Val His Trp Leu Asp Ser Leu Lys Asp Asn Asp Asp Lys Phe Ser
195 200 205

Tyr Gly Gly Trp Trp Ser Val Trp Trp Thr Gly Thr Tyr Ser Met Val

210 215 220

Leu Ser Lys Ala Ala Phe Phe His Lys Lys Tyr Phe Asn Ile Tyr Thr
225 230 235 240

Asn Glu Met Pro Ser Ser Ile Arg Glu Tyr Ile Thr Lys Asn Arg Asn
245 250 255

Cys Glu Asp Ile Ala Met Ser Phe Leu Val Ala Asn Ala Thr Gly Ala
260 265 270

Pro Pro Ile Trp Val Lys Gly Lys Ile Phe Glu Ile Gly Ser Thr Gly
275 280 285

Ile Ser Ser Leu Gly Gly His Ser Glu Arg Arg Thr Glu Cys Val Asn
290 295 300

Arg Phe Ala Ala Val Tyr Gly Arg Met Pro Leu Val Ser Thr Ser Val
305 310 315 320

Lys Ala Val Asp Ser Arg Asn Ile Trp Phe Trp
325 330

<210> 1043
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<212> PRT
<213> Garbanzo

<400> 1043

Met Arg Gly Ser Cys Trp Leu Asn Arg Arg Ile Glu Gln Arg Phe Arg
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Leu Leu Ala Ile Ser Thr Val Lys Ser Val Lys Ile Lys Leu Leu Leu
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Cys Cys Cys Val Ala Leu Thr Leu Leu Ala Phe Ser Thr Ser Gly Ser
35 40 45

Thr Phe Leu Leu Trp Asn Asn Gln Thr Ser Ser Leu Arg Arg Phe Pro
50 55 60

Asp Ser Arg Lys Gly Tyr Ser Ile Val Met Asn Thr Trp Lys Arg Tyr
65 70 75 80

Asp Leu Leu Lys Gln Ser Ile Lys His Tyr Ser Ser Cys Pro Arg Leu
85 90 95

Glu Ser Val His Ile Val Trp Ser Glu Pro Asn Pro Pro Ser Glu Ser
100 105 110

Leu Leu Lys Phe Leu His Gln Ala Val Lys Ser Lys Ala Arg Asp Gly
115 120 125

Gln Tyr Val Lys Leu Arg Phe Asp Ile Asn Lys Glu Asp Ser Leu Asn
130 135 140

Asn Arg Phe Lys Glu Ile Asp Asp Leu Glu Thr Asp Ala Val Phe Ser
145 150 155 160

Ile Asp Asp Asp Val Ile Phe Pro Cys Ser Ser Val Glu Phe Ala Phe
165 170 175

Asp Val Trp Gln Ser Ala Pro Asp Ala Met Val Gly Phe Val Pro Arg
180 185 190

Val His Trp Val Asp Ser Leu Asn Gly Asn Asp Asn Val Phe Lys Tyr
195 200 205

Gly Gly Trp Trp Ser Val Trp Trp Thr Gly Thr Tyr Ser Met Val Leu
210 215 220

Ser Lys Ala Ala Phe Phe His Lys Lys Tyr Phe Ile Leu Tyr Thr Asn
225 230 235 240

Glu Met Pro Ser Ser Ile Arg Glu Tyr Val Thr Lys Asn Arg Asn Cys
245 250 255

Glu Asp Ile Ala Met Ser Phe Leu Val Ala Asn Ala Thr Gly Ala Pro
260 265 270

Pro Leu Trp Val Lys Gly Lys Ile Phe Glu Ile Gly Ser Thr Gly Ile
275 280 285

Ser Ser Leu Gly Gly His Ser Glu Arg Arg Ser Glu Cys Val Asn Ile
290 295 300

Phe Thr Ala Val Tyr Gly Arg Met Pro Leu Val Tyr Thr Ser Val Lys
305 310 315 320

Ala Val Asp Ser Arg Asn Thr Trp Phe Trp
325 330

<210> 1044
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<213> Medicago

<400> 1044

Met Arg Gly Ser Cys Trp Leu Asn Arg Arg Ile Glu Gln Arg Phe Arg
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Leu Leu Ala Ile Ser Thr Val Lys Ser Ala Lys Ile Lys Leu Leu Leu
20 25 30

Phe Cys Cys Val Ala Leu Thr Leu Leu Ala Phe Ser Ser Thr Gly Ser
35 40 45

Ser Phe Leu Leu Trp Asn Asn Thr Asn Gln Thr Pro Gln Ile Pro Ser
50 55 60

Phe Thr Asp Ser Arg Lys Gly Tyr Ser Ile Val Met Asn Thr Trp Lys
65 70 75 80

Arg Tyr Asp Leu Leu Lys Gln Ser Ile Lys His Tyr Ser Ser Cys Pro
85 90 95

Arg Leu Glu Ser Val His Ile Val Trp Ser Glu Pro Asn Pro Pro Ser
100 105 110

Glu Ser Leu Leu Lys Tyr Leu His His Val Val Lys Ser Lys Ser Arg
115 120 125

Asp Gly Arg Tyr Val Lys Leu Arg Phe Asp Ile Asn Thr Glu Asp Ser
130 135 140

Leu Asn Asn Arg Phe Lys Glu Ile Lys Asp Leu Glu Thr Asp Ala Val
145 150 155 160

Phe Ser Ile Asp Asp Asp Val Ile Phe Pro Cys Ser Ser Val Glu Phe
165 170 175

Ala Phe Asp Val Trp Gln Ser Ala Pro Asp Ala Met Val Gly Phe Val
180 185 190

Pro Arg Val His Trp Val Asp Ser Leu Asn Gly Asp Ser Asn Lys Phe
195 200 205

Arg Tyr Gly Gly Trp Trp Ser Val Trp Trp Thr Gly Thr Tyr Ser Met
210 215 220

Val Leu Ser Lys Ala Ala Phe Phe His Lys Lys Tyr Phe Ser Leu Tyr
225 230 235 240

Thr Asn Glu Met Pro Ser Ser Ile Arg Glu Phe Val Thr Lys Asn Arg
245 250 255

Asn Cys Glu Asp Ile Ala Met Ser Phe Leu Val Ala Asn Ala Thr Gly
260 265 270

Ala Pro Pro Leu Trp Val Lys Gly Lys Ile Tyr Glu Ile Gly Ser Thr
275 280 285

Gly Ile Ser Ser Leu Gly Gly His Ser Glu Arg Arg Ser Asp Cys Val
290 295 300

Asn Ile Phe Thr Ser Val Tyr Gly Arg Met Pro Leu Val Tyr Thr Ser
305 310 315 320

Val Lys Ala Val Asp Ser Arg Asn Val Trp Phe Trp
325 330

<210> 1045
<211> 257
<212> PRT

<213> Maní

<400> 1045

Met Asn Thr Trp Lys Arg Tyr Asp Leu Leu Lys Gln Ser Ile Lys His
1 5 10 15

Tyr Ser Ser Cys Pro Arg Leu Asp Ser Val His Ile Val Trp Ser Glu
20 25 30

Pro Asp Pro Pro Ser Asp Ser Leu Leu Lys Tyr Leu Tyr His Val Val
35 40 45

Lys Ser Val Pro Lys Asp Gly His Gln Val Lys Leu Lys Phe Asp Ile
50 55 60

Asn Lys Glu Asp Ser Leu Asn Asn Arg Phe Lys Glu Ile Lys Asp Leu
65 70 75 80

Glu Ser Asp Ala Val Phe Ser Ile Asp Asp Asp Val Ile Phe Pro Cys
85 90 95

Ser Ser Val Glu Phe Ala Phe Asp Val Trp Gln Ser Ala Pro Asp Thr
100 105 110

Met Val Gly Phe Val Pro Arg Val His Trp Val Asp Tyr Ser Lys Gly
115 120 125

Gly Gly Ser Lys Phe Lys Tyr Gly Gly Trp Trp Ser Val Trp Trp Thr
130 135 140

Gly Thr Tyr Ser Met Val Leu Ser Lys Ala Ala Phe Phe His Lys Lys
145 150 155 160

Tyr Phe Ile Leu Tyr Thr Asn Gln Met Pro Thr Ser Leu Lys Glu Tyr
165 170 175

Ile Thr Lys Asn Arg Asn Cys Glu Asp Ile Ala Met Ser Phe Leu Val
180 185 190

Ala Asn Ala Thr Gly Ala Pro Pro Ile Trp Val Lys Gly Lys Ile Phe
195 200 205

Glu Ile Gly Ser Thr Gly Ile Ser Ser Leu Gly Gly His Ser Glu Lys
210 215 220

Arg Ser Glu Cys Val Asn Arg Phe Ala Ser Val Phe Gly Arg Met Pro
225 230 235 240

Leu Val Ser Thr Ser Val Lys Ala Val Asp Ser Arg Asn Ile Trp Phe
245 250 255

Trp

<210> 1046
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<212> PRT
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<400> 1046

Met Arg Gly Ser Trp Phe Leu Lys Arg Arg Pro Glu Gln Arg Phe Arg
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Leu Leu Ala Ala Ser Ala Val Lys Ser Ala Arg Ile Asn Leu Leu Leu
20 25 30

Cys Cys Cys Ile Ala Leu Val Leu Ile Val Leu Ala Thr Thr Ile Ser
35 40 45

Thr Phe Val Val Phe Ser Asp Phe Pro Pro Ser Leu Pro Arg Ser His
50 55 60

Ala Ser Gly Lys Gly Tyr Ser Ile Val Met Asn Thr Trp Lys Arg Tyr
65 70 75 80

Asp Leu Leu Lys Gln Ser Ile Ala His Tyr Ser Ser Cys Pro Arg Leu
85 90 95

Glu Ser Val His Ile Val Trp Ser Glu Pro Asp Pro Pro Ser Asp Asp
100 105 110

Leu Leu Lys Phe Leu Leu His Ala Ile Gln Ser Lys Ser Ile Asp Arg

115 120 125

Arg Gln Val Lys Leu Lys Ile Asp Ile Asn Lys Glu Asp Ser Leu Asn
130 135 140

Asn Arg Phe Lys Val Ile Lys Asp Leu Glu Thr Asp Ala Val Phe Ser
145 150 155 160

Ile Asp Asp Asp Val Ile Phe Pro Cys Ser Ser Val Glu Phe Ala Phe
165 170 175

Asp Val Trp Gln Ser Ala Pro Asp Thr Met Val Gly Phe Val Pro Arg
180 185 190

Ala His Trp Leu Asp Ser Ser Glu Ser Gly Gly Ile Lys Phe Arg Tyr
195 200 205

Ala Gly Trp Trp Ser Val Trp Trp Thr Gly Thr Tyr Ser Met Val Leu
210 215 220

Ser Lys Ala Ala Phe Phe His Lys Lys Tyr Phe Ser Val Tyr Thr Asn
225 230 235 240

Glu Met Pro Ala Ser Ile Arg Glu Tyr Val Thr His Asn Arg Asn Cys
245 250 255

Glu Asp Ile Ala Met Ser Phe Leu Val Ala Asn Ala Thr Asp Ala Pro

260 265 270

Pro Ile Trp Val Gln Gly Lys Ile Phe Glu Ile Gly Ser Thr Gly Ile
275 280 285

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

Phe Thr Ala Val Tyr Gly Arg Met Pro Leu Val Ser Thr Ser Val Lys
305 310 315 320

Ala Val Asp Ser Arg Asn Ile Trp Phe Trp
325 330

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<212> ADN
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<400> 662
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cgaaccggtt ttggtttttt ttttatttag attttgttgt tattagcggc ggtgatgaga 360

gggagctgtt ggttgaaccg tcggattgaa cagaggtttc ggttacttgc gatctccacc 420

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<210> 663
<211> 1507
<212> ADN
<213> Maní

<400> 663
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<210> 664
<211> 1684
<212> ADN
<213> Maní

<400> 664
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cggagcagag gttccggttg ctggcggctt ccgccgtcaa atctgccagg atcaacctcc 360

tcctctgctg ttgtattgct ttggtgctca tcgtactcgc caccaccatt tccaccttcg 420

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<210> 665
<211> 200
<212> PRT
<213> Soja

<400> 665

Met Ser Phe Ile Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Asp Gln Leu Ser Ala Asp Gly Thr Ala Tyr His Lys
20 25 30

Ala Cys Phe Arg Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Ser Gly Ser Phe Ser Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Leu Ala Asp Lys Thr Thr His Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Ser Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Gly Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Thr Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Thr Lys Ser
165 170 175

Ala Ser Val Lys Arg Ala Ala Ala Ala Ala Ala Thr Ala Thr Ala Thr
180 185 190

Thr Val Ala Ser Val Pro Glu Ser
195 200

<210> 666
<211> 194
<212> PRT
<213> Poroto

<400> 666

Met Ser Phe Ile Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Asp Gln Leu Ser Ala Asp Gly Thr Ala Tyr His Lys
20 25 30

Ala Cys Phe Arg Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Tyr Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Thr Phe Ser Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Leu Ala Asp Lys Thr Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Ser Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Gly Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Thr Pro

130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Thr Lys Ser
165 170 175

Ala Ser Ile Lys Arg Ala Ala Ala Ala Ala Ala Ala Ala Thr Val Pro
180 185 190

Glu Ser

<210> 667
<211> 193
<212> PRT
<213> Chícharo salvaje

<400> 667

Met Ser Phe Ile Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Asp Gln Leu Ser Ala Asp Gly Thr Ala Tyr His Lys
20 25 30

Ala Cys Phe Arg Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Tyr Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Thr Phe Ser Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Leu Ala Asp Lys Thr Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Ser Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Gly Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Thr Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Thr Lys Ser
165 170 175

Ala Ser Ile Lys Arg Ala Ala Ala Ala Ala Ala Ala Thr Val Pro Glu
180 185 190

Ser

<210> 668
<211> 190
<212> PRT
<213> Guandú

<400> 668

Met Ser Phe Ile Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Asp Gln Leu Ser Ala Asp Gly Thr Ala Tyr His Lys
20 25 30

Ala Cys Phe Arg Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Tyr Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Thr Phe Ser Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Leu Ala Asp Lys Thr Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Ser Met Phe Ser Gly Thr Gln Asp Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Gly Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Thr Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Ile Lys Arg Ala Ala Ala Ala Ser Val Pro Glu Ser
180 185 190

<210> 669
<211> 189
<212> PRT
<213> Lotus

<400> 669

Met Ser Phe Leu Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Asp Gln Leu Ser Ala Asp Gly Thr Ser Tyr His Lys
20 25 30

Ala Cys Phe Arg Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Tyr Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Thr Phe Lys Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Leu Ala Asp Lys Asn Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Ser Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Thr Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Ile Lys Arg Ala Ala Ala Ser Val Pro Glu Ser
180 185

<210> 670
<211> 189
<212> PRT
<213> Garbanzo

<400> 670

Met Ser Phe Ile Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Asp Gln Leu Ser Ala Asp Gly Thr Ser Tyr His Lys
20 25 30

Ala Cys Phe Arg Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Ser
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Tyr Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Thr Phe Lys Lys Asn Phe Thr Ser Pro Ala
65 70 75 80

Lys Leu Ala Asp Lys Thr Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys

85 90 95

Ala Ala Ser Met Phe Ser Gly Thr Gln Asp Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Ser Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Thr Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Ile Lys Arg Ala Ala Thr Ser Val Pro Glu Ser
180 185

<210> 671
<211> 189
<212> PRT
<213> Maní

<400> 671

Met Ser Phe Ile Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Asp Gln Leu Ser Ala Asp Gly Thr Ala Tyr His Lys
20 25 30

Ala Cys Phe Arg Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Tyr Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Ser Phe Thr Lys Asn Phe Gln Ser Ser Ala
65 70 75 80

Lys Leu Ala Asp Lys Ala Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Ser Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Gly Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Thr Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Val Lys Ser
165 170 175

Ala Ser Ile Lys Arg Ala Ala Thr Ser Val Pro Asp Ser
180 185

<210> 672
<211> 191
<212> PRT
<213> Medicago

<400> 672

Met Ser Phe Ile Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Asp Gln Leu Ser Ala Asp Gly Thr Ser Tyr His Lys
20 25 30

Ala Cys Phe Arg Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Ser
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu His Gly Asn Phe Ser Lys Asn Lys Asn Phe Gln Ser
65 70 75 80

Pro Ala Lys Val Ala Asp Gly Thr Thr Pro Val Leu Thr Arg Thr Pro
85 90 95

Ser Lys Ala Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr
100 105 110

Cys Gly Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Ser Gln
115 120 125

Ala Tyr His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile
130 135 140

Thr Pro Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His
145 150 155 160

His Phe Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile
165 170 175

Lys Ser Ala Ser Ile Lys Arg Ala Ala Ala Ser Val Pro Glu Ser
180 185 190

<210> 673
<211> 191
<212> PRT
<213> Trigonella

<400> 673

Met Ser Phe Ile Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Asp Gln Leu Ser Ala Asp Gly Thr Ser Tyr His Lys
20 25 30

Ala Cys Phe Arg Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu His Gly Asn Phe Ser Lys Asn Lys Asn Phe Gln Ser
65 70 75 80

Pro Ala Lys Val Ala Asp Ser Thr Thr Pro Val Leu Thr Arg Thr Pro
85 90 95

Ser Lys Ala Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr
100 105 110

Cys Gly Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Ser Gln
115 120 125

Ser Tyr His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile
130 135 140

Thr Pro Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His
145 150 155 160

His Phe Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile
165 170 175

Lys Ser Ala Ser Ile Lys Arg Ala Ala Ala Ser Val Pro Glu Ser
180 185 190

<210> 674
<211> 199
<212> PRT
<213> Manzana

<400> 674

Met Ser Phe Ile Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Glu Leu Ser Ala Asp Gly Ile Ser Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Thr His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala

65 70 75 80

Lys Ser Ala Glu Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Ser Met Phe Ser Gly Thr Gln Asp Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Ser Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Thr Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Ile Lys Arg Thr Ala Ala Ala Ala Ala Ala Ala Thr Ala Ala
180 185 190

Val Ala Ser Ile Pro Glu Ala
195

<210> 675

<211> 192
<212> PRT
<213> Prunus

<400> 675

Met Ser Phe Ile Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Glu Leu Ser Ala Asp Gly Val Ser Tyr His Lys
20 25 30

Ala Cys Phe Lys Cys Thr His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Glu Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Ser Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Ser Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Thr Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Ile Lys Arg Ala Ala Ala Ala Ala Ala Ser Ile Pro Glu Ala
180 185 190

<210> 676
<211> 200
<212> PRT
<213> Manzana

<400> 676

Met Ser Phe Ile Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Glu Leu Ser Ala Asp Gly Ile Ser Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Thr His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Ala Lys Ser Ala Glu Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser
85 90 95

Lys Ala Ala Ser Met Phe Ser Gly Thr Gln Asp Lys Cys Ala Thr Cys
100 105 110

Gly Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Ser Gln Ala
115 120 125

Tyr His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Thr
130 135 140

Pro Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His
145 150 155 160

Phe Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys
165 170 175

Ser Ala Ser Ile Lys Arg Thr Ala Ala Ala Ala Ala Ala Ala Ala Ala
180 185 190

Thr Val Ala Ser Ile Pro Glu Ala
195 200

<210> 677
<211> 189
<212> PRT
<213> Soja

<400> 677

Met Ser Phe Ile Gly Thr Gln Gln Lys Cys Glu Ala Cys Asp Lys Thr
1 5 10 15

Val Tyr Pro Val Asp Gln Leu Ser Ala Asp Gly Thr Ala Tyr His Lys
20 25 30

Ala Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Tyr Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Ser Phe Lys Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Gln Ala Val Lys Thr Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Ser Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Gly Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Ser Cys Pro Ile Thr Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Val Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Ile Lys Arg Glu Ala Asn Ser Val Pro Gln Ala
180 185

<210> 678
<211> 191
<212> PRT
<213> Nueces

<400> 678

Met Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Val Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Gln Leu Ser Ala Asp Gly Val Val Tyr His Lys

20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Glu Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Ser Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Ser Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Thr Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser

165 170 175

Ala Ser Ile Lys Arg Ala Ala Ala Ala Ala Ser Ile Pro Glu Ala
180 185 190

<210> 679
<211> 200
<212> PRT
<213> Fresa

<400> 679

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

Val Tyr Pro Val Glu Glu Leu Ser Ala Asp Gly Ile Ser Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Thr His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Glu Lys Leu Thr Pro Glu Met Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Ser Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Thr Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Ile Lys Arg Ala Ala Ala Ala Thr Ala Thr Ala Ala Ala Ala
180 185 190

Ala Val Ala Ser Ile Pro Glu Ala
195 200

<210> 680
<211> 189
<212> PRT
<213> Castaño, roble

<400> 680

Met Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Val Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Gln Leu Ser Ala Asp Gly Val Val Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Ser Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Glu Lys Leu Ser Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Ser Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Ser Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Thr Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Met Lys Arg Ala Ala Ala Ser Thr Pro Glu Ala
180 185

<210> 681
<211> 201
<212> PRT
<213> Centaurea, Cirsium

<400> 681

Met Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Gly Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Ile Asp Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Ser Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ala Ala Asp Lys Ser Ser Pro Met Leu Thr Lys Ser Pro Ser Lys
85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Asn Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Ile Lys Arg Ser Ala Ala Ala Ala Thr Ala Ala Ala Ala Ser
180 185 190

Pro Thr Thr Ala Ser Ile Pro Glu Val
195 200

<210> 682
<211> 199
<212> PRT
<213> Ambrosia

<400> 682

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

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Ile Asp Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Ser Gly Asn Phe Asn Lys Asn Phe Thr Ser Pro Ala
65 70 75 80

Lys Ala Ala Asp Lys Leu Ser Pro Met Leu Thr Lys Ser Pro Ser Lys
85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Asn Gln Ala Tyr

115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Glu Ser
165 170 175

Ala Ser Ile Lys Arg Thr Ala Ala Ala Thr Ala Ala Ala Ala Thr Pro
180 185 190

Glu Ala Ala Ser Ile Pro Glu
195

<210> 683
<211> 199
<212> PRT
<213> Lechuga

<400> 683

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

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Val Asp Tyr His Lys
20 25 30

Ser Cys Phe Arg Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Asp Gln
50 55 60

Leu Phe Lys Glu Ser Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Arg Phe Ala Glu Asn Leu Thr Pro His Leu Thr Lys Ser Pro Ser Lys
85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Asn Glu Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Val Lys Arg Ser Ala Ala Ala Thr Ala Ala Ala Ala Val Ala
180 185 190

Ala Thr Ala Val Pro Glu Ala
195

<210> 684
<211> 190
<212> PRT
<213> Tripterygium

<400> 684

Met Ser Phe Ile Gly Thr Gln Glu Lys Cys Lys Ala Cys Gln Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Val Asn Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Thr His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Glu Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Ser Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Asn
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Gly Gln Ser Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Ile Lys Arg Ala Ala Ala Ala Ser Val Pro Glu Ala
180 185 190

<210> 685
<211> 200
<212> PRT
<213> Ambrosia

<400> 685

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

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Ile Asp Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Ser Gly Asn Phe Asn Lys Asn Phe Thr Ser Pro Ala
65 70 75 80

Lys Ala Ala Asp Lys Leu Ser Pro Met Leu Thr Lys Ser Pro Ser Lys
85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Asn Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Ile Lys Arg Thr Ala Ala Ala Thr Ala Ala Ala Ala Ala Thr
180 185 190

Pro Glu Ala Ala Ser Ile Pro Glu
195 200

<210> 686
<211> 201
<212> PRT
<213> Cirsium

<400> 686

Met Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Gly Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Ile Asp Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln

50 55 60

Leu Phe Lys Glu Ser Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Thr Ala Glu Lys Ser Ser Pro Met Leu Thr Lys Ser Pro Ser Lys
85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Asn Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Ile Lys Arg Ser Ala Ala Ala Ala Thr Ala Ala Ala Ala Ser
180 185 190

Pro Thr Thr Ala Ser Ile Pro Glu Val

195 200

<210> 687
<211> 200
<212> PRT
<213> Cynara

<400> 687

Met Pro Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Gly Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Ile Asp Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Ser Gly Asn Phe Asp Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ala Ala Glu Lys Ser Ser Pro Met Leu Thr Lys Ser Pro Ser Lys
85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Asn Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Ile Lys Arg Ser Ala Ala Ala Ala Thr Ala Ala Ala Ala Pro
180 185 190

Thr Thr Ala Ser Ile Pro Glu Val
195 200

<210> 688
<211> 198
<212> PRT
<213> Guizotia

<400> 688

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

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Ile Asp Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Ser Gly Asn Phe Asn Lys Asn Phe Thr Ser Pro Ala
65 70 75 80

Lys Ala Ala Glu Lys Leu Ser Pro Met Leu Thr Lys Ser Pro Ser Lys
85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Asp Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Asn Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Val Lys Arg Thr Ala Ala Thr Thr Ala Ala Ala Ala Ala Ala
180 185 190

Ala Ala Ser Ile Pro Glu
195

<210> 689
<211> 189
<212> PRT
<213> Haya

<400> 689

Met Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Val Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Gln Leu Ser Ala Asp Gly Val Val Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Ser Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Glu Lys Leu Thr Pro Glu Met Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Ser Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Ser Gln Ser Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Thr Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Leu Lys Arg Ala Ala Ala Ser Val Pro Glu Ala
180 185

<210> 690
<211> 189
<212> PRT
<213> Gossypium raimondii

<400> 690

Met Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Ile Pro Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Gly Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Val Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Ser Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Glu Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Ser Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Gly Gln Ser Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Thr Pro

130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Ile Lys Arg Ala Ala Ala Ser Val Pro Glu Ala
180 185

<210> 691
<211> 190
<212> PRT
<213> Tripterygium

<400> 691

Met Ser Phe Ile Gly Thr Gln Glu Lys Cys Lys Ala Cys Gln Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Val Asn Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Thr His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Glu Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Asn
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Gly Gln Ser Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Ile Lys Arg Ala Ala Ala Ala Ser Val Pro Glu Ala
180 185 190

<210> 692
<211> 201

<212> PRT
<213> Arnica

<400> 692

Met Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Gly Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Ile Asp Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Ser Gly Asn Phe Asn Lys Asn Phe Thr Ser Pro Ala
65 70 75 80

Lys Ala Ala Glu Lys Leu Ser Pro Met Leu Thr Lys Ser Pro Ser Lys
85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Asn Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Ile Lys Arg Ala Ala Ala Thr Ala Ala Ala Ala Ala Thr Ala
180 185 190

Thr Ala Thr Ala Ala Ser Ile Pro Glu
195 200

<210> 693
<211> 201
<212> PRT
<213> Diente de león

<400> 693

Met Ser Phe Met Gly Thr Gln Gln Lys Cys Lys Ala Cys Gly Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Ile Asp Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Tyr Lys Glu Ser Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Thr Val Asp Lys Ser Ser Pro Met Leu Thr Lys Ser Pro Ser Lys
85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Asn Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Ile Lys Arg Ser Ala Ala Ala Ala Thr Ala Ala Ala Ala Ser
180 185 190

Ala Ala Val Ala Ser Ile Pro Glu Ala
195 200

<210> 694
<211> 199
<212> PRT
<213> Girasol

<400> 694

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

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Ile Asp Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Ser Gly Asn Phe Asn Lys Asn Phe Thr Ser Pro Ala
65 70 75 80

Lys Ala Ala Glu Lys Leu Ser Pro Met Leu Thr Lys Ser Pro Ser Lys

85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Asp Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Asn Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Ile Lys Arg Thr Ala Ala Ala Ala Ala Ala Ala Ala Thr Pro
180 185 190

Asp Ala Ala Ser Ile Pro Glu
195

<210> 695
<211> 189
<212> PRT
<213> Algodón

<400> 695

Met Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Gln Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Ile Pro Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Gly Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Val Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Ser Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Glu Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Ser Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Gly Gln Ser Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Thr Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Ile Lys Arg Ala Ala Ala Ser Val Pro Glu Ala
180 185

<210> 696
<211> 189
<212> PRT
<213> Algodón

<400> 696

Met Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Ile Pro Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Gly Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Val Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Ser Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Arg Ser Ala Glu Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Ser Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Gly Gln Ser Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Thr Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Ile Lys Arg Ala Ala Ala Ser Val Pro Glu Ala
180 185

<210> 697
<211> 189
<212> PRT

<213> Uva

<400> 697

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

Val Tyr Pro Val Glu Gln Leu Ser Ala Asp Gly Val Val Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Asn Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Ser Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Glu Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Ser Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Ser Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ala Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Met Lys Arg Ser Ala Ala Ser Val Pro Asp Ala
180 185

<210> 698
<211> 189
<212> PRT
<213> Kiwi

<220>
<221> misc_feature
<222> (183)..(183)
<223> Xaa puede ser cualquier aminoácido de origen natural

<220>
<221> misc_feature
<222> (186)..(186)
<223> Xaa puede ser cualquier aminoácido de origen natural

<400> 698

Met Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Val Ser Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Ser Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Asp Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Ser Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Ser Gln Ala Tyr
115 120 125

His Lys Thr Cys Phe Lys Cys Ser His Gly Gly Cys Ser Ile Thr Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Leu Lys Ser
165 170 175

Ala Ser Met Lys Arg Pro Xaa Ala Ser Xaa Pro Glu Ala
180 185

<210> 699
<211> 195
<212> PRT
<213> Sandía

<400> 699

Met Ser Phe Ile Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Asp Gln Leu Ser Ala Asp Gly Val Ala Phe His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Ile Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Asn Phe Ser Lys Asn Phe Leu Ser Pro Ala
65 70 75 80

Lys Ser Ser Glu Lys Pro Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Ser Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Ser Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Asp Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Met Lys Arg Gln Ala Ala Thr Ser Asp Leu Asp Pro Ser Lys
180 185 190

Val Glu Ser
195

<210> 700
<211> 197
<212> PRT

<213> Artemisia

<400> 700

Met Asn Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Gly Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Ile Asp Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Ser Gly Asn Phe Asn Lys Asn Phe Thr Ser Pro Ala
65 70 75 80

Lys Ala Ala Asp Ser Pro Met Leu Thr Lys Ser Pro Ser Lys Ala Ala
85 90 95

Gly Met Phe Ser Gly Thr Gln Asp Lys Cys Ala Thr Cys Gly Lys Thr
100 105 110

Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Asn Gln Ala Tyr His Lys
115 120 125

Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Ser Pro Ser Asn
130 135 140

Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe Ser Gln
145 150 155 160

Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser Ala Ser
165 170 175

Ile Lys Arg Asn Ala Ala Ala Thr Ala Ala Ala Ala Thr Ala Ala Ala
180 185 190

Ala Ser Ile Pro Glu
195

<210> 701
<211> 200
<212> PRT
<213> Lechuga

<400> 701

Met Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Gly Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Ile Asp Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn

35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Ser Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ala Ala Glu Lys Leu Ser Pro Met Leu Thr Lys Ser Pro Ser Lys
85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Asn Glu Ser Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Ile Lys Arg Ala Ser Ala Ala Ser Ala Ala Ala Ala Thr Ala

180 185 190

Ala Ala Ala Ser Ile Pro Glu Val
195 200

<210> 702
<211> 190
<212> PRT
<213> Cacao

<400> 702

Met Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Val Pro Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Gly Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Ala Lys Ser Ala Glu Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser
85 90 95

Lys Ala Ala Ser Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys
100 105 110

Gly Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Gly Gln Ser
115 120 125

Tyr His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Ser
130 135 140

Pro Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His
145 150 155 160

Phe Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys
165 170 175

Ser Ala Ser Ile Lys Arg Ala Ala Ala Ser Val Pro Glu Ala
180 185 190

<210> 703
<211> 198
<212> PRT
<213> Flaveria

<400> 703

Met Asn Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Gly Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Val Asp Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Ser Gly Asn Phe Asn Lys Asn Phe Thr Ser Pro Ala
65 70 75 80

Lys Ala Ala Glu Lys Leu Ser Pro Met Leu Thr Lys Ser Pro Ser Lys
85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Asn Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Ile Lys Arg Thr Ala Ala Thr Thr Ala Ala Ala Ala Ala Ala
180 185 190

Ala Ala Ser Ile Pro Glu
195

<210> 704
<211> 189
<212> PRT
<213> Eucalyptus

<400> 704

Met Ser Phe Thr Gly Thr Gln Val Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Gln Leu Ser Ala Asp Gly Val Ala Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Ser
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Asp Lys Leu Thr Pro Glu Leu Ala Arg Ser Pro Ser Lys
85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Asp Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Ser Gln Ser Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Thr Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Met Lys Arg Ala Ala Ala Ser Ile Pro Glu Ala
180 185

<210> 705
<211> 189
<212> PRT
<213> Ipomoea nil

<400> 705

Met Ser Phe Ile Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Ile Asn Tyr His Lys
20 25 30

Ser Cys Phe Arg Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Ser Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Asp Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Ser Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Asn Gln Ser Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Thr Pro

130 135 140

Ser Asn Tyr Ala Ala Leu Asp Gly Ile Leu Tyr Cys Lys Pro His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Val Lys Arg Pro Thr Thr Pro Val Pro Glu Ala
180 185

<210> 706
<211> 194
<212> PRT
<213> Lechuga

<400> 706

Met Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Gly Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Ile Asp Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Ser Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ala Ala Asp Lys Leu Ser Pro Met Leu Thr Lys Ser Pro Ser Lys
85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Asn Glu Ser Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Lys Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Ile Lys Arg Ser Ala Ala Ala Thr Ala Ala Ala Ser Ile Pro
180 185 190

Glu Val

<210> 707
<211> 198
<212> PRT
<213> Tragopogon

<400> 707

Met Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Gly Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Val Asp Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Ser Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Glu Lys Leu Ser Pro Met Leu Thr Lys Ser Pro Ser Lys
85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Asn Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Ile Lys Arg Ser Ala Ala Ala Ala Thr Ala Ala Ala Ala Val
180 185 190

Asp Ser Ile Pro Glu Val
195

<210> 708
<211> 199
<212> PRT
<213> Flaveria

<400> 708

Met Asn Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Gly Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Val Asp Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Ser Gly Asn Phe Asn Lys Asn Phe Thr Ser Pro Ala
65 70 75 80

Lys Ala Ala Glu Lys Leu Ser Pro Met Leu Thr Lys Ser Pro Ser Lys
85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Asn Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Ile Lys Arg Thr Ala Ala Thr Thr Thr Ala Ala Ala Ala Ala
180 185 190

Ala Ala Ala Ser Ile Pro Glu
195

<210> 709
<211> 85
<212> PRT
<213> Sarracenia

<400> 709

Met Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Val Ser Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Ile
35 40 45

Thr Pro Arg Trp Lys Val Phe Tyr Thr Ala Ser Leu Thr Leu Ser Ser
50 55 60

Ser Ser Arg Arg Pro Val Val Ser Thr Arg Ile Ser Asn His Leu Gln

65 70 75 80

Ser Gln Leu Lys Ser
85

<210> 710
<211> 210
<212> PRT
<213> Palma aceitera

<400> 710

Met Ala Phe Ser Gly Thr Gln Gln Lys Cys Lys Ala Cys Asn Lys Thr
1 5 10 15

Val Tyr Leu Met Asp Gln Leu Ser Ala Asp Gly Ile Ala Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Asn His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Leu Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Ser Phe Asn Lys Ser Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Glu Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Gly Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Glu Leu Gln Pro Ser His Gln Met
165 170 175

Cys Phe His Gln Ala His Ser Ser Ile His Pro Arg Ser Leu Ser Ser
180 185 190

Phe Cys Leu Leu Lys Trp Ile Phe Thr Gln Val Cys Asp Leu Ile Ile
195 200 205

Tyr Phe
210

<210> 711
<211> 139

<212> PRT
<213> Phlya

<400> 711

Met Glu Gly Val Leu Tyr Cys Lys Pro His Tyr Glu Gln Leu Phe Lys
1 5 10 15

Glu Thr Gly Ser Phe Thr Lys Asn Phe Gln Ser Pro Ala Lys Ser Ala
20 25 30

Glu Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys Ala Ala Gly
35 40 45

Met Phe Ser Gly Thr Gln Asp Lys Cys Ala Thr Cys Gly Lys Thr Ala
50 55 60

Tyr Pro Leu Glu Lys Val Thr Val Glu Ser Gln Ser Tyr His Lys Ser
65 70 75 80

Cys Phe Arg Cys Ser His Gly Gly Cys Ser Leu Asn Pro Ser Asn Tyr
85 90 95

Ala Ala Leu Asp Gly Ile Leu Tyr Cys Lys Pro His Phe Ser Gln Leu
100 105 110

Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser Ala Ser Met
115 120 125

Lys Arg Pro Thr Ala Ala Ala Val Pro Asp Ser
130 135

<210> 712
<211> 195
<212> PRT
<213> Momordica

<400> 712

Met Ser Phe Ile Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Asp Gln Leu Ser Ala Asp Gly Val Ala Phe His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Asn Phe Ser Lys Asn Phe Leu Ser Pro Ala
65 70 75 80

Lys Ser Thr Asp Lys Pro Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Ser Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Ser Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Asp Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Met Lys Arg Gln Ala Ala Thr Ser Val Pro Asp Ala Glu Asn
180 185 190

Val Glu Leu
195

<210> 713
<211> 189
<212> PRT
<213> Papaya

<400> 713

Met Ser Phe Ile Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr

1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Val Pro Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Thr His Cys Lys Gly Thr Leu Lys Leu Gly Asn
35 40 45

Tyr Ser Ser Met Glu Gly Ile Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Ser Phe Asn Lys Asn Phe Gln Ser Pro Val
65 70 75 80

Lys Ser Ala Glu Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Ser Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Gly Gln Ser Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe

145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Leu Lys Arg Ala Thr Ala Ser Val Pro Asp Ala
180 185

<210> 714
<211> 194
<212> PRT
<213> Senecio

<400> 714

Met Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Gly Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Val Asp Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Thr His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Ser Gly Asn Phe Asn Lys Asn Phe Thr Ser Pro Ala
65 70 75 80

Lys Asp Ala Asp Lys Leu Ser Pro Met Leu Thr Lys Ser Pro Ser Lys
85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Asp Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Asn Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Ile Lys Arg Asn Ala Ala Ala Thr Ala Ala Ala Ala Ala Ala
180 185 190

Ala Ala

<210> 715
<211> 200

<212> PRT
<213> Flaveria

<400> 715

Met Asn Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Gly Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Val Asp Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Ser Gly Asn Phe Asn Lys Asn Phe Thr Ser Pro Ala
65 70 75 80

Lys Ala Ala Glu Lys Leu Ser Pro Met Leu Thr Lys Ser Pro Ser Lys
85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Asn Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Ile Lys Arg Thr Ala Ala Ser Thr Thr Ala Ala Ala Ala Ala
180 185 190

Ala Ala Ala Ala Ser Ile Pro Glu
195 200

<210> 716
<211> 199
<212> PRT
<213> Centaurea

<400> 716

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

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Val Asp Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Thr His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Ser Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Glu Lys Leu Thr Pro Gln Leu Thr Lys Ser Gln Ser Lys
85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Asp Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Asn Glu Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Val Leu Ser
165 170 175

Ala Thr Ile Lys Arg Thr Ala Ala Ala Glu Ala Ala Ala Ala Ser Ala
180 185 190

Ala Ala Thr Val Pro Glu Val
195

<210> 717
<211> 188
<212> PRT
<213> Cártamo

<400> 717

Met Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Arg Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Ile Asp Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Ser Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ala Ala Asp Lys Pro Ser Pro Met Leu Thr Lys Ser Pro Ser Lys

85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Asn Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Ile Lys Arg Ser Ala Ala Ala Ala Thr Ala
180 185

<210> 718
<211> 172
<212> PRT
<213> Melón

<400> 718

Met Ser Phe Ile Gly Thr Gln Gln Lys Cys Lys Ala Cys Asp Lys Thr
1 5 10 15

Val Tyr Pro Val Asp Gln Leu Ser Ala Asp Gly Val Ser Phe His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Asp Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Asn Phe Ser Lys Asn Phe Leu Ser Pro Ala
65 70 75 80

Lys Ser Ser Glu Lys Pro Thr Pro Glu Leu Thr Arg Ser Pro Ser Arg
85 90 95

Ala Ala Ser Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Ser Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Arg Glu Ala Thr Thr Ile
165 170

<210> 719
<211> 192
<212> PRT
<213> Aguacate

<400> 719

Met Ala Phe Ser Gly Thr Gln Gln Lys Cys Lys Val Cys Asp Lys Thr
1 5 10 15

Val Tyr Val Val Asp Gln Leu Met Ala Asp Gly Ala Ala Tyr His Lys
20 25 30

Ser Cys Phe Arg Cys Asn His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Leu Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Ser Lys Lys Thr Gly Ser Phe Asn Lys Ser Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Glu Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Ser Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Arg Val Thr Val Glu Ser Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Thr Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Cys
165 170 175

Ala Ser Ile Lys Arg Thr Gly Ala Thr Ala Thr Pro Val Pro Glu Leu
180 185 190

<210> 720
<211> 189
<212> PRT
<213> Clementina, naranja

<400> 720

Met Ser Phe Ile Gly Thr Gln Gln Lys Cys Lys Val Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Gln Leu Ser Ala Asp Gly Val Val Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Ser Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Glu Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Ser Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Ser Cys Ser
100 105 110

Lys Thr Val Tyr Pro Leu Glu Lys Val Ala Val Glu Asn Gln Ala Tyr
115 120 125

His Lys Thr Cys Phe Lys Cys Ser His Gly Gly Cys Ser Ile Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Met Lys Arg Ala Ala Ala Ser Val Pro Glu Ala
180 185

<210> 721
<211> 189
<212> PRT
<213> Euonymus

<400> 721

Met Ser Phe Ile Gly Thr Gln Glu Lys Cys Lys Ala Cys Gln Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Val Asn Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Thr His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Glu Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys

85 90 95

Ala Ala Ser Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Asn
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Gly Gln Ser Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ala Ile Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Ile Lys Arg Ala Ala Ala Ser Val Pro Glu Ala
180 185

<210> 722
<211> 189
<212> PRT
<213> Nasturtium

<400> 722

Met Ser Phe Leu Gly Thr Gln Gln Lys Cys Lys Ala Cys Val Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Val Ser Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Thr His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Ser Gly Ser Phe Thr Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Asp Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Ser Gln Ser Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ala Leu Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Cys
165 170 175

Ala Ser Ile Lys Arg Ala Ala Ala Ser Val Pro Glu Ala
180 185

<210> 723
<211> 189
<212> PRT
<213> Álamo

<400> 723

Met Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Met Glu Leu Leu Ser Ala Asp Gly Val Ala Tyr His Lys
20 25 30

Thr Cys Phe Lys Cys Phe His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Glu Lys Leu Asn Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Ser Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Ser Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ala Ile Thr Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Val Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Thr Met Lys Arg Ala Ala Ala Ser Val Pro Glu Ala
180 185

<210> 724
<211> 201
<212> PRT
<213> Flaveria

<400> 724

Met Asn Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Gly Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Val Asp Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Ser Gly Asn Phe Asn Lys Asn Phe Thr Ser Pro Ala
65 70 75 80

Lys Ala Ala Glu Lys Leu Ser Pro Met Leu Thr Lys Ser Pro Ser Lys
85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Asn Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Ile Lys Arg Thr Ala Ala Thr Thr Thr Ala Ala Ala Ala Ala
180 185 190

Ala Ala Ala Ala Ala Ser Ile Pro Glu
195 200

<210> 725
<211> 201
<212> PRT
<213> Cirsium

<400> 725

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

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Val Asp Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln

50 55 60

Leu Phe Lys Glu Ser Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Glu Lys Leu Thr Pro Gln Leu Thr Lys Ser Gln Ser Lys
85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Asp Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Asn Glu Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Thr Ile Lys Arg Ser Ala Ala Ile Glu Ala Ala Ala Ala Ala Ala
180 185 190

Ala Ala Glu Thr Thr Val Pro Glu Val

195 200

<210> 726
<211> 200
<212> PRT
<213> Arabidopsis lyrata

<400> 726

Met Ser Phe Thr Gly Thr Gln Gln Lys Cys Arg Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Ile Ser Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Ser Arg Leu Gln Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Val Tyr Cys Arg Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Ser Gly Ser Phe Ser Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Pro Leu Thr Asp Lys Pro Thr Pro Glu Leu Thr Arg Thr Pro Ser
85 90 95

Arg Leu Ala Gly Met Phe Ser Gly Thr Gln Asp Lys Cys Ala Thr Cys
100 105 110

Ser Lys Thr Val Tyr Pro Ile Glu Lys Val Thr Val Glu Ser Gln Cys
115 120 125

Tyr His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Ser
130 135 140

Pro Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His
145 150 155 160

Phe Ala Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys
165 170 175

Ser Ala Ser Ile Lys Arg Ala Thr Ala Ala Ala Thr Ala Ala Ala Ala
180 185 190

Ala Val Ala Ala Val Pro Glu Ser
195 200

<210> 727
<211> 200
<212> PRT
<213> Arabidopsis

<400> 727

Met Ser Phe Thr Gly Thr Gln Gln Lys Cys Arg Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Ile Ser Tyr His Lys
20 25 30

Ala Cys Phe Lys Cys Ser His Cys Lys Ser Arg Leu Gln Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Val Tyr Cys Arg Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Ser Gly Ser Phe Ser Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Pro Leu Thr Asp Lys Pro Thr Pro Glu Leu Asn Arg Thr Pro Ser
85 90 95

Arg Leu Ala Gly Met Phe Ser Gly Thr Gln Asp Lys Cys Ala Thr Cys
100 105 110

Thr Lys Thr Val Tyr Pro Ile Glu Lys Val Thr Val Glu Ser Gln Cys
115 120 125

Tyr His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Ser
130 135 140

Pro Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His
145 150 155 160

Phe Ala Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys
165 170 175

Ser Ala Ser Ile Lys Arg Ala Thr Ala Ala Ala Thr Ala Ala Ala Ala
180 185 190

Ala Val Ala Ala Val Pro Glu Ser
195 200

<210> 728
<211> 148
<212> PRT
<213> Flaveria

<400> 728

Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln Leu Phe Lys
1 5 10 15

Glu Ser Gly Asn Phe Asn Lys Asn Phe Thr Ser Pro Ala Lys Ala Ala
20 25 30

Glu Lys Leu Ser Pro Met Leu Thr Lys Ser Pro Ser Lys Ala Ala Gly
35 40 45

Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly Lys Thr Ala
50 55 60

Tyr Pro Leu Glu Lys Val Thr Val Glu Asn Gln Ala Tyr His Lys Ser
65 70 75 80

Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Ser Pro Ser Asn Tyr
85 90 95

Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe Ser Gln Leu
100 105 110

Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser Ala Ser Ile
115 120 125

Lys Arg Thr Ala Ala Thr Thr Thr Ala Ala Val Ala Ala Ala Ala Ala
130 135 140

Ser Ile Pro Glu
145

<210> 729
<211> 199
<212> PRT
<213> Arabidopsis lyrata

<400> 729

Met Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Ala Val Glu Leu Leu Ser Ala Asp Gly Val Gly Tyr His Lys

20 25 30

Ser Cys Phe Lys Cys Thr His Cys Lys Ser Arg Leu Gln Leu Ser Ser
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Ser Gly Ser Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Pro Ala Asp Lys Ser Thr Pro Glu Leu Thr Arg Thr Pro Ser Arg
85 90 95

Val Ala Ser Arg Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Ser
100 105 110

Lys Thr Val Tyr Pro Ile Glu Lys Val Thr Val Glu Ser Gln Thr Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ala Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser

165 170 175

Ala Ser Ile Lys Arg Ser Ala Ala Ala Ala Val Ala Ala Gly Val Pro
180 185 190

Ala Ala Ser Gly Pro Glu Ser
195

<210> 730
<211> 199
<212> PRT
<213> Arabidopsis

<400> 730

Met Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Ala Val Glu Leu Leu Ser Ala Asp Gly Val Gly Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Thr His Cys Lys Ser Arg Leu Gln Leu Ser Ser
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Ser Gly Ser Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Asp Lys Ser Thr Pro Glu Leu Thr Arg Thr Pro Ser Arg
85 90 95

Val Ala Gly Arg Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Ser
100 105 110

Lys Thr Val Tyr Pro Ile Glu Lys Val Thr Val Glu Ser Gln Thr Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ala Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Ile Lys Arg Ser Ala Ala Ala Ala Val Ala Ala Gly Val Pro
180 185 190

Ala Ala Ser Val Pro Glu Ser
195

<210> 731
<211> 189

<212> PRT
<213> Euphorbia

<400> 731

Met Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Met Glu Leu Leu Ser Ala Asp Gly Ile Pro Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Phe His Cys Lys Gly Thr Leu Lys Leu Ser Ser
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Ser Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Glu Arg Leu Asn Pro Glu Phe Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Ser Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Ile Lys Arg Ala Ala Ala Ser Val Ser Glu Ser
180 185

<210> 732
<211> 206
<212> PRT
<213> Rábano

<220>
<221> misc_feature
<222> (192)..(192)
<223> Xaa puede ser cualquier aminoácido de origen natural

<400> 732

Met Ser Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys
1 5 10 15

Thr Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Val Ser Tyr His
20 25 30

Lys Ser Cys Phe Lys Cys Ser His Cys Lys Ser Arg Leu Gln Leu Ser
35 40 45

Arg Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Tyr Glu
50 55 60

Gln Leu Phe Lys Glu Ser Gly Ser Phe Thr Lys Asn Phe Gln Ser Pro
65 70 75 80

Ala Lys Pro Ala Glu Lys Ser Ser Pro Glu Leu Thr Arg Thr Pro Ser
85 90 95

Arg Val Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys
100 105 110

Ser Lys Thr Val Tyr Pro Ile Glu Lys Val Thr Val Glu Ser Gln Thr
115 120 125

Tyr His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Ser
130 135 140

Pro Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His
145 150 155 160

Phe Ala Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys
165 170 175

Ser Ala Ser Ile Lys Arg Ser Ala Ala Ala Ala Val Ala Ala Gly Xaa
180 185 190

Gln Gln Gln Arg Phe Leu Asn Leu Lys Phe Lys Asn His Leu
195 200 205

<210> 733
<211> 189
<212> PRT
<213> Mandioca

<400> 733

Met Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Met Glu Leu Leu Ser Ala Asp Gly Val Pro Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Phe His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Glu Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Ser Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Ser Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Val Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Met Lys Arg Ala Ala Ala Ser Val Pro Glu Ala
180 185

<210> 734
<211> 189
<212> PRT
<213> Mandioca

<400> 734

Met Ser Phe Thr Gly Thr Gln Gln Lys Cys Thr Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Met Glu Leu Leu Ser Ala Asp Gly Val Ser Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Phe His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Val Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Glu Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Ser Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Ser Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Ile Thr Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Val Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Met Lys Arg Ala Ala Ala Ser Val Pro Glu Ala
180 185

<210> 735
<211> 189
<212> PRT
<213> Ricino

<400> 735

Met Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Met Glu Leu Leu Ser Ala Asp Gly Val Pro Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Phe His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Val Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala

65 70 75 80

Lys Ser Ala Glu Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Ser Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Ser Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Ile Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Val Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Met Lys Arg Ala Ala Ala Ser Val Pro Glu Ala
180 185

<210> 736
<211> 189
<212> PRT
<213> Algodón, Gossypium raimondii

<400> 736

Met Ser Phe Ile Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Val Pro Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ala Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Asn Phe Asn Lys Asn Phe Gln Ser Ser Ala
65 70 75 80

Lys Ala Ala Glu Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Ser Met Phe Ser Gly Thr Val Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Gly Gln Ser Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Ile Lys Arg Thr Ala Ala Ser Val Pro Glu Ala
180 185

<210> 737
<211> 189
<212> PRT
<213> Algodón

<400> 737

Met Ser Phe Ile Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Val Pro Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ala Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Asn Phe Asn Lys Asn Phe Gln Ser Ser Ala
65 70 75 80

Lys Ala Ala Glu Lys Leu Thr Pro Glu Met Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Ser Met Phe Ser Gly Thr Val Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Gly Gln Ser Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Ile Lys Arg Ala Ala Ala Ser Val Pro Glu Ala
180 185

<210> 738
<211> 189
<212> PRT

<213> Pepino, melón

<400> 738

Met Ser Phe Ile Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Gln Leu Ser Ala Asp Gly Val Ser Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Glu Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Asp Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Val Tyr Pro Leu Glu Lys Val Thr Val Glu Ser Gln Ser Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ala Leu Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Met Lys Arg Ser Ala Ala Pro Val Pro Glu Ala
180 185

<210> 739
<211> 189
<212> PRT
<213> Cucurbita

<400> 739

Met Ser Phe Ile Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Gln Leu Ser Val Asp Gly Val Ser Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Thr His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln

50 55 60

Leu Phe Lys Glu Ser Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Glu Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Asp Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Val Tyr Pro Leu Glu Lys Val Thr Val Glu Ser Gln Ser Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Ile Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Met Lys Arg Pro Ala Ala Ser Val Pro Glu Ala
180 185

<210> 740

<211> 189
<212> PRT
<213> Sandía

<400> 740

Met Ser Phe Ile Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Gln Leu Ser Ala Asp Gly Val Ser Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Cys Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Asn Phe Gln Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Glu Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Asp Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Val Tyr Pro Leu Glu Lys Val Thr Val Glu Ser Gln Ser Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ala Ile Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Met Lys Arg Ser Ala Ala Pro Val Pro Glu Ala
180 185

<210> 741
<211> 195
<212> PRT
<213> Cannabis

<400> 741

Met Ser Phe Leu Gly Thr Gln Gln Lys Cys Lys Ala Cys Asp Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Gln Leu Ser Ala Asp Gly Val Ser Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Thr Gly Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Glu Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Ser Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Ser Leu Ser Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ala Leu Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Asn Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Ile Lys Arg Ala Ala Ala Ala Ala Ser Val Pro Glu Ala Glu
180 185 190

Ala Glu Ala
195

<210> 742
<211> 200
<212> PRT
<213> B. juncea

<400> 742

Met Ser Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys
1 5 10 15

Thr Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Val Ser Tyr His
20 25 30

Lys Ser Cys Phe Lys Cys Ser His Cys Lys Ser Arg Leu Gln Leu Ser
35 40 45

Arg Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Tyr Glu
50 55 60

Gln Leu Phe Lys Glu Ser Gly Ser Phe Asn Lys Asn Phe Gln Ser Pro
65 70 75 80

Ala Lys Pro Ala Glu Lys Ser Ser Pro Glu Leu Thr Arg Thr Pro Ser
85 90 95

Arg Val Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys
100 105 110

Ser Lys Thr Val Tyr Pro Ile Glu Lys Val Thr Val Glu Ser Gln Thr
115 120 125

Tyr His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Ser
130 135 140

Pro Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His
145 150 155 160

Phe Ala Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys
165 170 175

Ser Ala Ser Ile Lys Arg Ser Ala Ala Ala Ala Val Ala Ala Gly Thr
180 185 190

Pro Ala Thr Ala Val Pro Glu Ser
195 200

<210> 743
<211> 200
<212> PRT
<213> Rábano

<400> 743

Met Ser Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys

1 5 10 15

Thr Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Val Ser Tyr His
20 25 30

Lys Ser Cys Phe Lys Cys Ser His Cys Lys Ser Arg Leu Gln Leu Ser
35 40 45

Arg Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Tyr Glu
50 55 60

Gln Leu Phe Lys Glu Ser Gly Ser Phe Thr Lys Asn Phe Gln Ser Pro
65 70 75 80

Ala Lys Pro Ala Glu Lys Ser Ser Pro Glu Leu Thr Arg Thr Pro Ser
85 90 95

Arg Val Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys
100 105 110

Ser Lys Thr Val Tyr Pro Ile Glu Lys Val Thr Val Glu Ser Gln Thr
115 120 125

Tyr His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Ser
130 135 140

Pro Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His

145 150 155 160

Phe Ala Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys
165 170 175

Ser Ala Ser Ile Lys Arg Ser Ala Ala Ala Ala Val Ala Ala Gly Thr
180 185 190

Pro Ala Thr Ala Val Pro Glu Ser
195 200

<210> 744
<211> 190
<212> PRT
<213> Sarracenia

<400> 744

Met Ala Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Val Ser Tyr His Lys
20 25 30

Ser Cys Phe Arg Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Ser Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Ala Lys Leu Pro Glu Lys Ser Thr Pro Val Leu Thr Arg Ser Pro Ser
85 90 95

Lys Ala Ala Thr Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys
100 105 110

Gly Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Ser Gln Ala
115 120 125

Tyr His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ala Leu Ser
130 135 140

Pro Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His
145 150 155 160

Phe Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys
165 170 175

Ser Ala Ser Met Lys Arg Pro Thr Ala Ser Ile Pro Glu Ala
180 185 190

<210> 745
<211> 188

<212> PRT
<213> Gossypium raimondii

<400> 745

Met Ser Phe Ile Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Val Ser Val Asp Gly Val Pro Phe His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Trp Gly Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Ala Gly Asn Tyr Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Glu Lys Leu Thr Gln Leu Thr Arg Ser Pro Ser Lys Ala
85 90 95

Ala Gly Met Phe Ser Gly Thr Gln Asp Lys Cys Ala Thr Cys Gly Lys
100 105 110

Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Gly Gln Ser Tyr His
115 120 125

Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Ser Pro Ser
130 135 140

Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe Ser
145 150 155 160

Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser Ala
165 170 175

Ser Ile Lys Arg Thr Ala Ala Ser Val Pro Glu Ala
180 185

<210> 746
<211> 83
<212> PRT
<213> Heritiera

<400> 746

Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly Lys Thr Ala
1 5 10 15

Tyr Pro Leu Glu Lys Val Thr Val Glu Gly Gln Ser Tyr His Lys Ser
20 25 30

Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Ser Pro Ser Asn Tyr
35 40 45

Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe Ser Gln Leu
50 55 60

Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser Ala Ser Ile
65 70 75 80

Lys Arg Thr

<210> 747
<211> 189
<212> PRT
<213> Momordica

<400> 747

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

Val Tyr Pro Val Glu Gln Leu Ser Ala Asp Gly Val Ile Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Thr His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala

65 70 75 80

Lys Ser Ala Asp Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Asp Lys Cys Thr Thr Cys Gly
100 105 110

Lys Thr Val Tyr Pro Leu Glu Lys Val Thr Val Glu Ser Gln Cys Phe
115 120 125

His Lys Cys Cys Phe Lys Cys Ser His Gly Gly Cys Ala Ile Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Met Lys Arg Thr Ala Ala Ser Val Pro Glu Ala
180 185

<210> 748
<211> 189
<212> PRT
<213> Petunia

<400> 748

Met Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Ile Ser Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Thr His Cys Lys Gly Thr Leu Lys Leu Ser Ser
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Tyr Lys Glu Ser Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Glu Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Ser Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Asn Gln Ser Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Asn Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Asn Gly Ile Leu Tyr Cys Lys Pro His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Met Lys Arg Pro Ala Ala Thr Val Pro Asp Ser
180 185

<210> 749
<211> 190
<212> PRT
<213> Cichorium

<400> 749

Met Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Gly Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Ile Asp Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Ser Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Glu Lys Leu Ser Pro Met Leu Thr Lys Ser Pro Ser Lys
85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Asn Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Ile Lys Arg Ser Thr Pro Glu Ser Ile Pro Glu Val
180 185 190

<210> 750
<211> 196
<212> PRT

<213> Cleome gynandra

<400> 750

Met Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Thr Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Val Gly Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Thr His Cys Lys Ser Arg Leu Gln Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Ser Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Pro Ala Glu Lys Pro Thr Pro Glu Leu Thr Arg Thr Pro Ser Lys
85 90 95

Val Ala Ser Met Phe Ser Gly Thr Gln Asp Lys Cys Ala Thr Cys Ser
100 105 110

Lys Thr Val Tyr Pro Leu Glu Lys Val Thr Val Glu Ser Gln Ser Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ala Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Ile Lys Arg Thr Ala Ala Ala Ala Gly Val Ala Ala Thr Thr
180 185 190

Val Pro Glu Ser
195

<210> 751
<211> 189
<212> PRT
<213> Hevea

<400> 751

Met Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Met Glu Leu Leu Ser Ala Asp Gly Val Pro Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Phe His Cys Lys Gly Thr Leu Lys Leu Ser Asn

35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Glu Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Ser Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Ser Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Val Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Cys
165 170 175

Ala Ser Met Lys Arg Ala Ala Ala Ser Val Pro Glu Ala

180 185

<210> 752
<211> 189
<212> PRT
<213> Álamo

<400> 752

Met Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Met Glu Leu Leu Ser Thr Asp Gly Val Ala Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Phe His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Asp Gln
50 55 60

Leu Phe Lys Glu Thr Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Glu Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Ser Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ala Ile Thr Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Val Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Cys
165 170 175

Ala Ser Met Lys Arg Ala Ala Ala Pro Val Pro Glu Ala
180 185

<210> 753
<211> 206
<212> PRT
<213> Rosa

<400> 753

Asp Ile Arg Gln Leu Cys Phe His Trp His Pro Ala Glu Cys Lys Ala
1 5 10 15

Cys Ala Lys Thr Val Tyr Pro Val Glu Glu Leu Ser Ala Asp Gly Ile
20 25 30

Ser Tyr His Lys Ser Cys Phe Lys Cys Thr His Cys Lys Gly Thr Leu
35 40 45

Lys Leu Ser Asn Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro
50 55 60

His Phe Glu Gln Leu Phe Lys Glu Thr Gly Asn Phe Asn Lys Asn Phe
65 70 75 80

Gln Ser Pro Ala Lys Ser Ala Glu Lys Leu Thr Pro Glu Leu Thr Arg
85 90 95

Ser Pro Ser Lys Ala Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys
100 105 110

Ala Thr Cys Gly Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu
115 120 125

Ser Gln Ala Tyr His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys
130 135 140

Pro Ile Thr Pro Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys
145 150 155 160

Lys His His Phe Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His
165 170 175

Leu Ile Lys Ser Ala Ser Ile Lys Arg Ala Ala Ala Ala Thr Ala Thr
180 185 190

Ala Thr Ala Ala Ala Ala Ala Val Ala Ser Ile Pro Glu Ala
195 200 205

<210> 754
<211> 199
<212> PRT
<213> Aquilegia

<400> 754

Met Ser Phe Ile Gly Thr Gln Glu Lys Cys Lys Ala Cys Asp Lys Thr
1 5 10 15

Val Tyr Val Met Asp Gln Leu Ser Ala Asp Gly Val Ser Tyr His Lys
20 25 30

Ala Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Arg Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Ser Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Val
65 70 75 80

Ala Lys Ser Val Glu Lys Leu Thr Pro Gln Met Thr Arg Ser Pro Ser
85 90 95

Lys Ala Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys
100 105 110

Gly Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Asn Gln Ala
115 120 125

Tyr His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Ser
130 135 140

Pro Ser Asn Tyr Ala Ala Leu Asp Gly Ile Leu Tyr Cys Lys His His
145 150 155 160

Phe Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys
165 170 175

Cys Ala Ser Ile Lys Arg Ser Pro Gly Thr Ala Thr Ala Ala Ala Ala
180 185 190

Ala Thr Val Pro Asp Asp Ala
195

<210> 755
<211> 200
<212> PRT
<213> B. oleracea

<220>
<221> misc_feature
<222> (81)..(81)
<223> Xaa puede ser cualquier aminoácido de origen natural

<400> 755

Met Ser Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys
1 5 10 15

Thr Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Val Ser Tyr His
20 25 30

Lys Ser Cys Phe Lys Cys Ser His Cys Lys Ser Arg Leu Gln Leu Ser
35 40 45

Arg Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Tyr Glu
50 55 60

Gln Leu Phe Lys Glu Ser Gly Ser Phe Thr Lys Asn Phe Gln Ser Pro
65 70 75 80

Xaa Lys Pro Ala Glu Lys Ser Asn Pro Glu Leu Thr Arg Thr Pro Ser
85 90 95

Arg Val Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys
100 105 110

Ser Lys Thr Val Tyr Pro Ile Glu Lys Val Thr Val Glu Ser Gln Thr
115 120 125

Tyr His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Ser
130 135 140

Pro Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His
145 150 155 160

Phe Ala Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys
165 170 175

Ser Ala Ser Ile Lys Arg Ser Ala Ala Ala Ala Val Ala Ala Gly Thr
180 185 190

Pro Ala Thr Ala Val Pro Glu Ser
195 200

<210> 756
<211> 122
<212> PRT
<213> Canola

<400> 756

Met Ser Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys
1 5 10 15

Thr Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Val Ser Tyr His
20 25 30

Lys Ser Cys Phe Lys Cys Ser His Cys Lys Ser Arg Leu Gln Leu Ser
35 40 45

Arg Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Tyr Glu
50 55 60

Gln Leu Phe Lys Glu Ser Gly Ser Phe Thr Lys Asn Phe Gln Ser Pro
65 70 75 80

Val Lys Pro Ala Ala Glu Lys Ser Ser Pro Glu Leu Thr Arg Thr Pro
85 90 95

Ser Arg Val Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Ala Pro Leu
100 105 110

Ala Val Lys Leu Cys Ile Leu Ser Lys Arg
115 120

<210> 757
<211> 200
<212> PRT
<213> Rábano

<400> 757

Met Ser Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys

1 5 10 15

Thr Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Val Ser Tyr His
5 20 25 30

Lys Ser Cys Phe Lys Cys Thr His Cys Lys Ser Arg Leu Gln Leu Ser
35 40 45
10

Arg Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Tyr Glu
50 55 60

15

Gln Leu Phe Lys Glu Ser Gly Ser Phe Thr Lys Asn Phe Gln Ser Pro
65 70 75 80

20 Val Lys Pro Ala Glu Lys Ser Ser Pro Glu Leu Thr Arg Thr Pro Ser
85 90 95

Arg Val Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys
25 100 105 110

Ser Lys Thr Val Tyr Pro Ile Glu Lys Val Thr Val Glu Ser Gln Thr
115 120 125
30

Tyr His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Ser
130 135 140

35

Pro Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His

145 150 155 160

Phe Ala Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys
165 170 175

Ser Ala Ser Ile Lys Arg Ser Ala Ala Ala Ala Val Ala Ala Gly Thr
180 185 190

Pro Ala Ala Ala Val Pro Glu Ser
195 200

<210> 758
<211> 190
<212> PRT
<213> Aristolochia

<400> 758

Met Ala Phe Phe Ser Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys
1 5 10 15

Thr Val Tyr Val Val Asp Gln Leu Ser Ala Asp Gly Val Ser Tyr His
20 25 30

Lys Ala Cys Phe Lys Cys Asn His Cys Lys Gly Thr Leu Lys Leu Ser
35 40 45

Asn Tyr Ser Ser Leu Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu
50 55 60

Gln Leu Phe Lys Glu Thr Gly Ser Phe Asn Lys Ser Phe Gln Ser Pro
65 70 75 80

Ala Lys Pro Val Glu Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser
85 90 95

Lys Ala Ala Ser Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys
100 105 110

Gly Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Gly Gln Pro
115 120 125

Tyr His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Ser
130 135 140

Pro Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His
145 150 155 160

Phe Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys
165 170 175

Cys Ala Ser Met Lys Arg Pro Thr Thr Pro Ile Pro Glu Ala
180 185 190

<210> 759
<211> 196

<212> PRT
<213> B. juncea

<400> 759

Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr Val Tyr Pro
1 5 10 15

Val Glu Leu Leu Ser Ala Asp Gly Val Ser Tyr His Lys Ser Cys Phe
20 25 30

Lys Cys Ser His Cys Lys Ser Arg Leu Gln Leu Ser Arg Tyr Ser Ser
35 40 45

Met Glu Gly Val Leu Tyr Cys Lys Pro His Tyr Glu Gln Leu Phe Lys
50 55 60

Glu Ser Gly Ser Phe Thr Lys Asn Phe Gln Ser Pro Ala Lys Pro Ala
65 70 75 80

Glu Lys Ser Ser Pro Glu Leu Thr Arg Thr Pro Ser Arg Val Ala Gly
85 90 95

Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Ser Lys Thr Val
100 105 110

Tyr Pro Ile Glu Lys Val Thr Val Glu Ser Gln Thr Tyr His Lys Ser
115 120 125

Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Ser Pro Ser Asn Tyr
130 135 140

Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe Ala Gln Leu
145 150 155 160

Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser Ala Ser Ile
165 170 175

Lys Arg Ser Ala Ala Ala Ala Val Ala Ala Gly Ala Pro Ala Ala Ala
180 185 190

Val Pro Glu Ser
195

<210> 760
<211> 189
<212> PRT
<213> Amborella

<400> 760

Met Ala Phe Ser Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Val Met Asp Gln Leu Ser Ala Asp Gly Val Leu Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Asn His Cys Lys Gly Thr Leu Lys Leu Gly Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Ser Phe Asn Lys Ser Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Val Glu Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Ser Met Phe Ser Gly Thr Gln Asp Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Ser Gln Ser Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Thr Pro
130 135 140

Ser Thr Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Cys
165 170 175

Ala Thr Met Lys Arg Gln Ala Ala Pro Val Pro Glu Ala
180 185

<210> 761
<211> 185
<212> PRT
<213> Cirsium

<400> 761

Met Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Gly Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Ile Asp Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Ser Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ala Ala Asp Lys Ser Ser Pro Met Leu Thr Lys Ser Pro Ser Lys
85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly

100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Asn Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Cys Thr Ala Asn Ile Ile Ser
145 150 155 160

His Ser Tyr Ser Arg Arg Arg Ala Ala Thr Ile Ile Ser Ser Ser Leu
165 170 175

His Pro Ser Ser Ala Leu Gln Gln Arg
180 185

<210> 762
<211> 189
<212> PRT
<213> Algodón

<400> 762

Met Ser Phe Ile Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Val Ser Val Asp Gly Val Pro Phe His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Trp Gly Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Ala Gly Asn Tyr Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Glu Lys Leu Thr Gln Leu Thr Arg Ser Pro Ser Lys Ala
85 90 95

Ala Gly Met Phe Ser Gly Thr Gln Asp Lys Cys Ala Thr Cys Gly Lys
100 105 110

Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Gly Gln Ser Tyr His
115 120 125

Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Ser Pro Ser
130 135 140

Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe Ser
145 150 155 160

Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser Ala
165 170 175

Ser Ile Lys Arg Thr Ala Thr Ser Val Pro Glu Ala Ser
180 185

<210> 763
<211> 189
<212> PRT
<213> Pimiento

<400> 763

Met Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Ile Ser Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Thr His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Tyr Lys Glu Ser Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Val
65 70 75 80

Lys Ser Ala Glu Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Asn Gln Ser Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Asn Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Asp Gly Ile Leu Tyr Cys Lys Pro His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Met Lys Arg Pro Ala Ala Thr Val Pro Asp Ser
180 185

<210> 764
<211> 184
<212> PRT
<213> Ambrosia

<400> 764

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

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Ile Asp Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Ser Gly Asn Phe Asn Lys Asn Phe Thr Ser Pro Ala
65 70 75 80

Lys Ala Ala Asp Lys Leu Ser Pro Met Leu Thr Lys Ser Pro Ser Lys
85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Asn Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Ile Lys Arg Thr Ala Ala
180

<210> 765
<211> 189
<212> PRT
<213> Basilicum

<400> 765

Met Ser Phe Ile Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Val Ser Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Ser
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Tyr Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Ser Phe Ser Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Glu Lys Leu Thr Pro Glu Met Thr Arg Ser Pro Ser Lys

85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Asp Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Ser Gln Ser Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Thr Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Asp Gly Ile Leu Tyr Cys Lys Pro His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Met Lys Arg Pro Thr Ala Val Val Pro Asp Ser
180 185

<210> 766
<211> 184
<212> PRT
<213> Liriodendron

<400> 766

Met Ala Phe Ser Gly Thr Gln Gln Lys Cys Lys Ala Cys Asp Lys Thr
1 5 10 15

Val Tyr Val Val Asp Gln Leu Ser Ala Asp Gly Val Ala Tyr His Lys
20 25 30

Ala Cys Phe Lys Cys Asn His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Leu Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Ser Phe Asn Lys Ser Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Glu Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Ser Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Cys
165 170 175

Ala Thr Ile Lys Arg Thr Ser Ala
180

<210> 767
<211> 201
<212> PRT
<213> Canola

<400> 767

Met Ser Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys
1 5 10 15

Thr Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Val Ser Tyr His
20 25 30

Lys Ser Cys Phe Lys Cys Ser His Cys Lys Ser Arg Leu Gln Leu Ser
35 40 45

Arg Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Tyr Glu
50 55 60

Gln Leu Phe Lys Glu Ser Gly Ser Phe Thr Lys Asn Phe Gln Ser Pro
65 70 75 80

Val Lys Pro Ala Ala Glu Lys Ser Ser Pro Glu Leu Thr Arg Thr Pro
85 90 95

Ser Arg Val Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr
100 105 110

Cys Ser Lys Thr Val Tyr Pro Ile Glu Lys Val Thr Val Glu Ser Gln
115 120 125

Thr Tyr His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile
130 135 140

Ser Pro Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His
145 150 155 160

His Phe Ala Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile
165 170 175

Lys Ser Ala Ser Ile Lys Arg Ser Ala Ala Ala Ala Val Ala Ala Gly
180 185 190

Ala Pro Ala Ala Ala Val Pro Glu Ser
195 200

<210> 768
<211> 201
<212> PRT

<213> Rábano

<400> 768

Met Ser Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys
1 5 10 15

Thr Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Val Ser Tyr His
20 25 30

Lys Ser Cys Phe Lys Cys Thr His Cys Lys Ser Arg Leu Gln Leu Ser
35 40 45

Arg Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Tyr Glu
50 55 60

Gln Leu Phe Lys Glu Ser Gly Ser Phe Thr Lys Asn Phe Gln Ser Pro
65 70 75 80

Val Lys Pro Ala Ala Glu Lys Ser Ser Pro Glu Leu Thr Arg Thr Pro
85 90 95

Ser Arg Val Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr
100 105 110

Cys Ser Lys Thr Val Tyr Pro Ile Glu Lys Val Thr Val Glu Ser Gln
115 120 125

Thr Tyr His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile
130 135 140

Ser Pro Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His
145 150 155 160

His Phe Ala Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile
165 170 175

Lys Ser Ala Ser Ile Lys Arg Phe Ala Ala Ala Ala Val Ala Ala Gly
180 185 190

Thr Pro Ala Ala Ala Val Pro Glu Ser
195 200

<210> 769
<211> 201
<212> PRT
<213> Rábano

<400> 769

Met Ser Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys
1 5 10 15

Thr Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Val Ser Tyr His
20 25 30

Lys Ser Cys Phe Lys Cys Thr His Cys Lys Ser Arg Leu Gln Leu Ser

35 40 45

Arg Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Tyr Glu
50 55 60

Gln Leu Phe Lys Glu Ser Gly Ser Phe Thr Lys Asn Phe Gln Ser Pro
65 70 75 80

Val Lys Pro Ala Ala Glu Lys Ser Ser Pro Glu Leu Thr Arg Thr Pro
85 90 95

Ser Arg Val Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr
100 105 110

Cys Ser Lys Thr Val Tyr Pro Ile Glu Lys Val Thr Val Glu Ser Gln
115 120 125

Thr Tyr His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile
130 135 140

Ser Pro Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His
145 150 155 160

His Phe Ala Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile
165 170 175

Lys Ser Ala Ser Ile Lys Arg Ser Ala Ala Ala Ala Val Ala Ala Gly

180 185 190

Thr Pro Ala Ala Ala Val Pro Glu Ser
195 200

<210> 770
<211> 189
<212> PRT
<213> Amorphophallus

<400> 770

Met Ala Phe Leu Gly Thr Gln Gln Lys Cys Lys Ala Cys Asp Lys Thr
1 5 10 15

Val Tyr Val Met Asp Gln Leu Thr Thr Asp Gly Val Val Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Asn His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ala Ala Glu Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Ser Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Gly Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Ile Thr Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Cys
165 170 175

Ala Ser Val Lys Arg Pro Val Thr Pro Ala Pro Asp Ser
180 185

<210> 771
<211> 190
<212> PRT
<213> Antirrhinum

<400> 771

Met Ser Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys
1 5 10 15

Thr Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Ile Asn Tyr His
20 25 30

Lys Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser
35 40 45

Ser Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Tyr Glu
50 55 60

Gln Leu Phe Lys Glu Thr Gly Ser Phe Thr Lys Asn Phe Gln Ser Pro
65 70 75 80

Ala Lys Ser Ala Glu Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser
85 90 95

Lys Ala Ala Gly Met Phe Ser Gly Thr Gln Asp Lys Cys Ala Thr Cys
100 105 110

Gly Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Asn Gln Ser
115 120 125

Tyr His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Thr
130 135 140

Pro Ser Asn Tyr Ala Ala Leu Asn Gly Val Leu Tyr Cys Lys Pro His
145 150 155 160

Phe Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Asn Lys
165 170 175

Ser Ser Ser Met Lys Arg Pro Thr Ala Val Val Pro Asp Ser
180 185 190

<210> 772
<211> 189
<212> PRT
<213> Catharanthus

<400> 772

Met Ser Phe Ile Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Ile Ser Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Ser
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Tyr Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Ser Phe Ser Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Glu Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Asp Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Ser Gln Ser Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Asn Gly Val Leu Tyr Cys Lys Pro His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Thr His Val Leu Lys Ser
165 170 175

Ala Ser Met Lys Arg Pro Thr Thr Pro Val Pro Asp Ser
180 185

<210> 773
<211> 168
<212> PRT
<213> Cynara

<220>
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<222> (164)..(164)
<223> Xaa puede ser cualquier aminoácido de origen natural

<220>
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<222> (167)..(167)
<223> Xaa puede ser cualquier aminoácido de origen natural

<400> 773

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

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Val Asp Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Ser Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Glu Lys Leu Thr Pro Gln Leu Thr Lys Ser Gln Ser Lys
85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Asp Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Asn Glu Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Xaa Lys Glu Xaa Gly
165

<210> 774
<211> 189
<212> PRT
<213> Euonymus

<400> 774

Met Ser Phe Ile Gly Thr Gln Glu Lys Cys Lys Ala Cys Gln Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Val Asn Tyr His Arg
20 25 30

Ser Cys Phe Lys Cys Thr His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Ala Thr Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Glu Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Ser Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Asn
100 105 110

Lys Thr Ala Tyr Pro Val Glu Lys Val Thr Val Glu Gly Lys Ser Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Ile Arg Arg Ala Ala Ala Ser Val Pro Glu Ala
180 185

<210> 775
<211> 189
<212> PRT
<213> Orobanche

<400> 775

Met Ser Phe Ile Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Val Ser Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Arg Gly Thr Leu Lys Leu Ser Thr
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Tyr Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Ser Phe Thr Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Glu Met Leu Thr Pro Glu Phe Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Asp Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Ser Gln Ser Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Cys His Gly Gly Cys Ser Leu Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Asp Gly Ile Leu Tyr Cys Lys Pro His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Val Lys Arg Pro Val Ala Val Val Pro Asp Ser
180 185

<210> 776
<211> 63
<212> PRT
<213> Phlya

<400> 776

Met Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Val Ser Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Ser

35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Tyr Glu
50 55 60

<210> 777
<211> 189
<212> PRT
<213> Tabaco

<400> 777

Met Ser Phe Ile Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Val Asn Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Phe Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Phe Glu Gln
50 55 60

Leu Phe Lys Glu Ser Gly Asn Phe Asn Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Glu Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Asn Gln Ser Tyr
115 120 125

His Lys Thr Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Asn Gly Ile Leu Tyr Cys Lys Pro His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys Ser
165 170 175

Ala Ser Met Lys Arg Pro Ala Ala Thr Val Pro Asp Ser
180 185

<210> 778
<211> 189
<212> PRT
<213> Triphysaria

<400> 778

Met Ser Phe Ile Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Val Asp Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Val Tyr Cys Lys Pro His Tyr Glu Gln
50 55 60

Leu Phe Lys Glu Ala Gly Asn Phe Thr Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Glu Lys Leu Ser Pro Glu Phe Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Ser Met Phe Ser Gly Thr Val Asp Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Ser Val Glu Asn Gln Ser Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Thr Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Asp Gly Ile Leu Tyr Cys Lys Pro His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Val Leu Lys Ser
165 170 175

Ala Ser Ile Lys Arg Pro Ala Ala Val Val Pro Asp Ser
180 185

<210> 779
<211> 189
<212> PRT
<213> Vinca

<400> 779

Met Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Ile Ser Tyr His Lys
20 25 30

Ser Cys Phe Lys Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Ser
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Tyr Glu Gln
50 55 60

Leu Phe Lys Glu Thr Gly Ser Phe Thr Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Ser Ala Glu Lys Leu Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Gly Met Phe Ser Gly Thr Gln Asp Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Asn Gln Ser Tyr
115 120 125

His Lys Thr Cys Phe Lys Cys Ser His Gly Gly Cys Ser Leu Ser Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Lys Gly Val Leu Tyr Cys Lys Pro His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Thr His Val Leu Lys Ser
165 170 175

Ala Ser Met Lys Arg Pro Thr Thr Pro Val Pro Glu Ser
180 185

<210> 780
<211> 201
<212> PRT
<213> B. rapa

<400> 780

Met Ser Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys

1 5 10 15

Thr Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Val Ser Tyr His
20 25 30

Lys Ser Cys Phe Lys Cys Ser His Cys Lys Ser Arg Leu Gln Leu Ser
35 40 45

Arg Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Tyr Glu
50 55 60

Gln Leu Phe Lys Glu Ser Gly Ser Phe Thr Lys Asn Phe Gln Ser Pro
65 70 75 80

Val Lys Pro Ala Ala Glu Lys Ser Ser Pro Glu Leu Thr Arg Thr Pro
85 90 95

Ser Arg Val Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr
100 105 110

Cys Ser Lys Thr Val Tyr Pro Ile Glu Lys Val Thr Val Glu Ser Gln
115 120 125

Thr Tyr His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile
130 135 140

Ser Pro Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His

145 150 155 160

His Phe Ala Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile
165 170 175

Lys Ser Ala Ser Ile Lys His Ser Ala Ala Ala Ala Val Ala Ala Gly
180 185 190

Ala Pro Ala Ala Ala Val Pro Glu Ser
195 200

<210> 781
<211> 200
<212> PRT
<213> Rábano

<400> 781

Met Ser Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys
1 5 10 15

Thr Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Val Ser Tyr His
20 25 30

Lys Ser Cys Phe Lys Cys Thr His Cys Lys Ser Arg Leu Gln Leu Ser
35 40 45

Arg Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Tyr Glu
50 55 60

Gln Leu Phe Lys Glu Ser Gly Ser Phe Thr Lys Asn Phe Gln Ser Pro
65 70 75 80

Val Lys Pro Val Glu Lys Ser Ser Pro Glu Leu Thr Arg Thr Pro Ser
85 90 95

Arg Val Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys
100 105 110

Ser Lys Thr Val Tyr Pro Ile Glu Lys Val Thr Val Glu Ser Gln Thr
115 120 125

Tyr His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Ser
130 135 140

Pro Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His
145 150 155 160

Phe Ala Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Ile Lys
165 170 175

Ser Ala Ser Ile Lys Arg Ser Ala Ala Ala Ala Val Ala Ala Gly Thr
180 185 190

Pro Ala Ala Ala Ala Pro Glu Ser
195 200

<210> 782
<211> 174
<212> PRT
<213> Rábano

<400> 782

Met Ser Ser Phe Thr Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys
1 5 10 15

Thr Val Tyr Pro Val Glu Leu Leu Ser Ala Asp Gly Val Ser Tyr His
20 25 30

Lys Ser Cys Phe Lys Cys Thr His Cys Lys Ser Arg Leu Gln Leu Ser
35 40 45

Arg Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Tyr Glu
50 55 60

Gln Leu Phe Lys Glu Ser Gly Ser Phe Thr Lys Asn Phe Gln Ser Pro
65 70 75 80

Val Lys Pro Ala Ala Glu Lys Ser Ser Pro Glu Leu Thr Arg Thr Pro
85 90 95

Ser Arg Val Ala Gly Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr
100 105 110

Cys Ser Lys Thr Val Tyr Pro Ile Glu Lys Val Thr Val Glu Ser Gln
115 120 125

Thr Tyr His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile
130 135 140

Ser Pro Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His
145 150 155 160

His Phe Ala Gln Leu Phe Lys Glu Lys Glu Ala Thr Thr Thr
165 170

<210> 783
<211> 248
<212> PRT
<213> Guandú

<400> 783

Met Ala Thr Ile Leu Gly Lys Glu Ser Gly Leu Asn Leu Lys Glu Thr
1 5 10 15

Glu Leu Cys Leu Gly Leu Pro Gly Gly Gly Gly Val Gly Gly Gly Gly
20 25 30

Gly Gly Gly Gly Gly Gly Gly Ser Ser Glu Val Glu Thr Pro Arg Ala
35 40 45

Thr Gly Lys Arg Gly Phe Ser Glu Thr Val Asp Leu Lys Leu Asn Leu
50 55 60

Gln Ser Lys Glu Asp Leu Asn Glu Asn Leu Lys Asn Val Ser Lys Glu
65 70 75 80

Lys Thr Leu Leu Lys Asp Pro Ala Lys Pro Pro Ala Lys Ala Gln Val
85 90 95

Val Gly Trp Pro Pro Val Arg Ser Tyr Arg Lys Asn Met Met Ala Gln
100 105 110

Lys Val Ser Thr Glu Asp Val Ala Glu Lys Thr Thr Ser Ser Thr Ala
115 120 125

Ser Gly Ala Phe Val Lys Val Ser Met Asp Gly Ala Pro Tyr Leu Arg
130 135 140

Lys Val Asp Leu Thr Met Tyr Lys Ser Tyr Lys Asp Leu Ser Asp Ala
145 150 155 160

Leu Ala Lys Met Phe Ser Ser Phe Thr Met Gly Asn Tyr Gly Ala Gln
165 170 175

Gly Met Ile Asp Phe Met Asn Glu Ser Lys Leu Met Asp Leu Leu Asn
180 185 190

Ser Ser Glu Tyr Val Pro Thr Tyr Glu Asp Lys Asp Gly Asp Trp Met
195 200 205

Leu Val Gly Asp Val Pro Trp Glu Met Phe Val Glu Ser Cys Lys Arg
210 215 220

Leu Arg Ile Met Lys Gly Ser Glu Ala Ile Gly Leu Ala Pro Arg Ala
225 230 235 240

Met Glu Lys Cys Lys Ser Arg Ser
245

<210> 784
<211> 244
<212> PRT
<213> Poroto

<400> 784

Met Ala Thr Met Leu Gly Lys Glu His His Leu Asn Leu Lys Glu Thr
1 5 10 15

Glu Leu Cys Leu Gly Leu Pro Gly Ala Gly Gly Gly Gly Gly Ser Gly
20 25 30

Gly Gly Gly Gly Ser Glu Val Glu Thr Pro Arg Ala Thr Gly Lys Arg
35 40 45

Gly Phe Ser Glu Thr Val Asp Leu Lys Leu Asn Leu Gln Ala Lys Glu

50 55 60

Asp Leu Asn Glu Asn Leu Lys Asn Ala Pro Glu Glu Lys Thr Leu Leu
65 70 75 80

Lys Asp Pro Thr Lys Gln Pro Ala Lys Ala Gln Val Val Gly Trp Pro
85 90 95

Pro Val Arg Ser Tyr Arg Lys Asn Met Met Thr Gln Lys Val Ser Thr
100 105 110

Glu Asp Gly Ala Glu Lys Thr Thr Ser Ser Thr Ala Ser Gly Ala Phe
115 120 125

Val Lys Val Ser Met Asp Gly Ala Pro Tyr Leu Arg Lys Val Asp Leu
130 135 140

Thr Met Tyr Lys Ser Tyr Lys Asp Leu Ser Asp Ala Leu Ala Lys Met
145 150 155 160

Phe Ser Ser Phe Thr Met Gly Asn Tyr Gly Ala Gln Gly Met Ile Asp
165 170 175

Phe Met Asn Glu Arg Lys Leu Met Asp Leu Leu Asn Ser Ser Glu Tyr
180 185 190

Val Pro Thr Tyr Glu Asp Lys Asp Gly Asp Trp Met Leu Val Gly Asp

195 200 205

Val Pro Trp Glu Met Phe Val Glu Ser Cys Lys Arg Leu Arg Ile Met
210 215 220

Lys Gly Ser Glu Ala Ile Gly Leu Ala Pro Arg Ala Met Glu Lys Cys
225 230 235 240

Lys Ser Arg Ser

<210> 785
<211> 245
<212> PRT
<213> Chícharo salvaje

<400> 785

Met Ala Thr Met Leu Ala Lys Asp His Ala Leu Asn Leu Lys Glu Thr
1 5 10 15

Glu Leu Cys Leu Gly Leu Pro Gly Ala Gly Gly Gly Gly Gly Gly Gly
20 25 30

Gly Gly Gly Gly Gly Ser Glu Val Glu Thr Pro Arg Ala Thr Gly Lys
35 40 45

Arg Gly Phe Ser Glu Thr Val Asp Leu Lys Leu Asn Leu Gln Ala Lys
50 55 60

Glu Asp Leu Asn Asp Asn Leu Lys Asn Ala Ser Glu Glu Lys Thr Leu
65 70 75 80

Leu Lys Asp Pro Thr Lys Gln Pro Ala Lys Ala Gln Val Val Gly Trp
85 90 95

Pro Pro Val Arg Ser Tyr Arg Lys Asn Met Met Ser Gln Lys Val Ser
100 105 110

Ser Glu Glu Gly Ala Glu Lys Thr Thr Ser Ser Thr Gly Ser Gly Ala
115 120 125

Phe Val Lys Val Ser Met Asp Gly Ala Pro Tyr Leu Arg Lys Val Asp
130 135 140

Leu Thr Met Tyr Lys Ser Tyr Lys Asp Leu Ser Asp Ala Leu Ala Lys
145 150 155 160

Met Phe Ser Ser Phe Thr Met Gly Asn Tyr Gly Ala Gln Gly Met Ile
165 170 175

Asp Phe Met Asn Glu Arg Lys Leu Met Asp Leu Leu Asn Ser Ser Glu
180 185 190

Tyr Val Pro Thr Tyr Glu Asp Lys Asp Gly Asp Trp Met Leu Val Gly
195 200 205

Asp Val Pro Trp Glu Met Phe Val Glu Ser Cys Lys Arg Leu Arg Ile
210 215 220

Met Lys Gly Ser Glu Ala Ile Gly Leu Ala Pro Arg Ala Met Glu Lys
225 230 235 240

Cys Lys Ser Arg Ser
245

<210> 786
<211> 239
<212> PRT
<213> Soja

<400> 786

Met Thr Thr Met Leu Thr Asn Glu His Gly Leu Ser Leu Asn Leu Lys
1 5 10 15

Glu Thr Glu Leu Cys Leu Gly Leu Pro Gly Gly Gly Ser Glu Val Glu
20 25 30

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

Lys Leu Asn Leu Gln Thr Lys Glu Asp Leu Asn Glu Asn Leu Lys Asn
50 55 60

Val Ser Lys Glu Lys Thr Leu Leu Lys Asp Pro Ala Lys Pro Pro Ala
65 70 75 80

Lys Ala Gln Val Val Gly Trp Pro Pro Val Arg Ser Tyr Arg Lys Asn
85 90 95

Met Met Ala Val Gln Lys Val Ser Asn Glu Glu Val Ala Glu Lys Thr
100 105 110

Thr Ser Ser Thr Ile Ala Asn Ser Gly Ala Phe Val Lys Val Ser Met
115 120 125

Asp Gly Ala Pro Tyr Leu Arg Lys Val Asp Leu Thr Met Tyr Lys Ser
130 135 140

Tyr Lys Asp Leu Ser Asp Ala Leu Ala Lys Met Phe Ser Ser Phe Thr
145 150 155 160

Met Gly Asn Tyr Gly Ala Gln Gly Met Ile Asp Phe Met Asn Glu Ser
165 170 175

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

Asp Lys Asp Gly Asp Trp Met Leu Val Gly Asp Val Pro Trp Glu Met
195 200 205

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

Ile Gly Leu Ala Pro Arg Ala Met Glu Lys Cys Lys Ser Arg Ser
225 230 235

<210> 787
<211> 242
<212> PRT
<213> Lotus

<400> 787

Met Ala Thr Leu Leu Gly Lys Val Gln Asn Asp Leu Asn Leu Lys Glu
1 5 10 15

Thr Glu Leu Cys Leu Gly Leu Pro Gly Gly Gly Gly Gly Gly Gly Gly
20 25 30

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

Glu Thr Val Asp Leu Lys Leu Asn Leu Gln Ser Lys Glu Asp Leu Asn
50 55 60

Asp Asp Val Lys Asn Val Ser Lys Glu Lys Thr Leu Leu Lys Asp Pro
65 70 75 80

Ala Lys Pro Pro Ala Lys Ala Gln Val Val Gly Trp Pro Pro Val Arg
85 90 95

Ser Tyr Arg Lys Asn Met Met Val Gln Lys Val Asn Asn Glu Asp Gln
100 105 110

Gly Thr Glu Lys Thr Thr Ser Ser Thr Ala Gly Gly Ala Phe Val Lys
115 120 125

Val Ser Met Asp Gly Ala Pro Tyr Leu Arg Lys Val Asp Leu Thr Met
130 135 140

Tyr Lys Ser Tyr Lys Glu Leu Ser Asp Ala Leu Ala Lys Met Phe Ser
145 150 155 160

Ser Phe Thr Met Gly Asn Tyr Gly Ala Gln Gly Met Ile Asp Phe Met
165 170 175

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

Thr Tyr Glu Asp Lys Asp Gly Asp Trp Met Leu Val Gly Asp Val Pro
195 200 205

Trp Glu Met Phe Val Gly Ser Cys Lys Arg Leu Arg Ile Met Lys Gly
210 215 220

Ser Glu Ala Ile Gly Leu Ala Pro Arg Ala Met Glu Lys Cys Lys Asn
225 230 235 240

Arg Ser

<210> 788
<211> 236
<212> PRT
<213> Medicago

<400> 788

Met Ala Thr Met Gly His Gly Leu Asn Leu Lys Glu Thr Glu Leu Cys
1 5 10 15

Leu Gly Leu Pro Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Ser Glu
20 25 30

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

Asp Leu Lys Leu Asn Leu Gln Thr Lys Glu Asp Leu Asn Glu Lys Ser
50 55 60

Ala Ser Lys Glu Lys Thr Leu Leu Lys Asp Pro Ala Lys Pro Pro Ala
65 70 75 80

Lys Ala Gln Val Val Gly Trp Pro Pro Val Arg Ser Tyr Arg Lys Asn

85 90 95

Met Met Ala Gln Lys Val Asn Asn Thr Glu Asp Thr Glu Lys Thr Thr
100 105 110

Ser Asn Thr Thr Ala Ala Ala Phe Val Lys Val Ser Met Asp Gly Ala
115 120 125

Pro Tyr Leu Arg Lys Val Asp Leu Thr Met Tyr Lys Thr Tyr Lys Asp
130 135 140

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

Tyr Gly Ala Gln Gly Met Ile Asp Phe Met Asn Glu Ser Lys Leu Met
165 170 175

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

Gly Asp Trp Met Leu Val Gly Asp Val Pro Trp Glu Met Phe Val Gly
195 200 205

Ser Cys Lys Arg Leu Arg Ile Met Lys Gly Ser Glu Ala Ile Gly Leu
210 215 220

Ala Pro Arg Ala Met Glu Lys Cys Lys Asn Arg Ser

225 230 235

<210> 789
<211> 240
<212> PRT
<213> Garbanzo

<400> 789

Met Ala Thr Leu Ile Gly Lys Glu Ser Gly Leu Asn Leu Lys Glu Thr
1 5 10 15

Glu Leu Cys Leu Gly Leu Pro Gly Gly Gly Gly Ser Gly Ser Glu Val
20 25 30

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

Leu Lys Leu Asn Leu Gln Ser Asn Lys Glu Asp Leu Asn Asp Asn Ser
50 55 60

Lys Asn Val Ser Lys Asp Lys Thr Leu Leu Lys Asp Pro Ala Lys Pro
65 70 75 80

Pro Ala Lys Ala Gln Val Val Gly Trp Pro Pro Val Arg Ser Tyr Arg
85 90 95

Lys Asn Met Met Ala Gln Lys Val Asn Asn Ser Asp Gln Asp Gly Asn
100 105 110

Glu Lys Thr Thr Ser Ser Thr Thr Ala Gly Thr Phe Val Lys Val Ser
115 120 125

Met Asp Gly Ala Pro Tyr Leu Arg Lys Val Asp Leu Thr Met Tyr Asn
130 135 140

Thr Tyr Lys Asp Leu Ser Asp Ala Leu Ala Lys Met Phe Ser Ser Phe
145 150 155 160

Thr Thr Gly Lys Tyr Gly Ala Gln Gly Met Ile Asp Phe Met Asn Glu
165 170 175

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

Glu Asp Lys Asp Gly Asp Trp Met Leu Val Gly Asp Val Pro Trp Glu
195 200 205

Met Phe Val Glu Ser Cys Lys Arg Leu Arg Ile Met Lys Gly Ser Glu
210 215 220

Ala Ile Gly Leu Ala Pro Arg Ala Met Glu Lys Cys Lys Asn Arg Ser
225 230 235 240

<210> 790
<211> 260

<212> PRT
<213> Maní

<400> 790

Met Ala Thr Met Leu Ala Lys Glu His Gly Leu Asn Leu Lys Glu Thr
1 5 10 15

Glu Leu Cys Leu Gly Leu Pro Gly Gly Gly Gly Gly Gly Gly Gly Asp
20 25 30

Thr Ala Thr Ala Glu Thr Pro Arg Ala Thr Gly Lys Arg Gly Phe Ser
35 40 45

Glu Thr Val Asp Leu Lys Leu Asn Leu Gln Gly Asn Asp Thr Asn Lys
50 55 60

Glu Asp Leu Asn Glu Asn Leu Lys Asn Val Pro Lys Glu Lys Thr Leu
65 70 75 80

Leu Lys Asp Pro Ala Lys Pro Pro Ala Lys Ala Gln Val Val Gly Trp
85 90 95

Pro Pro Val Arg Ser Tyr Arg Lys Asn Met Met Ala Gln Lys Val Ser
100 105 110

Thr Glu Glu Asn Asn Asn Gly Ser Ala Thr Thr Glu Lys Thr Thr Ser
115 120 125

Ser Ala Ala Ala Ala Ala Thr Thr Ala Ala Ser Thr Gly Gly Ser Phe
130 135 140

Val Lys Val Ser Met Asp Gly Ala Pro Tyr Leu Arg Lys Val Asp Leu
145 150 155 160

Thr Met Tyr Lys Ser Tyr Gln Asp Leu Ser Asp Ala Leu Ala Lys Met
165 170 175

Phe Ser Ser Phe Thr Met Gly Asn Tyr Gly Ser Gln Gly Met Ile Asp
180 185 190

Phe Met Asn Glu Ser Lys Leu Met Asp Leu Leu Asn Ser Ser Glu Tyr
195 200 205

Val Pro Thr Tyr Glu Asp Lys Asp Gly Asp Trp Met Leu Val Gly Asp
210 215 220

Val Pro Trp Glu Met Phe Val Gly Ser Cys Lys Arg Leu Arg Ile Met
225 230 235 240

Lys Gly Ser Glu Ala Ile Gly Leu Ala Pro Arg Ala Met Glu Lys Cys
245 250 255

Lys Ser Arg Ser
260

<210> 791
<211> 248
<212> PRT
<213> Cacao

<400> 791

Met Ala Asn Met Leu Gly Ala Glu Arg Asp Leu Asn Phe Lys Glu Thr
1 5 10 15

Glu Leu Cys Leu Gly Leu Pro Gly Gly Gly Gly Gly Gly Gly Gly Gly
20 25 30

Gly Gly Asn Glu Val Glu Thr Pro Lys Thr Thr Gly Lys Arg Gly Phe
35 40 45

Ser Glu Thr Val Asp Leu Lys Leu Asn Leu Gln Ser Lys Glu Thr Gly
50 55 60

Met Asp Leu Asn Lys Asn Ile Glu Asn Gly Ser Lys Glu Lys Thr Leu
65 70 75 80

Leu Pro Ala Cys Thr Lys Asp Pro Ala Lys Pro Pro Ala Lys Ala Gln
85 90 95

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

Asn Gln Lys Asn Ser Cys Glu Glu Ser Asp Lys Lys Ala Ser Ser Gly
115 120 125

Gly Ala Ala Phe Val Lys Val Ser Met Asp Gly Ala Pro Tyr Leu Arg
130 135 140

Lys Val Asp Leu Lys Met Tyr Lys Ser Tyr Gln Glu Leu Ser Asp Ala
145 150 155 160

Leu Ala Lys Met Phe Ser Ser Phe Thr Met Gly Asn Tyr Gly Ala Gln
165 170 175

Gly Met Ile Asp Phe Met Asn Glu Ser Lys Leu Met Asp Leu Leu Asn
180 185 190

Ser Ser Asp Tyr Val Pro Thr Tyr Glu Asp Lys Asp Gly Asp Trp Met
195 200 205

Leu Val Gly Asp Val Pro Trp Glu Met Phe Val Asp Ser Cys Lys Arg
210 215 220

Leu Arg Ile Met Lys Gly Ser Glu Ala Ile Gly Leu Ala Pro Arg Ala
225 230 235 240

Met Glu Lys Cys Lys Ser Arg Ala
245

<210> 792
<211> 241
<212> PRT
<213> Trébol

<400> 792

Met Ala Thr Met Ile Gly Lys Asp Asn Asp Leu Ser Leu Lys Thr Glu
1 5 10 15

Leu Cys Leu Gly Leu Pro Gly Gly Gly Gly Gly Gly Gly Ser Glu Gln
20 25 30

Val Glu Thr Pro Arg Ala Ser Ala Lys Arg Gly Phe Ser Glu Thr Ile
35 40 45

Asp Leu Lys Leu Asn Leu Gln Thr Lys Glu Asp Leu Asn Gly Asn Ile
50 55 60

Lys Asn Ala Ser Lys Asp Lys Ser Leu Leu Lys Asp Pro Ser Lys Pro
65 70 75 80

Pro Ala Lys Ala Gln Val Val Gly Trp Pro Pro Val Arg Ser Tyr Arg
85 90 95

Lys Asn Met Met Ala Gln Lys Val Asn Asn Ile Ser Glu Asp Gly Asn
100 105 110

Asn Glu Lys Thr Thr Ser Ser Thr Thr Ser Gly Ala Phe Val Lys Val

115 120 125

Ser Met Asp Gly Ala Pro Tyr Leu Arg Lys Val Asp Leu Thr Met Tyr
130 135 140

Lys Thr Tyr Lys Asp Leu Ser Asp Ala Leu Ala Lys Met Phe Ser Ser
145 150 155 160

Phe Thr Thr Gly Asn Tyr Gly Ala Gln Gly Met Ile Asp Phe Met Asn
165 170 175

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

Tyr Glu Asp Lys Asp Gly Asp Trp Met Leu Val Gly Asp Val Pro Trp
195 200 205

Glu Met Phe Val Gly Ser Cys Lys Arg Leu Arg Ile Met Lys Gly Ser
210 215 220

Glu Ala Ile Gly Leu Ala Pro Arg Ala Met Glu Lys Cys Lys Asn Arg
225 230 235 240

Ser

<210> 793

<211> 595
<212> PRT
<213> Soja

<400> 793

Met Lys Arg Asp His Lys Asp Ser Cys Gly Gly Gly Gly Ala Ala Gly
1 5 10 15

Gly Thr Val Lys Gly Glu Cys Ser Ser Met Gln Ser Asn Gly Lys Ala
20 25 30

Lys Met Trp Glu Glu Glu Gln Gln Gln Gln Gln Gln Gln Gln Gln
35 40 45

Gln Gln Gln Gln Gly Met Asp Glu Leu Leu Ala Ala Leu Gly Tyr Lys
50 55 60

Val Arg Ala Ser Asp Met Ala Asp Val Ala Gln Lys Leu Glu Gln Leu
65 70 75 80

Glu Met Val Met Gly Cys Ala Gln Glu Asp Gly Ile Ser His Leu Ala
85 90 95

Ser Asp Thr Val His Tyr Asp Pro Thr Asp Leu Tyr Ser Trp Val Gln
100 105 110

Ser Met Leu Thr Glu Leu Asn Pro Glu Pro Asn Asn Asn Leu Asp Pro
115 120 125

Ser Ser Phe Leu Ile Asp Asn Asn Asn Asn Ile Ile Asn Ser Thr Ala
130 135 140

Pro Val Phe Asn Asp Asp Ser Glu Tyr Asp Leu Arg Ala Ile Pro Gly
145 150 155 160

Ile Ala Ala Tyr Pro Pro Pro Leu Pro Gln Asp Asn His Leu Asp Glu
165 170 175

Ile Glu Thr Ala Asn Asn Ile Asn Lys Arg Leu Lys Pro Ser Pro Ala
180 185 190

Glu Ser Ala Asp Ser Ala Ala Ser Glu Pro Thr Arg His Val Val Leu
195 200 205

Val Asp His Gln Glu Ala Gly Val Arg Leu Val His Thr Leu Leu Ala
210 215 220

Cys Ala Glu Ala Val Gln Gln Glu Asn Leu Lys Leu Ala Asp Ala Leu
225 230 235 240

Val Lys His Val Gly Ile Leu Ala Ala Ser Gln Ala Gly Ala Met Arg
245 250 255

Lys Val Ala Ser Tyr Phe Ala Gln Ala Leu Ala Arg Arg Ile Tyr Gly
260 265 270

Ile Phe Pro Glu Glu Thr Leu Asp Ser Ser Phe Ser Asp Val Leu His
275 280 285

Met His Phe Tyr Glu Ser Cys Pro Tyr Leu Lys Phe Ala His Phe Thr
290 295 300

Ala Asn Gln Ala Ile Leu Glu Ala Phe Ala Thr Ala Gly Lys Val His
305 310 315 320

Val Ile Asp Phe Gly Leu Lys Gln Gly Met Gln Trp Pro Ala Leu Met
325 330 335

Gln Ala Leu Ala Leu Arg Pro Gly Gly Pro Pro Thr Phe Arg Leu Thr
340 345 350

Gly Ile Gly Pro Pro Gln Pro Asp Asn Thr Asp Ala Leu Gln Gln Val
355 360 365

Gly Leu Lys Leu Ala Gln Leu Ala Gln Ile Ile Gly Val Gln Phe Glu
370 375 380

Phe Arg Gly Phe Val Cys Asn Ser Leu Ala Asp Leu Asp Pro Asn Met
385 390 395 400

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

Leu His Arg Met Leu Ala Arg Ser Gly Ser Val Asp Lys Val Leu Asp
420 425 430

Thr Val Lys Lys Ile Asn Pro Gln Ile Val Thr Ile Val Glu Gln Glu
435 440 445

Ala Asn His Asn Gly Pro Gly Phe Leu Asp Arg Phe Thr Glu Ala Leu
450 455 460

His Tyr Tyr Ser Ser Leu Phe Asp Ser Leu Glu Gly Ser Ser Ser Ser
465 470 475 480

Ser Thr Gly Leu Gly Ser Pro Ser Gln Asp Leu Leu Met Ser Glu Leu
485 490 495

Tyr Leu Gly Arg Gln Ile Cys Asn Val Val Ala Tyr Glu Gly Pro Asp
500 505 510

Arg Val Glu Arg His Glu Thr Leu Thr Gln Trp Arg Gly Arg Leu Asp
515 520 525

Ser Ala Gly Phe Asp Pro Val His Leu Gly Ser Asn Ala Phe Lys Gln
530 535 540

Ala Ser Met Leu Leu Ala Leu Phe Ala Gly Gly Asp Gly Tyr Arg Val
545 550 555 560

Glu Glu Asn Asn Gly Cys Leu Met Leu Gly Trp His Thr Arg Pro Leu
565 570 575

Ile Ala Thr Ser Ala Trp Lys Leu Pro Ser Ser Ser Glu Ser Ser Gly
580 585 590

Leu Thr Gln
595

<210> 794
<211> 563
<212> PRT
<213> Guandú

<400> 794

Met Lys Arg Asp His Glu Asp Arg Gly Gly Val Ser Ser Ser Met Ser
1 5 10 15

Asn Ser Ser Gly Lys Ala Lys Met Trp Glu Glu Glu Gln Gln Gln Gly
20 25 30

Gly Asn Asp Glu Leu Leu Ala Ala Leu Gly Tyr Lys Val Arg Ser Ser
35 40 45

Asp Met Ala Asp Val Ala Gln Lys Leu Glu Gln Leu Glu Met Val Met
50 55 60

Gly Ser Ala Gln Glu Glu Gly Ile Ser His Leu Ala Ser Asp Thr Val
65 70 75 80

His Tyr Asp Pro Thr Asp Leu Tyr Ser Trp Val Gln Thr Met Leu Thr
85 90 95

Glu Leu Asn Pro Pro Pro Asn Asn Leu Asp His Leu Leu Ile Gln Asp
100 105 110

Pro Ile Leu Thr Pro Ser Arg Val Phe Asn Asp Asp Ser Glu Tyr Asp
115 120 125

Leu Arg Ala Ile Pro Gly Ile Ala Ala Tyr Pro Pro Gln Asn Thr Asn
130 135 140

Asn Asn Ile Glu Glu Ile Glu Ala Asn Asn His Asn Asn Asn Asn Asn
145 150 155 160

Lys Arg Leu Lys Pro Ser Pro Ile Glu Ser Thr Asp Ser Val Ser Glu
165 170 175

Pro Thr Arg Pro Val Val Leu Val Asp Ser Gln Glu Thr Gly Val Arg
180 185 190

Leu Val His Thr Leu Met Ala Cys Ala Glu Ala Val Gln Gln Lys Asn
195 200 205

Leu Lys Leu Ala Glu Ala Leu Val Lys His Val Gly Ile Leu Ala Ala
210 215 220

Ser Gln Ala Gly Ala Met Arg Lys Val Ala Phe Tyr Phe Ala Gln Ala
225 230 235 240

Leu Ala His Arg Ile Tyr Gly Ala Phe Pro Glu Glu Pro Leu Asp Ser
245 250 255

Ser Phe Ser Asp Leu Leu His Met His Phe Tyr Glu Ser Cys Pro Tyr
260 265 270

Leu Lys Phe Ala His Phe Thr Ala Asn Gln Ala Ile Leu Glu Ala Phe
275 280 285

Ala Thr Ala Gly Arg Val His Val Ile Asp Phe Gly Leu Lys Gln Gly
290 295 300

Met Gln Trp Pro Ala Leu Met Gln Ala Leu Ala Leu Arg Pro Gly Gly
305 310 315 320

Pro Pro Thr Phe Arg Leu Thr Gly Ile Gly Pro Pro Gln Pro Asp Asn
325 330 335

Thr Asp Ala Leu Gln Gln Val Gly Leu Lys Leu Ala Gln Leu Ala Glu
340 345 350

Thr Ile Gly Val Arg Phe Glu Phe Arg Gly Phe Val Cys Asn Ser Leu
355 360 365

Ala Asp Leu Asp Pro Asn Met Leu Glu Ile Arg Pro Gly Glu Ala Val
370 375 380

Ala Val Asn Ser Val Phe Glu Leu His Arg Met Leu Ala Arg Pro Gly
385 390 395 400

Ser Val Glu Lys Val Leu Asp Thr Val Lys Lys Ile Lys Pro Lys Ile
405 410 415

Ile Thr Val Val Glu Gln Glu Ala Asn His Asn Gly Pro Val Phe Leu
420 425 430

Asp Arg Phe Thr Glu Ala Leu His Tyr Tyr Ser Ser Leu Phe Asp Ser
435 440 445

Leu Glu Gly Ser Ser Ser Ser Thr Gly Leu Gly Ser Pro Ser Gln Asp
450 455 460

His Leu Met Ser Glu Val Tyr Leu Gly Arg Gln Ile Cys Asn Val Val
465 470 475 480

Ala Tyr Glu Gly Val Asp Arg Val Glu Arg His Glu Thr Leu Thr Gln
485 490 495

Trp Arg Gly Arg Leu Gly Ser Gly Gly Phe Asp Pro Val His Leu Gly
500 505 510

Ser Asn Ala Phe Lys Gln Ala Ser Thr Leu Leu Ala Leu Phe Ala Gly
515 520 525

Gly Asp Gly Tyr Arg Val Glu Glu Asn Asn Gly Cys Leu Leu Leu Gly
530 535 540

Trp His Thr Arg Pro Leu Ile Ala Thr Ser Ala Trp Lys Leu Pro Ser
545 550 555 560

Ser Glu Ser

<210> 795
<211> 596
<212> PRT
<213> Poroto

<400> 795

Met Lys Arg Asp Phe Gln Gln Ala Cys Ala Gly Gly Pro Val Lys Gly
1 5 10 15

Asp Ser Ser Ser Met Pro Asn Gly Lys Ala Lys Met Trp Glu Glu Asp
20 25 30

Arg His Gln Gln Gly Gly Gly Met Asp Glu Leu Leu Ala Ala Leu Gly
35 40 45

Tyr Lys Val Arg Ala Ser Asp Met Ala Asp Val Ala Gln Lys Leu Glu
50 55 60

Gln Leu Glu Met Val Met Gly Ser Ala Gln Glu Glu Gly Ile Ser His
65 70 75 80

Leu Ser Ser Tyr Thr Val His Tyr Asp Pro Thr Asp Leu His Ser Trp
85 90 95

Val Gln Ser Met Leu Ser Glu Leu Asn Pro Glu Pro Thr Thr Ile Leu
100 105 110

Asp Pro Ser Ser Phe Leu Ile Asp Asn Pro Val His Ser Ser Pro Ile
115 120 125

Leu Thr Thr Thr Ser Arg Val Phe Asn Asp Asp Ser Glu Tyr Asp Leu
130 135 140

Arg Ala Ile Pro Gly Ile Ala Ala Tyr Pro Pro Gln His Ala Thr Asn
145 150 155 160

Asn Ala Thr Thr Ile Ser Thr Thr Thr Ala Thr Ser Pro Thr Thr Thr
165 170 175

Val Ala Thr Thr Asn Thr Gln Thr Val Glu Glu Ile Glu Pro Gly Thr
180 185 190

Asn Lys Arg Leu Lys Ala Ser Pro Ile Glu Ser Ser Glu Ser Ala Ser
195 200 205

Glu Pro Thr Arg Pro Val Val Leu Val Asp Ser Gln Glu Ala Gly Val
210 215 220

Arg Leu Val His Thr Leu Met Ala Cys Ala Glu Ala Val Gln Gln Glu
225 230 235 240

Asn Leu Lys Leu Ala Asp Ala Leu Val Lys His Val Gly Ile Leu Ala
245 250 255

Ala Ser Gln Ala Gly Ala Met Arg Lys Val Ala Thr Tyr Phe Ala Gln
260 265 270

Ala Leu Ala Arg Arg Ile Tyr Gly Ile Phe Pro Glu Glu Thr Leu Asp
275 280 285

Ser Ser Leu Ser Asp Leu Leu His Met His Phe Tyr Glu Ser Cys Pro
290 295 300

Tyr Leu Lys Phe Ala His Phe Thr Ala Asn Gln Ala Ile Leu Glu Ala
305 310 315 320

Phe Ala Thr Ala Gly Arg Val His Val Ile Asp Phe Gly Leu Lys Gln
325 330 335

Gly Met Gln Trp Pro Ala Leu Met Gln Ala Leu Ala Leu Arg Pro Gly
340 345 350

Gly Pro Pro Thr Phe Arg Leu Thr Gly Ile Gly Pro Pro Gln Pro Asp
355 360 365

Asn Thr Asp Ala Leu Gln Gln Val Gly Trp Lys Leu Ala Gln Leu Ala
370 375 380

Gln Thr Ile Gly Val Gln Phe Glu Phe Arg Gly Phe Val Cys Ser Ser
385 390 395 400

Leu Ala Asp Leu Asp Pro Asn Met Leu Glu Ile Arg Pro Gly Glu Ala
405 410 415

Val Ala Val Asn Ser Val Phe Glu Leu His Arg Met Leu Ala Arg Pro
420 425 430

Gly Ser Val Asp Lys Val Met Asp Thr Val Lys Asn Leu Asn Pro Lys
435 440 445

Ile Val Thr Ile Val Glu Gln Glu Ala Asn His Asn Gly Pro Val Phe
450 455 460

Leu Asp Arg Phe Thr Glu Ala Leu His Tyr Tyr Ser Ser Leu Phe Asp
465 470 475 480

Ser Leu Glu Gly Ser Ser Ser Ser Thr Gly Leu Gly Ser Pro Ser Gln
485 490 495

Asp Leu Leu Met Ser Glu Val Tyr Leu Gly Lys Gln Ile Cys Asn Val
500 505 510

Val Ala Tyr Glu Gly Val Glu Arg Val Glu Arg His Glu Thr Leu Ser
515 520 525

Gln Trp Arg Gly Arg Met Gly Ser Ala Gly Phe Asp Pro Val His Leu
530 535 540

Gly Ser Asn Ala Phe Lys Gln Ala Ser Met Leu Leu Ala Leu Phe Ala
545 550 555 560

Gly Gly Asp Gly Tyr Arg Val Glu Glu Asn Asn Gly Cys Leu Met Leu
565 570 575

Gly Trp His Thr Arg Pro Leu Ile Ala Thr Ser Ala Trp Lys Leu Pro
580 585 590

Ser Pro Glu Ser
595

<210> 796
<211> 1010
<212> PRT
<213> Soja

<400> 796

Leu Ser Leu Tyr Phe Phe Ser Val Val Gly Gln Leu Pro Ser Gln Asp
1 5 10 15

Ile Leu Ala Leu Leu Glu Phe Lys Lys Gly Ile Lys His Asp Pro Thr
20 25 30

Gly Tyr Val Leu Asn Ser Trp Asn Glu Glu Ser Ile Asp Phe Asp Gly
35 40 45

Cys Pro Ser Ser Trp Asn Gly Val Leu Cys Asn Ala Gly Asn Val Ala
50 55 60

Gly Val Val Leu Asp Asn Leu Gly Leu Ser Ala Asp Pro Asp Leu Ser
65 70 75 80

Val Phe Ser Asn Leu Thr Lys Leu Leu Arg Ser Leu Gln Asn Leu Ser
85 90 95

Leu Ala Gly Asn Asn Phe Ser Gly Pro Ile Pro Asp Ser Ile Ser Glu
100 105 110

Met Ala Ser Ile Lys Ser Leu Asp Leu Ser Arg Asn Ser Phe Ser Gly

115 120 125

Met Leu Pro Val Thr Leu Thr Lys Thr Thr Ser Leu Val Ser Leu Asn
130 135 140

Leu Ser His Asn Gly Phe Thr Gly Lys Val Pro Lys Gly Phe Glu Leu
145 150 155 160

Ile Pro Ala Leu Glu Lys Leu Asp Leu His Gly Asn Met Leu Glu Gly
165 170 175

Asn Leu Asp Val Val Phe Met Leu Leu Ser Ser Ala Ser Tyr Val Asp
180 185 190

Leu Ser Glu Asn Met Leu Ser Ser Ser Asp Ser Lys Lys Lys Phe Leu
195 200 205

Pro Arg Ile Ser Glu Ser Ile Lys His Leu Asn Leu Ser His Asn Lys
210 215 220

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

Leu Lys Val Leu Asp Leu Ser Tyr Asn Gln Leu Asp Gly Glu Leu Pro
245 250 255

Gly Phe Asp Phe Val Tyr Asp Leu Glu Val Leu Arg Leu Ser Asn Asn

260 265 270

Arg Phe Ser Gly Phe Ile Pro Asn Gly Leu Leu Lys Gly Asp Ser Leu
275 280 285

Val Leu Thr Glu Leu Asp Leu Ser Ala Asn Asn Leu Ser Gly Pro Leu
290 295 300

Ser Ile Ile Thr Ser Thr Thr Leu His Ser Leu Asn Leu Ser Ser Asn
305 310 315 320

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

Asp Leu Ser Asn Asn Lys Leu Glu Gly Asn Leu Thr Arg Met Leu Lys
340 345 350

Trp Gly Asn Ile Glu Phe Leu Asp Leu Ser Gly Asn His Leu Thr Gly
355 360 365

Thr Ile Pro Glu Glu Thr Pro Gln Phe Leu Arg Leu Ser Tyr Leu Asn
370 375 380

Leu Ser His Asn Ser Leu Ser Ser Ser Leu Pro Lys Val Leu Thr Gln
385 390 395 400

Tyr Pro Lys Leu Arg Val Leu Asp Ile Ser Phe Asn Gln Leu Asp Gly

405 410 415

Leu Leu Leu Ala Asn Leu Leu Thr Leu Ser Thr Leu Gln Glu Leu His
420 425 430

Leu Glu Asn Asn Met Ile Ser Gly Gly Ile Lys Phe Ser Ser Ser Ala
435 440 445

Asp Gln Ser Asp Leu Gln Ile Leu Asp Leu Ser His Asn Gln Leu Asn
450 455 460

Gly Tyr Phe Pro Asp Glu Phe Gly Ser Leu Thr Gly Leu Lys Val Leu
465 470 475 480

Asn Ile Ala Gly Asn Asn Phe Ser Gly Ser Leu Pro Thr Thr Ile Ala
485 490 495

Asp Met Ser Ser Leu Asp Ser Leu Asp Ile Ser Glu Asn His Phe Ala
500 505 510

Gly Pro Leu Pro Ser Asn Ile Pro Lys Gly Leu Gln Asn Phe Asn Ala
515 520 525

Ser Gln Asn Asp Leu Ser Gly Leu Val Pro Glu Val Leu Arg Lys Phe
530 535 540

Pro Ser Ser Ser Phe Phe Pro Gly Asn Thr Lys Leu His Phe Pro Asn

545 550 555 560

Gly Pro Pro Gly Ser Val Ser Ser Pro Ala Lys Ser Ser Lys Arg Lys
565 570 575

His Met Asn Thr Ile Val Lys Val Ile Ile Ile Val Ser Cys Val Val
580 585 590

Ala Leu Phe Ile Leu Ile Leu Leu Ala Val Phe Ile His Tyr Ile Arg
595 600 605

Ile Ser Arg Ser Pro Gln Glu Tyr Asp Ala Ser Lys Asp Ile His Arg
610 615 620

His Pro Gln Pro Ile Ile Ser Ala Pro Val Arg Thr Thr Asp Arg Gly
625 630 635 640

Gly Ala Leu Val Val Ser Ala Glu Asp Leu Val Thr Ser Arg Lys Glu
645 650 655

Ser Pro Ser Glu Ile Ile Ser Ser Asp Glu Lys Met Ala Ala Val Thr
660 665 670

Gly Phe Ser Pro Ser Lys Gln Ser His Phe Ser Trp Ser Pro Glu Ser
675 680 685

Gly Asp Ser Leu Thr Gly Glu Asn Leu Ala Arg Leu Asp Thr Arg Ser

690 695 700

Pro Asp Arg Leu Ile Gly Glu Leu His Phe Leu Asp Asp Thr Ile Thr
705 710 715 720

Leu Thr Pro Glu Glu Leu Ser Arg Ala Pro Ala Glu Val Leu Gly Arg
725 730 735

Ser Ser His Gly Thr Ser Tyr Lys Ala Thr Leu Glu Asn Gly Leu Leu
740 745 750

Leu Arg Val Lys Trp Leu Arg Glu Gly Val Ala Lys Gln Arg Lys Glu
755 760 765

Phe Val Lys Glu Met Lys Lys Phe Ala Asn Ile Arg His Pro Asn Val
770 775 780

Val Gly Leu Arg Gly Tyr Tyr Trp Gly Pro Thr Gln His Glu Lys Leu
785 790 795 800

Ile Leu Ser Asp Tyr Ile Ser Pro Gly Ser Leu Ala Ser Phe Leu Tyr
805 810 815

Asp Arg Pro Gly Arg Lys Gly Pro Pro Leu Thr Trp Ala Gln Arg Leu
820 825 830

Lys Ile Ala Val Asp Val Ala Arg Gly Leu Asn Tyr Leu His Phe Asp

835 840 845

Arg Ala Val Pro His Gly Asn Leu Lys Ala Thr Asn Val Leu Leu Asp
850 855 860

Thr Thr Asp Met Asn Ala Arg Val Ala Asp Tyr Cys Leu His Arg Leu
865 870 875 880

Met Thr Arg Ala Gly Asn Ile Glu Gln Ile Leu Asp Ala Gly Val Leu
885 890 895

Gly Tyr Arg Ala Pro Glu Leu Ala Ala Ser Lys Lys Pro Met Pro Ser
900 905 910

Phe Lys Ser Asp Val Tyr Ala Phe Gly Val Ile Leu Leu Glu Leu Leu
915 920 925

Thr Gly Arg Cys Ala Gly Asp Val Ile Ser Ser Glu Glu Gly Gly Val
930 935 940

Asp Leu Thr Asp Trp Val Arg Leu Arg Val Ala Glu Gly Arg Gly Ser
945 950 955 960

Glu Cys Phe Asp Ala Thr Leu Met Pro Glu Met Ser Asn Pro Ile Ala
965 970 975

Glu Lys Gly Met Lys Glu Val Leu Gly Ile Val Met Arg Cys Ile Arg

980 985 990

Ser Val Ser Glu Arg Pro Gly Ile Lys Thr Ile Tyr Glu Asp Leu Ser
995 1000 1005

Ser Ile
1010

<210> 797
<211> 1061
<212> PRT
<213> Poroto

<400> 797

Met Lys Leu Phe Ser Leu Leu Val Leu Ser Leu Tyr Phe Phe Ser Val
1 5 10 15

Val Gly Gln Leu Pro Ser Gln Asp Ile Leu Ala Leu Leu Glu Phe Lys
20 25 30

Lys Gly Val Lys His Asp Pro Ser Gly Tyr Val Leu Asn Ser Trp Asn
35 40 45

Glu Glu Ser Ile Asp Phe Asp Gly Cys Pro Ser Ser Trp Asn Gly Val
50 55 60

Leu Cys Asn Gly Gly Asn Val Ala Gly Val Val Leu Asp Asn Leu Gly
65 70 75 80

Leu Ser Ala Asp Thr Asp Leu Ser Met Phe Ser Asn Leu Thr Lys Leu
85 90 95

Val Lys Leu Ser Met Ala Asn Asn Ser Ile Thr Gly Ser Leu His Gly
100 105 110

Ser Ile Ala Glu Phe Lys Ser Leu Glu Phe Leu Asp Ile Ser Asn Asn
115 120 125

Leu Phe Ser Ser Ser Leu Pro Leu Asn Ile Gly Lys Leu Ser Ser Leu
130 135 140

Gln Asn Leu Ser Leu Ala Gly Asn Asn Phe Ser Gly Pro Ile Pro Asp
145 150 155 160

Ser Ile Ser Glu Met Ala Ser Ile Lys Ser Leu Asp Leu Ser Arg Asn
165 170 175

Ser Phe Ser Gly Glu Leu Pro Val Leu Leu Thr Lys Val Thr Ser Leu
180 185 190

Val Ser Leu Asn Leu Ser His Asn Gly Phe Thr Gly Lys Ile Pro Lys
195 200 205

Gly Phe Glu Met Ile Thr Val Leu Glu Lys Leu Asp Leu His Gly Asn
210 215 220

Met Leu Glu Gly Asn Leu Asp Val Glu Phe Leu Leu Leu Ser Ser Ala
225 230 235 240

Ser Tyr Val Asp Leu Ser Glu Asn Arg Leu Ser Ser Ser Asp Ser Lys
245 250 255

Gln Lys Phe Leu Pro Arg Leu Ser Glu Ser Ile Lys His Leu Asn Leu
260 265 270

Ser His Asn Gln Leu Thr Gly Ser Leu Ala Ser Gly Val Ala Glu Pro
275 280 285

Val Phe Glu Asn Leu Lys Val Leu Asp Leu Ser Tyr Asn Gln Leu Asp
290 295 300

Gly Glu Leu Pro Gly Phe Asp Phe Val Tyr Asp Leu Gln Val Leu Arg
305 310 315 320

Leu Ser Asn Asn Met Phe Ser Gly Phe Ile Pro Asn Gly Leu Leu Lys
325 330 335

Gly Asp Ser Leu Val Leu Thr Glu Leu Asp Leu Ser Ala Asn Asn Leu
340 345 350

Ser Gly Pro Leu Ser Ile Ile Thr Ser Thr Thr Leu His Ser Leu Asn
355 360 365

Leu Ser Ser Asn Gln Phe Thr Gly Glu Leu Pro Pro Leu Thr Gly Ser
370 375 380

Cys Ala Val Leu Asp Leu Ser Thr Asn Lys Leu Glu Gly Asn Leu Thr
385 390 395 400

Arg Met Leu Lys Trp Gly Asn Ile Glu Phe Leu Asp Leu Ser Gly Asn
405 410 415

His Leu Met Gly Thr Ile Pro Glu Glu Thr Pro Gln Phe Leu Arg Leu
420 425 430

Asn Tyr Leu Asn Leu Ser His Asn Ser Leu Ser Ser Ser Leu Pro Lys
435 440 445

Val Leu Thr Gln Tyr Pro Lys Leu Arg Val Leu Asp Ile Ser Phe Asn
450 455 460

Gln Leu Asp Gly Pro Leu Leu Ser Gly Leu Leu Thr Met Ser Thr Leu
465 470 475 480

Arg Glu Leu His Leu Glu Asn Asn Val Ile Ser Gly Gly Ile Asn Phe
485 490 495

Ser Ser Pro Asp Gln Ser Asp Leu Gln Ile Leu Asp Leu Ser His Asn
500 505 510

Gln Leu Asn Gly Tyr Phe Pro Asp Lys Phe Gly Ser Leu Thr Gly Leu
515 520 525

Lys Val Leu Asn Ile Ala Gly Asn Asn Phe Ser Gly Ser Leu Pro Thr
530 535 540

Thr Ile Ala Asp Met Asn Ser Leu Asp Ser Met Asp Ile Ser Glu Asn
545 550 555 560

His Phe Thr Gly Pro Leu Pro Asp Asn Met Pro Gln Gly Leu Gln Asn
565 570 575

Phe Asn Ala Ser Glu Asn Asp Leu Ser Gly Leu Val Pro Glu Val Leu
580 585 590

Arg Lys Phe Pro Ser Ser Ser Phe Phe Pro Gly Asn Ser Lys Leu His
595 600 605

Phe Pro Asn Gly Pro Pro Gly Ser Thr Ala Ser Pro Ala Glu Ser Ser
610 615 620

Lys Arg Lys His Leu Asn Thr Ile Val Lys Val Ile Ile Ile Val Ser
625 630 635 640

Cys Val Val Ala Leu Phe Ile Leu Ile Leu Leu Ala Val Phe Ile His
645 650 655

Tyr Ile Arg Ile Ser Arg Ser Pro Pro Glu Tyr Asp Thr Ser Lys Asp
660 665 670

Ile His Arg His Pro Gln Pro Ile Ile Ser Ala Pro Val Arg Thr Thr
675 680 685

Asp Arg Gly Gly Ala Leu Val Val Ser Ala Glu Asp Leu Val Thr Thr
690 695 700

Arg Lys Glu Ser Pro Ser Glu Val Ile Ser Ser Asp Glu Lys Ile Ala
705 710 715 720

Ala Val Thr Gly Phe Ser Pro Ser Lys Gln Ser His Phe Ser Trp Ser
725 730 735

Pro Glu Ser Gly Asp Ser Phe Thr Gly Glu Asn Leu Ala Arg Leu Asp
740 745 750

Thr Arg Ser Pro Asp Arg Leu Ile Gly Glu Leu His Phe Leu Asp Asp
755 760 765

Ser Ile Thr Leu Thr Pro Glu Glu Leu Ser Arg Ala Pro Ala Glu Val
770 775 780

Leu Gly Arg Ser Ser His Gly Thr Ser Tyr Lys Ala Thr Leu Glu Asn
785 790 795 800

Gly Leu Leu Leu Arg Val Lys Trp Leu Arg Glu Gly Val Ala Lys Gln
805 810 815

Arg Lys Glu Phe Val Lys Glu Thr Lys Lys Phe Ala Asn Ile Arg His
820 825 830

Pro Asn Val Val Gly Leu Arg Gly Tyr Tyr Trp Gly Pro Thr Gln His
835 840 845

Glu Lys Leu Ile Leu Ser Asp Tyr Ile Ser Pro Gly Ser Leu Ala Ser
850 855 860

Phe Leu Tyr Asp Arg Pro Gly Arg Lys Gly Pro Pro Leu Thr Trp Ile
865 870 875 880

Gln Arg Leu Lys Ile Ala Val Asp Val Ala Arg Gly Leu Asn Tyr Leu
885 890 895

His Phe Asp Arg Ala Ile Pro His Gly Asn Leu Lys Ala Thr Asn Val
900 905 910

Leu Leu Asp Thr Thr Asp Met Asn Ala Arg Val Ala Asp Tyr Cys Leu
915 920 925

His Arg Leu Met Thr Gln Ala Gly Thr Ile Glu Gln Ile Leu Asp Ala
930 935 940

Gly Val Leu Gly Tyr Arg Ala Pro Glu Leu Ala Ser Ser Lys Lys Pro
945 950 955 960

Met Pro Ser Phe Lys Ser Asp Val Tyr Ala Phe Gly Val Ile Leu Leu
965 970 975

Glu Leu Leu Thr Gly Arg Cys Ala Gly Asp Val Ile Ser Ser Glu Glu
980 985 990

Gly Gly Val Asp Leu Thr Asp Trp Val Arg Val Arg Val Ala Glu Gly
995 1000 1005

Arg Gly Ser Glu Cys Phe Asp Ala Thr Leu Met Pro Glu Met Ser
1010 1015 1020

Asn Pro Ile Val Glu Lys Gly Met Lys Glu Val Leu Gly Ile Ala
1025 1030 1035

Met Arg Cys Ile Arg Ser Val Ser Glu Arg Pro Gly Ile Lys Thr
1040 1045 1050

Ile Tyr Glu Asp Leu Ser Ser Ile
1055 1060

<210> 798
<211> 1045

<212> PRT
<213> Guandú

<400> 798

Gly Gln Leu Pro Ser Gln Asp Ile Leu Ala Leu Leu Glu Phe Lys Lys
1 5 10 15

Gly Ile Lys His Asp Pro Thr Gly Tyr Val Leu Asn Ser Trp Asn Glu
20 25 30

Glu Ser Ile Asp Phe Asp Gly Cys Pro Ser Ser Trp Asn Gly Val Leu
35 40 45

Cys Asn Gly Gly Asn Val Ala Gly Val Val Leu Asp Asn Leu Gly Leu
50 55 60

Ser Ala Asp Thr Asp Leu Ser Val Phe Ser Asn Leu Thr Lys Leu Val
65 70 75 80

Lys Leu Ser Met Ala Asn Asn Ser Ile Ser Gly Lys Leu Pro Asp Asn
85 90 95

Ile Ala Asp Phe Lys Ser Leu Glu Phe Leu Asp Ile Ser Asn Asn Leu
100 105 110

Phe Ser Ser Ser Leu Pro Leu Gly Ile Gly Lys Leu Gly Ser Leu Gln
115 120 125

Asn Leu Ser Leu Ala Gly Asn Asn Phe Ser Gly Pro Ile Pro Asp Ser
130 135 140

Ile Ser Gln Met Ala Ser Ile Lys Ser Leu Asp Leu Ser Arg Asn Ser
145 150 155 160

Phe Ser Gly Ala Leu Pro Ala Ser Leu Thr Glu Val Asn Ser Leu Val
165 170 175

Ser Leu Asn Leu Ser His Asn Gly Phe Thr Gly Lys Ile Pro Lys Gly
180 185 190

Phe Glu Leu Ile Pro Ala Leu Glu Lys Leu Asp Leu His Gly Asn Met
195 200 205

Leu Glu Gly Asn Leu Asp Val Glu Phe Met Leu Leu Ser Ser Ala Ser
210 215 220

Tyr Val Asp Leu Ser Glu Asn Met Leu Ser Ser Ser Asp Ser Lys Gln
225 230 235 240

Lys Phe Leu Pro Arg Leu Ser Glu Ser Ile Lys His Leu Asn Leu Ser
245 250 255

His Asn Gln Leu Thr Gly Ser Leu Ala Ser Gly Ala Thr Glu Pro Val
260 265 270

Phe Glu Asn Leu Lys Val Leu Asp Leu Ser Tyr Asn Gln Leu Asp Gly
275 280 285

Glu Leu Pro Gly Phe Asp Phe Val Tyr Asp Leu Glu Val Leu Arg Leu
290 295 300

Ser Asn Asn Arg Phe Ser Gly Phe Ile Pro Thr Gly Leu Leu Lys Gly
305 310 315 320

Asp Ser Leu Val Leu Thr Glu Leu Asp Leu Ser Ala Asn Asn Leu Thr
325 330 335

Gly Ser Leu Ser Ile Ile Ile Ser Thr Thr Leu Arg Ser Leu Asn Leu
340 345 350

Ser Ser Asn Glu Phe Thr Gly Glu Leu Pro Leu Leu Thr Gly Thr Cys
355 360 365

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

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

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

Tyr Leu Asn Leu Ser His Asn Ser Leu Thr Ser Ser Leu Pro Lys Val
420 425 430

Ile Thr Gln Tyr Pro Lys Leu Arg Val Leu Asp Ile Ser Phe Asn Gln
435 440 445

Leu Asp Gly Leu Leu Arg Ala Gly Leu Leu Thr Met Pro Thr Met Gln
450 455 460

Glu Leu His Leu Glu Asn Asn Met Ile Ser Gly Gly Ile Asn Leu Ser
465 470 475 480

Ser Ser Leu Gly Gln Ser Asp Leu Gln Ile Leu Asp Leu Ser His Asn
485 490 495

Gln Leu Asn Gly Tyr Phe Pro Asp Glu Phe Gly Ser Leu Thr Gly Leu
500 505 510

Lys Val Leu Asn Ile Ala Gly Asn Asn Phe Ser Gly Ser Leu Pro Thr
515 520 525

Thr Ile Ala Asp Met Ser Ser Leu Asp Ser Ile Asp Ile Ser Glu Asn
530 535 540

His Phe Thr Gly Pro Leu Pro Asn Asn Met Pro Lys Gly Ile Gln Ser
545 550 555 560

Phe Asn Ala Ser Gln Asn Asp Leu Ser Gly Val Val Pro Glu Val Leu
565 570 575

Arg Lys Phe Pro Ser Ser Ser Phe Phe Pro Gly Asn Thr Lys Leu His
580 585 590

Phe Pro Asn Gly Pro Pro Gly Ser Thr Ser Ser Pro Ala Glu Ser Ser
595 600 605

Lys Arg Arg His Met Asn Thr Ile Val Lys Val Ile Ile Ile Val Ser
610 615 620

Cys Val Val Ala Leu Phe Ile Leu Ile Leu Leu Ala Val Phe Ile His
625 630 635 640

Tyr Ile Arg Ile Ser Arg Ser Pro Pro Glu Tyr Asp Thr Gly Lys Asp
645 650 655

Val His Arg Arg Pro Gln Pro Ile Ile Ser Ala Pro Val Arg Thr Thr
660 665 670

Asp Arg Gly Gly Ala Leu Val Val Ser Thr Glu Asp Leu Val Thr Ser
675 680 685

His Lys Glu Ser Pro Ser Glu Ile Val Thr Pro Asp Glu Lys Met Ala
690 695 700

Ala Val Thr Gly Phe Ser Pro Ser Lys Gln Ser His Phe Ser Trp Ser
705 710 715 720

Pro Glu Ser Gly Asp Ser Phe Thr Gly Glu Asn Leu Ala Arg Leu Asp
725 730 735

Thr Arg Ser Pro Asp Arg Leu Ile Gly Glu Leu His Phe Leu Asp Asp
740 745 750

Thr Ile Thr Leu Thr Pro Glu Glu Leu Ser Arg Ala Pro Ala Glu Val
755 760 765

Leu Gly Arg Ser Ser His Gly Thr Ser Tyr Lys Ala Thr Leu Asp Asn
770 775 780

Gly Leu Leu Leu Arg Val Lys Trp Leu Arg Glu Gly Val Ala Lys Gln
785 790 795 800

Arg Lys Glu Phe Val Lys Glu Thr Lys Lys Phe Ala Asn Ile Arg His
805 810 815

Pro Asn Val Val Gly Leu Arg Gly Tyr Tyr Trp Gly Pro Thr Gln His
820 825 830

Glu Lys Leu Ile Leu Ser Asp Tyr Ile Ser Pro Gly Ser Leu Ala Ser
835 840 845

Phe Leu Tyr Asp Arg Pro Gly Arg Lys Gly Pro Pro Leu Thr Trp Ser
850 855 860

Gln Arg Leu Lys Ile Ala Val Asp Val Ala Arg Gly Leu Asn Tyr Leu
865 870 875 880

His Phe Asp Arg Ala Ile Pro His Gly Asn Leu Lys Ala Thr Asn Val
885 890 895

Leu Leu Asp Thr Thr Asp Met Asn Ala Arg Val Ala Asp Tyr Cys Leu
900 905 910

His Arg Leu Met Thr Gln Ala Gly Thr Ile Glu Gln Ile Leu Asp Ala
915 920 925

Gly Val Leu Gly Tyr Arg Ala Pro Glu Leu Ala Ala Ser Lys Lys Pro
930 935 940

Met Pro Ser Phe Lys Ser Asp Val Tyr Ala Phe Gly Val Ile Leu Leu
945 950 955 960

Glu Leu Leu Thr Gly Arg Cys Ala Gly Asp Val Ile Ser Ser Glu Glu
965 970 975

Gly Gly Val Asp Leu Thr Asp Trp Val Arg Leu Arg Val Ala Glu Gly
980 985 990

Arg Gly Ser Glu Cys Phe Asp Ala Ala Leu Met Ser Glu Thr Gly Asn
995 1000 1005

Ala Val Val Glu Lys Gly Met Lys Glu Val Leu Gly Ile Ala Met
1010 1015 1020

Arg Cys Ile Arg Ser Val Ser Glu Arg Pro Gly Ile Lys Thr Ile
1025 1030 1035

Tyr Glu Asp Leu Ser Ser Ile
1040 1045

<210> 799
<211> 976
<212> PRT
<213> Soja

<400> 799

Gln Leu Pro Ser Gln Asp Ile Leu Thr Leu Leu Glu Phe Lys Lys Gly
1 5 10 15

Ile Lys His Asp Pro Thr Gly Tyr Val Leu Asn Ser Trp Asn Glu Glu
20 25 30

Ser Ile Asp Phe Asp Gly Cys Pro Ser Ser Trp Asn Gly Val Leu Cys
35 40 45

Asn Gly Gly Asn Val Ala Gly Val Val Leu Asp Asn Leu Gly Leu Ser
50 55 60

Ala Asp Thr Asp Leu Ser Val Phe Thr Asn Leu Thr Lys Leu Val Lys
65 70 75 80

Leu Ser Leu Ser Asn Asn Ser Ile Ser Gly Thr Leu Leu Asp Ser Ile
85 90 95

Ala Asp Phe Lys Ser Leu Glu Phe Leu Asp Ile Ser Tyr Asn Leu Phe
100 105 110

Ser Ser Ser Leu Pro Leu Gly Ile Gly Lys Leu Gly Ser Leu Gln Asn
115 120 125

Leu Ser Leu Ala Gly Asn Asn Phe Ser Gly Pro Ile Pro Asp Ser Ile
130 135 140

Ser Glu Met Ala Ser Ile Lys Ser Leu Asp Leu Ser Cys Asn Ala Phe
145 150 155 160

Ser Gly Met Leu Pro Ala Ser Leu Thr Lys Thr Ile Ser Leu Val Ser
165 170 175

Leu Asn Leu Ser His Asn Gly Phe Asn Gly Lys Ile Pro Lys Gly Leu
180 185 190

Glu Leu Ile Pro Ala Leu Glu Lys Leu Asp Leu His Gly Asn Met Leu
195 200 205

Glu Gly Asn Leu Asp Val Val Phe Met Leu Ser Ser Ser Ala Ser Tyr
210 215 220

Val Asp Leu Ser Glu Asn Met Leu Ser Ser Ser Asp Ser Asn Gln Lys
225 230 235 240

Phe Leu Pro Arg Ile Ser Glu Ser Ile Lys His Leu Asn Leu Ser His
245 250 255

Asn Lys Leu Thr Gly Ser Leu Ala Ser Gly Ala Ala Glu Pro Val Phe
260 265 270

Glu Asn Leu Lys Val Leu Asp Leu Ser Tyr Asn Gln Leu Asp Gly Glu
275 280 285

Leu Pro Gly Phe Asp Phe Val Tyr Asp Leu Glu Val Leu Lys Leu Ser
290 295 300

Asn Asn Arg Phe Ser Gly Phe Ile Pro Asn Gly Leu Leu Lys Gly Asp
305 310 315 320

Ser Leu Val Leu Thr Glu Leu Asp Leu Ser Ala Asn Asn Leu Ser Gly
325 330 335

Pro Leu Ser Ile Ile Thr Ser Thr Thr Leu His Ser Leu Asn Leu Ser
340 345 350

Ser Asn Glu Phe Thr Gly Asp Met Pro Leu Leu Thr Gly Ser Cys Ala
355 360 365

Val Leu Asp Leu Ser Asn Asn Lys Leu Glu Gly Asn Leu Thr Arg Met
370 375 380

Leu Lys Trp Gly Asn Ile Glu Phe Leu Asp Leu Ser Arg Asn His Leu
385 390 395 400

Thr Gly Ala Ile Pro Glu Glu Thr Pro Gln Phe Leu Arg Leu Asn Tyr
405 410 415

Leu Asn Leu Ser His Asn Ser Leu Ser Ser Ser Leu Pro Lys Val Leu
420 425 430

Thr Gln Tyr Pro Lys Leu Arg Val Leu Asp Ile Ser Phe Asn Gln Leu
435 440 445

Asp Gly Leu Leu Pro Ala Asn Leu Leu Thr Leu Pro Thr Leu Gln Glu
450 455 460

Leu Arg Leu Glu Asn Asn Met Ile Ser Gly Gly Ile Lys Phe Ser Ser
465 470 475 480

Ser Pro Asp Gln Ser Asp Leu Gln Ile Leu Asp Leu Ser His Asn Gln
485 490 495

Leu Asn Gly Tyr Phe Pro Asp Glu Phe Gly Ser Leu Thr Gly Leu Lys
500 505 510

Val Leu Asn Ile Ala Gly Asn Asn Phe Ser Gly Ser Leu Pro Thr Thr
515 520 525

Ile Ala Asp Met Ser Ser Leu Asp Ser Leu Asp Ile Ser Glu Asn His
530 535 540

Phe Thr Gly Pro Leu Pro Ser Asn Met Pro Lys Gly Leu Gln Asn Phe
545 550 555 560

Asn Ala Ser Gln Asn Asp Leu Ser Gly Val Val Pro Glu Val Leu Arg
565 570 575

Lys Phe Pro Ser Ser Ser Phe Phe Pro Gly Asn Thr Lys Leu His Phe
580 585 590

Pro Asn Gly Pro Pro Gly Ser Ile Ser Ser Pro Ala Glu Ser Ser Lys
595 600 605

Arg Lys His Met Asn Thr Ile Val Lys Val Ile Ile Ile Val Ser Cys
610 615 620

Val Val Ala Leu Phe Ile Leu Ile Leu Leu Ala Val Phe Ile His Tyr
625 630 635 640

Ile Arg Phe Ser Pro Ser Lys Gln Ser His Phe Ser Trp Ser Pro Glu
645 650 655

Ser Gly Asp Ser Leu Ser Gly Glu Asn Leu Ala Arg Leu Asp Thr Arg
660 665 670

Ser Pro Asp Arg Leu Val Gly Glu Leu His Phe Leu Asp Asp Thr Ile
675 680 685

Thr Leu Thr Pro Glu Glu Leu Ser Arg Ala Pro Ala Glu Val Leu Gly
690 695 700

Arg Ser Ser His Gly Thr Ser Tyr Lys Ala Thr Leu Glu Asn Gly Leu
705 710 715 720

Leu Leu Arg Val Lys Trp Leu Arg Glu Gly Val Ala Lys Gln Arg Lys
725 730 735

Glu Phe Val Lys Glu Thr Lys Lys Phe Ala Asn Ile Arg His Pro Asn
740 745 750

Val Val Gly Leu Arg Gly Tyr Tyr Trp Gly Pro Thr Gln His Glu Lys
755 760 765

Leu Ile Leu Ser Asp Tyr Ile Ser Leu Gly Ser Leu Ala Ser Phe Leu
770 775 780

Tyr Gly Arg Lys Gly Pro Pro Leu Thr Trp Thr Gln Arg Leu Lys Ile
785 790 795 800

Ala Val Asp Val Ala Arg Gly Leu Asn Tyr Leu His Phe Asp Arg Ala
805 810 815

Val Pro His Gly Asn Leu Lys Ala Thr Asn Val Leu Leu Asp Thr Thr
820 825 830

Asp Met Asn Ala Arg Val Ala Asp Tyr Cys Leu His Arg Leu Met Thr
835 840 845

Gln Ala Gly Thr Ile Glu Gln Ile Leu Asp Ala Gly Val Leu Gly Tyr
850 855 860

Cys Ala Pro Glu Leu Ala Ala Ser Lys Lys Pro Met Pro Ser Phe Lys
865 870 875 880

Ser Asp Val Tyr Ala Phe Gly Val Ile Leu Leu Glu Leu Leu Thr Gly
885 890 895

Arg Cys Ala Gly Asp Val Ile Ser Ser Glu Glu Gly Gly Val Asp Leu
900 905 910

Thr Asp Trp Val Arg Leu Arg Val Ala Glu Gly Arg Gly Ser Glu Cys
915 920 925

Phe Glu Ala Thr Leu Met Pro Glu Met Ser Asn Pro Val Val Glu Lys
930 935 940

Gly Met Lys Glu Val Leu Gly Ile Ala Met Arg Cys Ile Arg Ser Ile
945 950 955 960

Ser Glu Arg Pro Gly Ile Lys Thr Ile Tyr Glu Asp Leu Ser Ser Ile
965 970 975

<210> 800
<211> 508
<212> PRT
<213> Garbanzo

<400> 800

Met Gly Gln Leu Pro Ser Gln Asp Ile Leu Ala Leu Leu Glu Phe Lys
1 5 10 15

Lys Cys Ile Lys His Asp Pro Thr Gly Tyr Val Leu Asn Ser Trp Asn
20 25 30

Glu Glu Ser Ile Asp Phe Asp Gly Cys Pro Ser Ser Trp Asn Gly Val
35 40 45

Leu Cys Asn Gly Gly Asn Val Ala Gly Val Val Leu Asp Asn Leu Gly

50 55 60

Leu Ser Ala Asp Thr Asp Leu Ser Val Phe Ser Asn Leu Ser Lys Leu
65 70 75 80

Val Lys Leu Ser Met Ala Asn Asn Ser Ile Ser Gly Lys Leu Thr Asn
85 90 95

Asn Val Ala Asp Phe Lys Ser Leu Gln Phe Leu Asp Ile Ser Asn Asn
100 105 110

Leu Phe Ser Ser Ser Ile Pro Ser Gly Ile Gly Lys Phe Asp Ser Leu
115 120 125

Gln Asn Leu Ser Leu Ala Gly Asn Asn Phe Ser Gly Pro Ile Pro Asn
130 135 140

Thr Ile Ser Glu Met Ala Ser Ile Glu Ser Leu Asp Leu Ser Arg Asn
145 150 155 160

Thr Leu Ser Glu Ala Leu Pro Pro Ser Leu Thr Lys Leu Asn Ser Ile
165 170 175

Val Ser Leu Asn Leu Ser His Asn Gly Phe Thr Gly Lys Ile Pro Lys
180 185 190

Gly Phe Glu Leu Ile Ser Ser Leu Glu Lys Leu Asp Leu His Ser Asn

195 200 205

Met Leu Asp Gly Pro Leu Asp Val Glu Phe Met Leu Leu Ser Gly Ala
210 215 220

Ser Tyr Val Asp Leu Ser Asp Asn Leu Leu Val Ser Ser Asp Ser Gly
225 230 235 240

Lys Phe Leu Pro Arg Ile Ser Glu Ser Ile Lys Tyr Leu Asn Leu Ser
245 250 255

His Asn Gln Leu Thr Gly Ser Leu Val Gly Gly Ala Glu Gln Pro Val
260 265 270

Phe Gln Asn Leu Lys Val Leu Asp Leu Ser Tyr Asn Gln Leu Asn Gly
275 280 285

Glu Leu Pro Gly Phe Asp Phe Val Tyr Asp Leu Gln Val Leu Lys Leu
290 295 300

Ser Asn Asn Arg Phe Ser Gly Phe Ile Pro Asn Gly Leu Leu Lys Gly
305 310 315 320

Asp Ser Leu Val Leu Thr Glu Leu Asp Leu Ser Ala Asn Asn Leu Ser
325 330 335

Gly Pro Leu Ser Met Ile Thr Ser Thr Thr Leu His Ser Leu Asn Leu

340 345 350

Ser Ser Asn Gly Phe Thr Gly Glu Leu Pro Leu Leu Thr Gly Ser Cys
355 360 365

Ala Val Leu Asp Leu Ser Asn Asn Lys Phe Glu Gly Asn Leu Thr Arg
370 375 380

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

Leu Ala Gly Asn Ile Pro Glu Val Thr Pro Gln Phe Leu Arg Met Asn
405 410 415

Tyr Leu Asn Leu Ser His Asn Asp Leu Ser His Asp Leu Pro Arg Val
420 425 430

Leu Thr Gln Tyr Pro Lys Leu Arg Val Leu Asp Ile Ser Ser Asn Gln
435 440 445

Phe Lys Gly Leu Leu Leu Pro Asp Phe Phe Thr Met Gln Thr Leu Gln
450 455 460

Glu Leu His Leu Glu Asp Asn Leu Ile Ser Gly Ser Ile Asn Leu Ser
465 470 475 480

Ser Ser Leu Asp Gln Ser His Leu Gln Val Leu Asp Leu Ser His Asn

485 490 495

Gln Leu Thr Ser Phe Phe Leu Met Ile Leu Ala His
500 505

<210> 801
<211> 1048
<212> PRT
<213> Medicago

<400> 801

Met Gly Gln Leu Pro Ser Gln Asp Ile Leu Ala Leu Leu Glu Phe Lys
1 5 10 15

Lys Cys Ile Lys His Asp Pro Thr Gly Tyr Val Leu Asn Ser Trp Asn
20 25 30

Glu Glu Ser Ile Asp Phe Asp Gly Cys Pro Ser Ser Trp Asn Gly Val
35 40 45

Leu Cys Asn Gly Gly Asn Val Ala Gly Val Val Leu Asp Asn Leu Gly
50 55 60

Leu Ser Ala Asp Ser Asp Leu Ser Val Phe Ser Asn Leu Ser Lys Leu
65 70 75 80

Val Lys Leu Ser Met Ser Asn Asn Ser Ile Ser Gly Lys Leu Pro Asn
85 90 95

Asn Ile Ala Asp Phe Lys Ser Leu Glu Phe Leu Asp Ile Ser Asn Asn
100 105 110

Leu Phe Ser Ser Ser Ile Pro Ala Gly Ile Gly Lys Phe Gly Ser Leu
115 120 125

Gln Asn Leu Ser Leu Ala Gly Asn Asn Phe Ser Gly Pro Ile Pro Asn
130 135 140

Ser Ile Ser Glu Met Ala Ser Ile Lys Ser Leu Asp Leu Ser Arg Asn
145 150 155 160

Ala Leu Ser Gly Ala Leu Pro Ser Ser Leu Pro Lys Leu Asn Ser Leu
165 170 175

Val Ser Leu Asn Leu Ser Tyr Asn Arg Leu Thr Gly Lys Ile Pro Lys
180 185 190

Gly Phe Glu Leu Ile Ser Ser Leu Asp Lys Leu Asp Leu His Gly Asn
195 200 205

Met Phe Asp Gly Pro Leu Asp Val Glu Phe Met Leu Leu Ser Ser Ala
210 215 220

Ser Tyr Val Asp Leu Ser Asp Asn Met Leu Leu Ser Ser Ser Ser Gly
225 230 235 240

Lys Phe Leu Pro Gly Ile Ser Glu Ser Ile Lys Tyr Leu Asn Leu Ser
245 250 255

His Asn Gln Leu Thr Gly Ile Leu Val Gly Gly Ala Glu Gln Pro Val
260 265 270

Phe Gln Asp Leu Lys Val Leu Asp Leu Ser Tyr Asn Gln Leu Asn Gly
275 280 285

Glu Leu Pro Gly Phe Asp Phe Val Tyr Asp Leu Gln Ile Leu Lys Leu
290 295 300

Ser Asn Asn Arg Phe Ser Gly Phe Ile Pro Asn Gly Leu Leu Lys Gly
305 310 315 320

Asp Ser Leu Val Leu Thr Glu Leu Asp Leu Ser Ala Asn Asn Leu Ser
325 330 335

Gly Pro Leu Ser Met Ile Thr Ser Thr Thr Leu His Phe Leu Asn Leu
340 345 350

Ser Ser Asn Gly Phe Thr Gly Glu Leu Pro Leu Leu Thr Gly Ser Cys
355 360 365

Ala Val Leu Asp Leu Ser Asn Asn Lys Phe Glu Gly Asn Leu Thr Arg
370 375 380

Met Leu Lys Trp Gly Asn Ile Glu Tyr Leu Asp Leu Gly Arg Asn Arg
385 390 395 400

Leu Ala Gly Asn Val Pro Glu Val Thr Pro Gln Phe Leu Arg Leu Asn
405 410 415

Tyr Leu Asn Leu Ser Asn Asn Arg Leu Ser Asp Asp Leu Pro Lys Val
420 425 430

Leu Thr Gln Tyr Pro Lys Leu Arg Val Leu Asp Ile Ser Ser Asn Gln
435 440 445

Leu Lys Gly Val Leu Leu Thr Glu Leu Phe Thr Met Pro Thr Leu Gln
450 455 460

Glu Leu His Leu Glu Asn Asn Leu Ile Asn Gly Gly Ile Asn Leu Ser
465 470 475 480

Ser Ser Leu Asp Gln Ser His Leu Gln Val Leu Asp Leu Ser His Asn
485 490 495

Gln Leu Ser Ser Phe Phe Pro Asp Glu Phe Gly Ser Leu Thr Ser Leu
500 505 510

Arg Val Leu Asn Ile Ala Gly Asn Asn Phe Ala Gly Ser Leu Pro Thr
515 520 525

Thr Ile Ala Asp Met Ser Ser Leu Asn Ser Leu Asp Ile Ser Asn Asn
530 535 540

Arg Phe Thr Gly Pro Leu Pro Asn Ser Met Pro Lys Gly Leu Arg Asp
545 550 555 560

Phe Asn Ala Ser Glu Asn Asp Leu Ser Gly Val Val Pro Glu Ile Leu
565 570 575

Arg Asn Phe Pro Ser Ser Ser Phe Phe Pro Gly Asn Ala Lys Leu His
580 585 590

Phe Pro Asn Ser Pro Pro Gly Ser Thr Val Ser Pro Thr Lys Ser Ser
595 600 605

Lys Gly Lys Ser Met Ser Thr Ala Val Lys Val Ile Ile Ile Val Ser
610 615 620

Cys Val Val Ala Leu Phe Ile Leu Ile Leu Leu Ala Val Phe Ile His
625 630 635 640

Tyr Ile Arg Met Ser Arg Ser Ser Thr Ser Glu Tyr Asp Thr Ala Thr
645 650 655

Gly Lys Asp Thr Arg Gly Arg Pro Gln Pro Val Ile Ser Gly Pro Ile
660 665 670

Arg Pro Thr Glu Arg Gly Ala Pro Leu Val Val Ser Ala Glu Asp Leu
675 680 685

Val Ala Ser Arg Lys Gly Ser Pro Ser Glu Ile Ile Ser Pro Asp Ala
690 695 700

Lys Thr Ala Ala Val Ala Gly Phe Ser Pro Ser Lys His Ser Gln Phe
705 710 715 720

Ser Trp Ser Pro Glu Ser Gly Asp Ser Leu Thr Ala Glu Asn Leu Thr
725 730 735

Arg Leu Asp Thr Arg Ser Pro Asp Arg Leu Ile Gly Glu Leu His Phe
740 745 750

Leu Asp Asp Thr Ile Ser Leu Thr Pro Glu Glu Leu Ser Arg Ala Pro
755 760 765

Ala Glu Val Leu Gly Arg Ser Ser His Gly Thr Ser Tyr Lys Ala Thr
770 775 780

Leu Asp Asn Gly Leu Leu Leu Arg Val Lys Trp Leu Arg Glu Gly Val
785 790 795 800

Ala Lys Gln Arg Lys Glu Phe Val Lys Glu Ile Arg Lys Phe Ala Asn
805 810 815

Ile Arg His Pro Asn Val Val Gly Leu Lys Gly Tyr Tyr Trp Gly Pro
820 825 830

Thr Gln His Glu Lys Leu Ile Leu Ser Asp Tyr Ile Ser Pro Gly Ser
835 840 845

Leu Ala Ser Phe Leu Tyr Asp Arg Pro Gly Arg Asn Gly Pro Pro Leu
850 855 860

Thr Trp Ala Gln Arg Leu Lys Ile Ala Val Asp Val Ala Arg Gly Leu
865 870 875 880

Asn Tyr Leu His Phe Asp Arg Ala Val Pro His Gly Asn Leu Lys Ala
885 890 895

Thr Asn Val Leu Leu Asp Thr Ala Asp Met Asn Ala Arg Val Ala Asp
900 905 910

Tyr Cys Leu His Arg Leu Met Thr Gln Ala Gly Thr Ile Glu Gln Ile
915 920 925

Leu Asp Ala Gly Val Leu Gly Tyr Arg Ala Pro Glu Leu Ala Ala Ser
930 935 940

Lys Lys Pro Met Pro Ser Phe Lys Ser Asp Val Tyr Ala Phe Gly Val
945 950 955 960

Ile Leu Leu Glu Leu Leu Thr Gly Arg Cys Ala Gly Asp Val Ile Thr
965 970 975

Gly Glu Glu Gly Gly Val Asp Leu Thr Asp Trp Leu Arg Leu Arg Val
980 985 990

Ala Glu Gly Arg Gly Ser Glu Cys Phe Asp Ala Thr Leu Met Ser Glu
995 1000 1005

Met Gly Asn Pro Val Val Glu Lys Gly Met Lys Glu Val Leu Gly
1010 1015 1020

Ile Ala Ile Arg Cys Ile Arg Ser Val Ser Glu Arg Pro Gly Ile
1025 1030 1035

Lys Thr Ile Tyr Glu Asp Leu Ser Ser Ile
1040 1045

<210> 802
<211> 510
<212> PRT
<213> Soja

<400> 802

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Thr Glu Ile Gln Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Lys Asn Gly Thr Tyr Gln Trp Val Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asn Thr His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Ile
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
100 105 110

Val Gly Ser Phe Gln Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asn Leu Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Asp
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Gln Gln
195 200 205

Ile Ile Lys Asp Ile Lys Glu Phe Lys Glu Ser Thr Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Leu Val
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Phe Ala Ser Leu Asp Arg
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Met Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Asn
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Glu Phe Lys Ala Glu
435 440 445

Asn Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 803
<211> 510
<212> PRT
<213> Guandú

<400> 803

Met Phe Val Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Thr Glu Ile Gln Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Gln Asn Lys Asn Gly Ala Tyr Gln Trp Val Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asn Thr His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Ile
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
100 105 110

Val Gly Ser Phe Gln Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asn Leu Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Asp
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Gln Gln
195 200 205

Ile Ile Lys Asp Ile Lys Glu Phe Lys Glu Thr Ser Lys Val Asp Arg
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val
225 230 235 240

Val Gly Leu Asn Asp Thr Val Glu Asn Leu Leu Ala Ser Leu Asp Arg
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Met Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Asn
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ala Glu
435 440 445

Asp Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Ser Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 804
<211> 510
<212> PRT
<213> Poroto

<400> 804

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Ser Glu Ile Glu Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Lys Asn Gly Thr Tyr Gln Trp Val Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asn Thr Arg Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Ile

85 90 95

Glu Lys Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
100 105 110

Val Gly Ser Phe Gln Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asn Leu Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Asp
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Gln Gln
195 200 205

Ile Ile Lys Asp Ile Lys Glu Phe Lys Glu Lys Ser Lys Val Asp Arg
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Ala

225 230 235 240

Val Gly Leu Asn Asp Thr Glu Glu Asn Leu Leu Ala Ser Leu Asp Arg
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Phe Ala Ile Ala Cys Val
260 265 270

Met Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Arg Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Asn
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val

370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ala Glu
435 440 445

Asp Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 805

<211> 510
<212> PRT
<213> Guandú

<400> 805

Met Phe Ile His Asn Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Thr Glu Ile Gln Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser
35 40 45

Val Lys Tyr Glu Phe Lys Thr Ser Thr His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Ile
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
100 105 110

Val Gly Ser Phe Gln Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Glu Asp
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Gln Gln
195 200 205

Ile Ile Lys Asp Ile Lys Glu Phe Lys Glu Ala Thr Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Leu Val
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Leu Asp Lys
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Met Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Asn
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ala Glu
435 440 445

Asn Glu Gly Lys Phe His Thr Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 806
<211> 510
<212> PRT
<213> Soja

<400> 806

Met Phe Ile Glu Asn Phe Lys Val Glu Cys Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Thr Glu Ile Gln Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asn Ile His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Ile
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
100 105 110

Val Gly Ser Phe Gln Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Leu Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Glu Glu
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Gln Glu Gln Val Gln Gln
195 200 205

Ile Ile Lys Asp Ile Lys Ala Phe Lys Glu Ala Thr Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Leu Val
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ala Val Asp Arg
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Met Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Ala Arg Asn Thr Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Asn
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ala Glu
435 440 445

Asn Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 807
<211> 510
<212> PRT
<213> Maní

<400> 807

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Thr Glu Ile Gln Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Lys Asn Gly Thr Tyr Gln Trp Val Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asn Thr His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Ile
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
100 105 110

Val Gly Ser Tyr Gln Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Glu Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asn Met Asn Leu Ala Asp Ala Met Gly Arg Ala Lys Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Glu Glu
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Gln Gln
195 200 205

Ile Ile Lys Asp Ile Lys Ala Phe Lys Glu Ala Asn Lys Val Glu Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ser Ala Leu Asp Arg
245 250 255

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

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ser Ile Asn Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Asn
355 360 365

Ser Asn Gly Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ala Glu
435 440 445

Asn Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 808
<211> 510
<212> PRT
<213> Chícharo salvaje

<400> 808

Met Phe Ile Glu Asn Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Thr Glu Ile Gln Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asn Thr His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Ile

85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
100 105 110

Val Gly Ser Phe Gln Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Gly Arg Ala Lys Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Glu Glu
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Ala Gln
195 200 205

Ile Ile Lys Asp Ile Lys Glu Phe Lys Ala Ala Thr Lys Val Asp Arg
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Leu Val

225 230 235 240

Val Gly Leu Asn Asp Thr Thr Glu Asn Leu Leu Ala Ala Leu Asp Arg
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Met Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Phe Ala Ile Glu Lys Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Asn
355 360 365

Ser Asn Ala Leu Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val

370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ala Glu
435 440 445

Lys Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 809

<211> 510
<212> PRT
<213> Lotus

<400> 809

Met Phe Ile Glu Asn Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Thr Glu Ile Gln Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Arg Asn Gly Ser Tyr Gln Trp Ile Val Lys Pro Lys Ser
35 40 45

Val Lys Tyr Glu Phe Lys Thr Ser Thr Asn Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Lys Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Ile
85 90 95

Glu Arg Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
100 105 110

Val Gly Ser Phe Gln Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Gly Arg Ala Arg Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Asp
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Ile Gln Gln
195 200 205

Ile Ile Lys Asp Ile Lys Glu Phe Lys Glu Ala Ser Lys Val Asp Arg
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Leu Val
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Val Asp Arg
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Met Glu Asn Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Lys Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Asn
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Ala Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ser Glu
435 440 445

Ala Glu Asp Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 810
<211> 510
<212> PRT
<213> Lotus

<400> 810

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Thr Glu Ile Gln Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Lys Asn Asn Ala Tyr Gln Trp Val Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Lys Thr Asn Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Lys Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Ile
85 90 95

Gln Gln Ser Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
100 105 110

Val Gly Ser Phe Gln Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asn Leu Asn Leu Ala Asp Ala Met Ala Arg Ala Arg Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asn Pro Asp Phe Ile Ala Ala Asn Gln Gly Glu
180 185 190

Arg Ala Asn Asn Val Leu Lys Gly Thr Lys Lys Glu Gln Val Gln Gln
195 200 205

Ile Ile Lys Asp Ile Lys Glu Phe Lys Glu Ala Asn Lys Val Asp Glu
210 215 220

Ile Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val
225 230 235 240

Val Gly Leu Asn Asp Thr Glu Glu Asn Leu Leu Ala Ser Leu Asp Arg
245 250 255

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

Met Glu Asn Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Arg Lys Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Asn
355 360 365

Ser Asn Ala Ile Leu Phe Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Ala Asp Ser Lys Arg Ala Met Asp
385 390 395 400

Glu Tyr Ile Ser Glu Ile Phe Met Gly Gly Lys Asn Thr Ile Val Met
405 410 415

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ala Glu
435 440 445

Asn Glu Ser Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Met Glu Tyr Lys
500 505 510

<210> 811
<211> 510
<212> PRT
<213> Maní

<400> 811

Met Phe Ile Glu Lys Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Ser
1 5 10 15

Glu Asp Glu Ile Glu Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Arg Asn Gly Ser Tyr Gln Trp Ile Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asn Thr His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Ile
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
100 105 110

Val Gly Ser Tyr Gln Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asn Ile Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Lys Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Gln Asp Phe Ile Ala Ala Asn Gln Glu Ala
180 185 190

Arg Ala Asp Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Ile Gln Gln
195 200 205

Ile Ile Lys Asp Ile Lys Glu Phe Lys Glu Gln Asn Lys Val Asp Arg
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Met Ala Ser Val Asp Lys
245 250 255

Asn Glu Ser Glu Ile Ser Pro Ser Thr Leu Phe Ala Ile Ala Cys Val
260 265 270

Met Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Ser Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Asn
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Phe Lys Ser Glu
435 440 445

Ala Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 812
<211> 510
<212> PRT
<213> Tabaco

<400> 812

Met Phe Ile Glu Asn Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Ser Glu Ile His Ser Val Tyr Asp Tyr Gln Thr Thr Glu Leu Val
20 25 30

His Glu Glu Lys Asn Gly Thr Tyr Gln Trp Thr Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asp Val His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val

85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
100 105 110

Val Gly Ser Phe Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asp Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
180 185 190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Ile Asp Gln
195 200 205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val

225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Phe Ala Ser Val Asp Arg
245 250 255

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

Leu Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Arg Asn Thr Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val

370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

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Gly Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
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LISTA DE SECUENCIAS

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Syngenta Participations AG
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KARCHI, Hagai
HUANG, Xiang

<120> **Composiciones y métodos para incrementar la resistencia a nematodos en plantas**

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<151> 2011-11-21

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Met Leu Thr Gln Glu Ile Arg Lys Ser Leu Asp Arg His Thr Ile Leu
180 185 190

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

Ala Val Trp Met Pro Asn Asp Gly Gly Thr Glu Met Asp Leu Thr His
210 215 220

Glu Leu Arg Gly Arg Gly Gly Tyr Gly Gly Cys Ser Val Ser Met Glu
225 230 235 240

Asp Leu Asp Val Val Arg Ile Arg Glu Ser Asp Glu Val Asn Val Leu
245 250 255

Ser Val Asp Ser Ser Ile Ala Arg Ala Ser Gly Gly Gly Gly Asp Val
260 265 270

Ser Glu Ile Gly Ala Val Ala Ala Ile Arg Met Pro Met Leu Arg Val
275 280 285

Ser Asp Phe Asn Gly Glu Leu Ser Tyr Ala Ile Leu Val Cys Val Leu
290 295 300

Pro Gly Gly Thr Pro Arg Asp Trp Thr Tyr Gln Glu Ile Glu Ile Val
305 310 315 320

Lys Val Val Ala Asp Gln Val Thr Val Ala Leu Asp His Ala Ala Val
325 330 335

Leu Glu Glu Ser Gln Leu Met Arg Glu Lys Leu Ala Glu Gln Asn Arg
340 345 350

Ala Leu Gln Met Ala Lys Arg Asp Ala Leu Arg Ala Ser Gln Ala Arg
355 360 365

Asn Ala Phe Gln Lys Thr Met Ser Glu Gly Met Arg Arg Pro Met His
370 375 380

Ser Ile Leu Gly Leu Leu Ser Met Ile Gln Asp Glu Lys Leu Ser Asp
385 390 395 400

Glu Gln Lys Met Ile Val Asp Thr Met Val Lys Thr Gly Asn Val Met
405 410 415

Ser Asn Leu Val Gly Asp Ser Met Asp Val Pro Asp Gly Arg Phe Gly
420 425 430

Thr Glu Met Lys Pro Phe Ser Leu His Arg Thr Ile His Glu Ala Ala
435 440 445

Cys Met Ala Arg Cys Leu Cys Leu Cys Asn Gly Ile Arg Phe Leu Val
450 455 460

Asp Ala Glu Lys Ser Leu Pro Asp Asn Val Val Gly Asp Glu Arg Arg
465 470 475 480

Val Phe Gln Val Ile Leu His Ile Val Gly Ser Leu Val Lys Pro Arg
485 490 495

Lys Arg Gln Glu Gly Ser Ser Leu Met Phe Lys Val Leu Lys Glu Arg
500 505 510

Gly Ser Leu Asp Arg Ser Asp His Arg Trp Ala Ala Trp Arg Ser Pro
515 520 525

Ala Ser Ser Ala Asp Gly Asp Val Tyr Ile Arg Phe Glu Met Asn Val
530 535 540

Glu Asn Asp Asp Ser Ser Ser Gln Ser Phe Ala Ser Val Ser Ser Arg
545 550 555 560

Asp Gln Glu Val Gly Asp Val Arg Phe Ser Gly Gly Tyr Gly Leu Gly
565 570 575

Gln Asp Leu Ser Phe Gly Val Cys Lys Lys Val Val Gln Leu Ile His
580 585 590

Gly Asn Ile Ser Val Val Pro Gly Ser Asp Gly Ser Pro Glu Thr Met
595 600 605

Ser Leu Leu Leu Arg Phe Arg Arg Arg Pro Ser Ile Ser Val His Gly
610 615 620

Ser Ser Glu Ser Pro Ala Pro Asp His His Ala His Pro His Ser Asn
625 630 635 640

Ser Leu Leu Arg Gly Leu Gln Val Leu Leu Val Asp Thr Asn Asp Ser
645 650 655

Asn Arg Ala Val Thr Arg Lys Leu Leu Glu Lys Leu Gly Cys Asp Val
660 665 670

Thr Ala Val Ser Ser Gly Phe Asp Cys Leu Thr Ala Ile Ala Pro Gly
675 680 685

Ser Ser Ser Pro Ser Thr Ser Phe Gln Val Val Val Leu Asp Leu Gln
690 695 700

Met Ala Glu Met Asp Gly Tyr Glu Val Ala Met Arg Ile Arg Ser Arg
705 710 715 720

Ser Trp Pro Leu Ile Val Ala Thr Thr Val Ser Leu Asp Glu Glu Met
725 730 735

Trp Asp Lys Cys Ala Gln Ile Gly Ile Asn Gly Val Val Arg Lys Pro
740 745 750

Val Val Leu Arg Ala Met Glu Ser Glu Leu Arg Arg Val Leu Leu Gln
755 760 765

Ala Asp Gln Leu Leu
770

<210> 31
<211> 253
<212> PRT
<213> Arabidopsis

<400> 31

Met Ala Thr Ser Gln Gln Phe Leu Asn Pro Thr Leu Phe Lys Ser Leu
1 5 10 15

Ala Ser Ser Asn Lys Asn Ser Cys Thr Leu Cys Pro Ser Pro Phe Leu
20 25 30

Gln Leu Lys Ser Ala Ser Thr Ile Phe Asn Tyr Lys Pro Leu Thr Ser
35 40 45

Ser Ser Ala Thr Ile Ile Thr Arg Val Ala Ala Ser Ser Ser Asp Ser
50 55 60

Gly Glu Ser Ile Thr Arg Glu Thr Phe His Gly Leu Cys Phe Val Leu
65 70 75 80

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

Leu Ile Pro Ser Ile Pro Glu Asp Arg Glu Lys Leu Gly Ser Phe Ala
100 105 110

Leu Asn Gly Leu Pro Lys Phe Tyr Asn Glu Arg Phe Val Val Pro Gly
115 120 125

Glu Met Lys Ser Lys Tyr Ser Val Ile Ile Gly Gly Asp Asn Phe Gly
130 135 140

Cys Gly Ser Ser Arg Glu His Ala Pro Val Cys Leu Gly Ala Ala Gly
145 150 155 160

Ala Lys Ala Val Val Ala Glu Ser Tyr Ala Arg Ile Phe Phe Arg Asn
165 170 175

Cys Val Ala Thr Gly Glu Ile Phe Pro Leu Glu Ser Glu Val Arg Ile
180 185 190

Cys Asp Glu Cys Lys Thr Gly Asp Val Val Thr Ile Glu His Lys Glu
195 200 205

Asp Gly Ser Ser Leu Leu Ile Asn His Thr Thr Arg Lys Glu Tyr Lys
210 215 220

Leu Lys Pro Leu Gly Asp Ala Gly Pro Val Ile Asp Ala Gly Gly Ile
225 230 235 240

Phe Ala Tyr Ala Arg Lys Ala Gly Met Ile Pro Ser Ala
245 250

<210> 32
<211> 575
<212> PRT
<213> Arabidopsis

<400> 32

Met Ala Ile Lys Glu Arg Ser Leu Glu Glu Thr Pro Thr Trp Ala Val
1 5 10 15

Ala Val Val Cys Phe Val Leu Leu Phe Ile Ser Ile Met Ile Glu Tyr
20 25 30

Phe Leu His Phe Ile Gly His Trp Phe Lys Lys Lys His Lys Lys Ala
35 40 45

Leu Ser Glu Ala Leu Glu Lys Val Lys Ala Glu Leu Met Leu Leu Gly
50 55 60

Phe Ile Ser Leu Leu Leu Val Val Leu Gln Thr Pro Val Ser Glu Ile
65 70 75 80

Cys Ile Pro Arg Asn Ile Ala Ala Thr Trp His Pro Cys Ser Asn His
85 90 95

Gln Glu Ile Ala Lys Tyr Gly Lys Asp Tyr Ile Asp Asp Gly Arg Lys
100 105 110

Ile Leu Glu Asp Phe Asp Ser Asn Asp Phe Tyr Ser Pro Arg Arg Asn

115 120 125

Leu Ala Thr Lys Gly Tyr Asp Lys Cys Ala Glu Lys Gly Lys Val Ala
130 135 140

Leu Val Ser Ala Tyr Gly Ile His Gln Leu His Ile Phe Ile Phe Val
145 150 155 160

Leu Ala Val Phe His Val Leu Tyr Cys Ile Ile Thr Tyr Ala Leu Gly
165 170 175

Lys Thr Lys Met Lys Lys Trp Lys Ser Trp Glu Arg Glu Thr Lys Thr
180 185 190

Ile Glu Tyr Gln Tyr Ala Asn Asp Pro Glu Arg Phe Arg Phe Ala Arg
195 200 205

Asp Thr Ser Phe Gly Arg Arg His Leu Asn Ile Trp Ser Lys Ser Thr
210 215 220

Phe Thr Leu Trp Ile Thr Cys Phe Phe Arg Gln Phe Phe Gly Ser Val
225 230 235 240

Thr Lys Val Asp Tyr Leu Thr Leu Arg His Gly Phe Ile Met Ala His
245 250 255

Leu Pro Ala Gly Ser Ala Ala Arg Phe Asp Phe Gln Lys Tyr Ile Glu

260 265 270

Arg Ser Leu Glu Gln Asp Phe Thr Val Val Val Gly Ile Ser Pro Leu
275 280 285

Ile Trp Cys Ile Ala Val Leu Phe Ile Leu Thr Asn Thr His Gly Trp
290 295 300

Asp Ser Tyr Leu Trp Leu Pro Phe Leu Pro Leu Ile Val Ile Leu Ile
305 310 315 320

Val Gly Ala Lys Leu Gln Met Ile Ile Ser Lys Leu Gly Leu Arg Ile
325 330 335

Gln Glu Lys Gly Asp Val Val Lys Gly Ala Pro Val Val Glu Pro Gly
340 345 350

Asp Asp Leu Phe Trp Phe Gly Arg Pro Arg Phe Ile Leu Phe Leu Ile
355 360 365

His Leu Val Leu Phe Thr Asn Ala Phe Gln Leu Ala Phe Phe Val Trp
370 375 380

Ser Thr Tyr Glu Phe Thr Leu Lys Asn Cys Phe His His Lys Thr Glu
385 390 395 400

Asp Ile Ala Ile Arg Ile Thr Met Gly Val Leu Ile Gln Val Leu Cys

405 410 415

Ser Tyr Ile Thr Leu Pro Leu Tyr Ala Leu Val Thr Gln Met Gly Thr
420 425 430

Ser Met Arg Pro Thr Ile Phe Asn Asp Arg Val Ala Asn Ala Leu Lys
435 440 445

Lys Trp His His Thr Ala Lys Lys Gln Thr Lys His Gly His Ser Gly
450 455 460

Ser Asn Thr Pro His Ser Ser Arg Pro Thr Thr Pro Thr His Gly Met
465 470 475 480

Ser Pro Val His Leu Leu His Asn Asn Asn Arg Ser Leu Asp Gln Gln
485 490 495

Thr Ser Phe Thr Ala Ser Pro Ser Pro Pro Arg Phe Ser Asp Tyr Ser
500 505 510

Gly Gln Gly His Gly His Gln His Phe Phe Asp Pro Glu Ser Gln Asn
515 520 525

His Ser Tyr Gln Arg Glu Ile Thr Asp Ser Glu Phe Ser Asn Ser His
530 535 540

His Pro Gln Val Asp Met Ala Ser Pro Val Arg Glu Glu Lys Glu Ile

545 550 555 560

Val Glu His Val Lys Val Asp Leu Ser Glu Phe Thr Phe Lys Lys
565 570 575

<210> 33
<211> 427
<212> PRT
<213> Arabidopsis

<400> 33

Met Ala Ile Pro Arg Phe Ser Ser Leu Leu Arg Cys Arg Lys Trp Ala
1 5 10 15

Lys Ser Asp Trp Leu Val Ala Ser Ile Gly Cys Val Leu Ile Val Phe
20 25 30

Phe Leu Ser Phe Phe Phe Asp Pro Thr Ser Asp Ser Val Pro Ser Val
35 40 45

Asp Arg Ser Arg Pro Ile Ile Ser Pro Ser Asp Leu Val Lys Leu Lys
50 55 60

Leu Ser Ser Val Ala Lys Glu Arg Gly Ala Phe Cys Leu Asp Gly Ser
65 70 75 80

Leu Pro Gly Tyr His Phe His Glu Gly Ser Gly Ser Gly Ser Gln Ser
85 90 95

Trp Leu Val His Leu Glu Gly Gly Gly Trp Cys Asn Thr Val Ala Ser
100 105 110

Cys Ser Ala Arg Ala Leu Thr Lys Leu Gly Ser Ser Asn Tyr Phe Glu
115 120 125

Gln Glu Val Ala Phe Gln Gly Val Leu Ser Ser Asp Pro Ser Gln Asn
130 135 140

Pro Glu Phe Phe Asn Trp Asn Lys Val Ala Ile Arg Tyr Cys Asp Gly
145 150 155 160

Ala Ser Phe Ser Gly Arg Pro Glu Ala Glu Phe Lys Asn Gly Thr Arg
165 170 175

Leu Phe Phe Arg Gly Gln Leu Ile Trp Glu Ala Ile Ile Asp Glu Leu
180 185 190

Leu Ser Met Gly Met Ser Asp Ala Lys Gln Ala Ile Leu Thr Gly Cys
195 200 205

Ser Ala Gly Gly Leu Ala Ser Leu Ile His Cys Asp Tyr Phe Arg Asp
210 215 220

His Leu Pro Lys Asp Ala Ala Val Lys Cys Val Ser Asp Gly Gly Tyr
225 230 235 240

Phe Leu Asn Val Pro Asp Val Leu Gly Asn Pro Thr Met Arg Ser Phe
245 250 255

Tyr His Asp Val Val Asn Leu Gln Gly Val Glu Lys Ser Leu Asp Gln
260 265 270

Lys Cys Val Ala Lys Thr Glu Pro Ser Lys Cys Met Phe Pro Gln Glu
275 280 285

Phe Leu Lys Asn Ile Arg Thr Pro Val Phe Leu Val Asn Pro Ala Tyr
290 295 300

Asp Phe Trp Gln Ile Gln His Val Leu Val Pro Thr Ser Ala Asp Pro
305 310 315 320

Asp Lys Ser Trp Ala Lys Cys Arg Leu Asn Ile Lys Glu Cys Asp Ala
325 330 335

Glu Gln Ile Lys Val Leu His Gly Phe Arg Ser Ser Met Met Thr Ala
340 345 350

Ile Gly Glu Phe His Gln Asn Lys Asp Gly Gly Met Phe Ile Asp Ser
355 360 365

Cys Tyr Ala His Cys Gln Thr Val Met Ser Val Thr Trp His Ser Leu
370 375 380

Thr Ser Pro Arg Ile Glu Asn Lys Thr Ile Ala Glu Ser Val Gly Asp
385 390 395 400

Trp Tyr Phe Asn Arg Lys Pro Val Lys Leu Ile Asp Cys Pro Tyr Pro
405 410 415

Cys Asn Pro Ser Cys Tyr Asn Met Asn Phe Thr
420 425

<210> 34
<211> 500
<212> PRT
<213> Arabidopsis

<400> 34

Met Val Gln Tyr Gln Arg Leu Ile Ile His His Gly Arg Lys Glu Asp
1 5 10 15

Lys Phe Arg Val Ser Ser Ala Glu Glu Ser Gly Gly Gly Gly Cys Cys
20 25 30

Tyr Ser Lys Arg Ala Lys Gln Lys Phe Arg Cys Leu Leu Phe Leu Ser
35 40 45

Ile Leu Ser Cys Cys Phe Val Leu Ser Pro Tyr Tyr Leu Phe Gly Phe
50 55 60

Ser Thr Leu Ser Leu Leu Asp Ser Phe Arg Arg Glu Ile Glu Gly Leu
65 70 75 80

Ser Ser Tyr Glu Pro Val Ile Thr Pro Leu Cys Ser Glu Ile Ser Asn
85 90 95

Gly Thr Ile Cys Cys Asp Arg Thr Gly Leu Arg Ser Asp Ile Cys Val
100 105 110

Met Lys Gly Asp Val Arg Thr Asn Ser Ala Ser Ser Ser Ile Phe Leu
115 120 125

Phe Thr Ser Ser Thr Asn Asn Asn Thr Lys Pro Glu Lys Ile Lys Pro
130 135 140

Tyr Thr Arg Lys Trp Glu Thr Ser Val Met Asp Thr Val Gln Glu Leu
145 150 155 160

Asn Leu Ile Thr Lys Asp Ser Asn Lys Ser Ser Asp Arg Val Cys Asp
165 170 175

Val Tyr His Asp Val Pro Ala Val Phe Phe Ser Thr Gly Gly Tyr Thr
180 185 190

Gly Asn Val Tyr His Glu Phe Asn Asp Gly Ile Ile Pro Leu Phe Ile
195 200 205

Thr Ser Gln His Tyr Asn Lys Lys Val Val Phe Val Ile Val Glu Tyr
210 215 220

His Asp Trp Trp Glu Met Lys Tyr Gly Asp Val Val Ser Gln Leu Ser
225 230 235 240

Asp Tyr Pro Leu Val Asp Phe Asn Gly Asp Thr Arg Thr His Cys Phe
245 250 255

Lys Glu Ala Thr Val Gly Leu Arg Ile His Asp Glu Leu Thr Val Asn
260 265 270

Ser Ser Leu Val Ile Gly Asn Gln Thr Ile Val Asp Phe Arg Asn Val
275 280 285

Leu Asp Arg Gly Tyr Ser His Arg Ile Gln Ser Leu Thr Gln Glu Glu
290 295 300

Thr Glu Ala Asn Val Thr Ala Leu Asp Phe Lys Lys Lys Pro Lys Leu
305 310 315 320

Val Ile Leu Ser Arg Asn Gly Ser Ser Arg Ala Ile Leu Asn Glu Asn
325 330 335

Leu Leu Val Glu Leu Ala Glu Lys Thr Gly Phe Asn Val Glu Val Leu
340 345 350

Arg Pro Gln Lys Thr Thr Glu Met Ala Lys Ile Tyr Arg Ser Leu Asn
355 360 365

Thr Ser Asp Val Met Ile Gly Val His Gly Ala Ala Met Thr His Phe
370 375 380

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

Thr Asp Trp Ala Ala Glu Thr Tyr Tyr Gly Glu Pro Ala Lys Lys Leu
405 410 415

Gly Leu Lys Tyr Val Gly Tyr Lys Ile Ala Pro Lys Glu Ser Ser Leu
420 425 430

Tyr Glu Glu Tyr Gly Lys Asp Asp Pro Val Ile Arg Asp Pro Asp Ser
435 440 445

Leu Asn Asp Lys Gly Trp Glu Tyr Thr Lys Lys Ile Tyr Leu Gln Gly
450 455 460

Gln Asn Val Lys Leu Asp Leu Arg Arg Phe Arg Glu Thr Leu Thr Arg
465 470 475 480

Ser Tyr Asp Phe Ser Ile Arg Arg Arg Phe Arg Glu Asp Tyr Leu Leu
485 490 495

His Arg Glu Asp
500

<210> 35
<211> 541
<212> PRT
<213> Medicago

<400> 35

Met Ser Gly Arg Lys Pro Tyr Ala Val Ala Gln Tyr Gly Cys Leu Leu
1 5 10 15

Val Thr His Ala Val Lys Lys Thr Val Glu Glu Val Asp Gly Asn Lys
20 25 30

Cys Val Ser Asp Trp Phe Gly Lys Gly Tyr Met Lys Val Glu Arg Gln
35 40 45

Lys Lys Lys Leu Ile Ser Asn Arg Asp Arg Val Arg Ala Gln Val Glu
50 55 60

Ala Ile Asp Ser Lys Thr Glu Lys Val Arg Asp Val Val Phe Glu Trp
65 70 75 80

Leu Lys Glu Ala Glu Ile Val Met Gln Lys Met Glu Asn Leu Lys Leu
85 90 95

Gln Ser Lys Pro Pro Ser Trp Ile Glu Phe Asn Lys Leu Gln Glu Lys
100 105 110

Ile Thr Ala Leu Asn Lys Lys Cys Asn Phe Glu Pro Phe Ser Thr Thr
115 120 125

Ile Pro Ser Leu Glu His Phe Ser Leu Gly Asn Asn Phe Glu Cys Phe
130 135 140

Lys Ser Thr Glu Lys Ala Ser Asp Glu Leu Leu Glu Ala Leu Gln Asp
145 150 155 160

Asp Asn Cys Cys Met Ile Gly Leu Tyr Gly Arg Arg Asp Ser Gly Lys
165 170 175

Thr Thr Leu Val Lys Val Met Glu Gln Lys Val Gln Tyr Leu Asn Ile
180 185 190

Phe Asp Glu Ile Leu Phe Val Asn Val Thr Lys Asn Pro Asn Ile Thr
195 200 205

Ala Met Gln Asp Glu Ile Ala Asp Ser Leu Asn Ile Arg Phe Asp Arg
210 215 220

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

Met Asp Arg Pro Ile Leu Val Ile Phe Asp Asp Val Arg Ala Lys Phe
245 250 255

Asp Leu Arg Asp Val Gly Ile Pro Ser Asn Ser Asn Arg Cys Lys Val
260 265 270

Leu Leu Thr Ala Arg Arg Gln Lys Tyr Cys Asp Leu Val Tyr Cys Gln
275 280 285

Arg Lys Ile Leu Leu Asp Pro Leu Ser Thr Glu Glu Ala Ser Thr Leu
290 295 300

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

Asp Leu Leu Asn Val Ala Arg Glu Ile Ala Phe Glu Cys Asp Gly Leu
325 330 335

Pro Gly Lys Ile Ile Lys Ala Gly Ser Ser Val Arg Ser Lys Pro Met
340 345 350

Glu Glu Trp Glu Lys Ser Leu Asp Asn Leu Arg His Ser Thr Ala Gln
355 360 365

Trp Glu Met Phe Leu Ser Phe Arg Gly Glu Asp Thr Arg Tyr Ser Phe
370 375 380

Thr Gly Ser Leu Phe Gln Ala Leu Ser Gln Gly Gly Phe Lys Thr Phe
385 390 395 400

Met Asp Asp Glu Gly Leu His Thr Gly Asp Arg Val Ser Pro Cys Leu
405 410 415

Arg Asn Ala Ile Glu Ala Ser Arg Leu Ser Ile Ile Val Leu Ser Glu
420 425 430

Asn Tyr Ala Asn Ser Thr Trp Cys Leu Asp Glu Leu Val Lys Ile Leu
435 440 445

Glu Cys Lys Lys Trp Asn Asn Gln Leu Val Trp Pro Ile Phe Tyr Lys
450 455 460

Val Glu Pro Ser Asp Ile Arg His Leu Arg Asn Gly Tyr Gly Lys Asp
465 470 475 480

Met Ala Gln His Glu Lys Lys Phe Gly Ile Asp Ser Glu Arg Val Gln
485 490 495

Lys Trp Lys Ser Ala Leu Leu Glu Val Ser Asn Leu Ser Gly Met Thr
500 505 510

Tyr Thr Thr Gly Tyr Glu Tyr Glu Phe Ile Gln Lys Ile Val Glu Asp
515 520 525

Ala Asn Asn Ile Lys Ser Arg Leu Gln Ile Arg Ser Val
530 535 540

<210> 36
<211> 543
<212> PRT
<213> Medicago

<400> 36

Met Ala Pro Asn Leu Val Leu Leu Cys Val Ser Val Tyr Leu Phe Ala
1 5 10 15

Ile Thr Thr Thr Ile Ile Val Ala Glu Asp Pro Tyr Arg Phe Phe Asn
20 25 30

Trp Asn Val Thr Tyr Gly Asp Ile Tyr Pro Leu Gly Val Arg Gln Gln
35 40 45

Gly Ile Leu Ile Asn Gly Gln Phe Pro Gly Pro Asp Ile His Ser Val
50 55 60

Thr Asn Asp Asn Leu Ile Ile Asn Val Phe Asn Ser Leu Asp Glu Pro
65 70 75 80

Phe Leu Ile Ser Trp Asn Gly Val Gln Gln Arg Arg Asn Ser Tyr Glu
85 90 95

Asp Gly Val Phe Gly Thr Thr Cys Pro Ile Pro Pro Gly Lys Asn Phe

100 105 110

Thr Tyr Ile Leu Gln Val Lys Asp Gln Ile Gly Ser Phe Tyr Tyr Phe
115 120 125

Pro Ser Leu Ala Phe His Lys Ala Ala Gly Gly Phe Gly Gly Ile Arg
130 135 140

Ile Leu Ser Arg Pro Arg Ile Pro Val Pro Phe Asp Asp Pro Ala Gly
145 150 155 160

Asp Tyr Thr Val Leu Ile Gly Asp Trp Tyr Lys Ser Asn His Thr Asp
165 170 175

Leu Lys Ala Gln Leu Asp Asn Gly Lys Lys Leu Pro Phe Pro Asp Gly
180 185 190

Ile Leu Ile Asn Gly Arg Gly Ser Gly Gly Ser Ser Leu Asn Val Glu
195 200 205

Gln Gly Lys Thr Tyr Arg Leu Arg Ile Ser Asn Val Gly Leu Glu Asn
210 215 220

Ser Leu Asn Phe Arg Ile Gln Asn His Lys Met Lys Leu Val Glu Val
225 230 235 240

Glu Gly Thr His Thr Leu Gln Thr Thr Tyr Ser Ser Leu Asp Val His

245 250 255

Val Gly Gln Ser Tyr Ser Val Leu Val Thr Ala Asp Gln Pro Ser Gln
260 265 270

Asp Tyr Tyr Ile Val Val Ser Ser Arg Phe Thr Asn Pro Val Leu Thr
275 280 285

Ser Thr Gly Ile Leu Arg Tyr Ser Asn Ser Ala Gly Pro Val Ser Gly
290 295 300

Pro Pro Pro Gly Gly Pro Thr Ile Gln Ile Asp Trp Ser Leu Asn Gln
305 310 315 320

Ala Arg Ser Ile Arg Thr Asn Leu Thr Ala Ser Gly Pro Arg Pro Asn
325 330 335

Pro Gln Gly Ser Tyr His Tyr Gly Met Ile Asn Leu Thr Arg Thr Ile
340 345 350

Val Leu Ser Ser Ser Ala Gly Gln Val Asn Gly Lys Gln Arg Tyr Ala
355 360 365

Ile Asn Ser Val Ser Tyr Val Ala Pro Asp Thr Pro Leu Lys Leu Ala
370 375 380

Asp Phe Phe Lys Ile Ala Gly Val Tyr Arg Pro Gly Ser Ile Ser Asp

385 390 395 400

Arg Pro Ser Gly Gly Gly Ile Tyr Leu Asp Thr Ser Val Met Gln Thr
405 410 415

Asp Tyr Arg Thr Phe Val Glu Ile Val Phe Gln Asn Asp Glu Asp Ile
420 425 430

Leu Gln Ser Tyr His Leu Asp Gly Tyr Ser Phe Phe Val Val Gly Met
435 440 445

Asp Gly Gly Gln Trp Thr Ser Asp Lys Arg Asn Gln Tyr Asn Leu Arg
450 455 460

Asp Ala Val Ser Arg Ser Thr Thr Gln Val Tyr Pro Lys Ser Trp Thr
465 470 475 480

Ala Ile Tyr Val Pro Leu Asp Asn Val Gly Met Trp Asn Leu Arg Ser
485 490 495

Glu Phe Trp Ala Arg Gln Tyr Leu Gly Gln Gln Phe Tyr Met Arg Val
500 505 510

Tyr Thr Thr Ser Thr Ser Leu Arg Asp Glu Tyr Pro Ile Pro Lys Asn
515 520 525

Ala Leu Leu Cys Gly Arg Ala Thr Gly Arg His Thr Arg Pro Leu

530 535 540

<210> 37
<211> 224
<212> PRT
<213> Arabidopsis

<400> 37

Met Ala Glu Lys Glu Glu Asp Val Lys Leu Leu Gly Phe Trp Ala Ser
1 5 10 15

Pro Phe Thr Arg Arg Val Glu Met Ala Phe Lys Leu Lys Gly Val Pro
20 25 30

Tyr Glu Tyr Leu Glu Gln Asp Ile Val Asn Lys Ser Pro Leu Leu Leu
35 40 45

Gln Ile Asn Pro Val Tyr Lys Lys Val Pro Val Leu Val Tyr Lys Gly
50 55 60

Lys Ile Leu Ser Glu Ser His Val Ile Leu Glu Tyr Ile Asp Gln Ile
65 70 75 80

Trp Lys Asn Asn Pro Ile Leu Pro Gln Asp Pro Tyr Glu Lys Ala Met
85 90 95

Ala Leu Phe Trp Ala Lys Phe Val Asp Glu Gln Val Gly Pro Val Ala
100 105 110

Phe Met Ser Val Ala Lys Ala Glu Lys Gly Val Glu Val Ala Ile Lys
115 120 125

Glu Ala Gln Glu Leu Phe Met Phe Leu Glu Lys Glu Val Thr Gly Lys
130 135 140

Asp Phe Phe Gly Gly Lys Thr Ile Gly Phe Leu Asp Leu Val Ala Gly
145 150 155 160

Ser Met Ile Pro Phe Cys Leu Ala Arg Gly Trp Glu Gly Met Gly Ile
165 170 175

Asp Met Ile Pro Glu Glu Lys Phe Pro Glu Leu Asn Arg Trp Ile Lys
180 185 190

Asn Leu Lys Glu Ile Glu Ile Val Arg Glu Cys Ile Pro Pro Arg Glu
195 200 205

Glu Gln Ile Glu His Met Lys Lys Val Val Glu Arg Ile Lys Ser Ala
210 215 220

<210> 38
<211> 87
<212> PRT
<213> Arabidopsis

<400> 38

Met Ala Asn Val Ser Ala Leu Leu Thr Ile Ala Leu Leu Leu Cys Ser
1 5 10 15

Thr Leu Met Cys Thr Ala Arg Pro Glu Pro Ala Ile Ser Ile Ser Ile
20 25 30

Thr Thr Ala Ala Asp Pro Cys Asn Met Glu Lys Lys Ile Glu Gly Lys
35 40 45

Leu Asp Asp Met His Met Val Asp Glu Asn Cys Gly Ala Asp Asp Glu
50 55 60

Asp Cys Leu Met Arg Arg Thr Leu Val Ala His Thr Asp Tyr Ile Tyr
65 70 75 80

Thr Gln Lys Lys Lys His Pro
85

<210> 39
<211> 1134
<212> PRT
<213> Medicago

<400> 39

Met Glu Ala Ser Ser Ser Ser Ser Cys Arg Ser Ser Ser Thr Thr Ser
1 5 10 15

Leu Cys Thr Tyr His Val Phe Leu Ser Phe Arg Gly Glu Asp Thr Arg
20 25 30

Lys Gly Phe Thr Asp His Leu Cys Ala Ala Leu Glu Arg Lys Gly Ile
35 40 45

Thr Thr Phe Lys Asp Asp Lys Asp Leu Glu Arg Gly Gln Val Ile Ser
50 55 60

Glu Lys Leu Ile Asn Ala Ile Lys Asp Ser Met Phe Ala Ile Thr Ile
65 70 75 80

Leu Ser Pro Asp Tyr Ala Ser Ser Thr Trp Cys Leu Asp Glu Leu Gln
85 90 95

Met Ile Met Glu Cys Ser Ser Lys Asn Asn Leu His Val Leu Pro Val
100 105 110

Phe Tyr Gly Val Asp Pro Ser Asp Val Arg His Gln Arg Gly Cys Phe
115 120 125

Glu Glu Ala Phe Arg Lys His Gln Glu Lys Phe Gly Gln His Ser Asp
130 135 140

Arg Val Asp Arg Trp Arg Asp Ala Phe Thr Gln Val Ala Ser Tyr Ser
145 150 155 160

Gly Trp Asp Ser Lys Gly Gln His Glu Ala Ser Leu Val Glu Asn Ile
165 170 175

Ala Gln His Ile His Arg Lys Leu Val Pro Lys Leu Pro Ser Cys Thr
180 185 190

Glu Asn Leu Val Gly Ile Val Ser Lys Val Glu Glu Val Asn Lys Phe
195 200 205

Leu Gly Met Gly Leu Asn Asp Val Arg Phe Ile Gly Ile Trp Gly Met
210 215 220

Gly Gly Ile Gly Lys Ser Thr Ile Ala Arg Ala Val Tyr Glu Thr Ile
225 230 235 240

Arg Cys Glu Phe Glu Leu Thr Cys Phe Leu Glu Asn Val Arg Glu Ile
245 250 255

Ser Glu Thr Asn Gly Leu Val His Leu Gln Arg Gln Leu Leu Ser His
260 265 270

Leu Ser Ile Ser Arg Asn Asp Phe His Asp Leu Tyr Asp Gly Lys Lys
275 280 285

Thr Ile Gln Asn Ser Leu Cys Arg Lys Lys Val Leu Leu Val Leu Asp
290 295 300

Asp Val Asn Glu Leu Asn Gln Leu Glu Asn Leu Val Gly Lys Gln Asp
305 310 315 320

Trp Phe Gly Pro Gly Ser Arg Val Ile Ile Thr Thr Arg Asp Lys His
325 330 335

Leu Leu Met Thr His Gly Val His Lys Thr Tyr Lys Thr Gly Met Leu
340 345 350

Cys Lys His Asp Ala Leu Val Leu Phe Cys Leu Lys Ala Phe Lys Gly
355 360 365

Asp Lys Pro Gln Glu Gly Tyr Leu Asp Leu Ser Lys Glu Val Val Asp
370 375 380

Tyr Cys Gly Gly Leu Pro Leu Ala Leu Glu Val Leu Gly Ser Tyr Leu
385 390 395 400

Tyr Gly Arg Asn Ile Asp Val Trp His Ser Ala Val Lys Lys Leu Arg
405 410 415

Ser Phe Pro His Pro Arg Val Gln Asp Asn Leu Lys Ile Ser Tyr Asp
420 425 430

Ser Leu Asp Thr Met Glu Lys Asp Ile Phe Leu Asp Ile Ala Cys Phe
435 440 445

Phe Lys Gly Met Lys Gly Asp Lys Val Ile Asp Ile Leu Glu Ser Cys
450 455 460

Gly Tyr Phe Pro Gln Ile Gly Ile Gln Ile Leu Ile Glu Arg Ser Leu
465 470 475 480

Ile Thr Leu Asp Ser Val Asn Asn Lys Leu Gly Met His Asp Leu Leu
485 490 495

Gln Glu Met Gly Arg Asp Ile Val Phe Gln Glu Ser Pro Asn Asp Pro
500 505 510

Cys Arg Arg Ser Arg Leu Trp Ser Gln Glu Asp Ile Asp Arg Val Leu
515 520 525

Thr Lys Asn Lys Gly Thr Glu Ala Ile Asn Ser Ile Asp Met Lys Leu
530 535 540

Leu Gln Pro Tyr Glu Ala His Trp Asn Thr Glu Ala Phe Ser Lys Thr
545 550 555 560

Ser Gln Leu Lys Phe Leu Ser Leu Cys Glu Met Gln Leu Pro Leu Gly
565 570 575

Leu Ser Cys Leu Pro Ser Ser Leu Lys Val Leu His Trp Arg Gly Cys
580 585 590

Pro Leu Lys Thr Leu Pro Ile Thr Thr Gln Leu Asp Glu Leu Val Asp
595 600 605

Ile Thr Leu Ser His Ser Lys Ile Glu Gln Leu Trp Gln Gly Val Lys
610 615 620

Phe Met Glu Lys Met Lys Tyr Leu Asn Leu Ala Phe Ser Lys Asn Leu
625 630 635 640

Lys Arg Leu Pro Asp Phe Ser Gly Val Pro Asn Leu Glu Lys Leu Ile
645 650 655

Leu Glu Gly Cys Glu Gly Leu Ile Glu Val His Pro Ser Leu Ala His
660 665 670

His Lys Lys Val Val Leu Val Asn Leu Lys Asp Cys Lys Ser Leu Lys
675 680 685

Ser Leu Ser Gly Lys Leu Glu Met Ser Ser Leu Lys Lys Leu Ile Leu
690 695 700

Ser Gly Ser Ser Lys Phe Lys Phe Leu Pro Glu Phe Gly Glu Lys Met
705 710 715 720

Glu Asn Leu Ser Met Leu Ala Leu Glu Gly Thr Asp Ile Arg Lys Leu
725 730 735

Pro Leu Ser Leu Gly Arg Leu Val Gly Leu Thr Asn Leu Asn Leu Lys
740 745 750

Asp Cys Lys Ser Leu Val Cys Leu Pro Asp Thr Ile His Gly Leu Asn
755 760 765

Ser Leu Ile Thr Leu Asp Ile Ser Gly Cys Ser Lys Leu Cys Arg Leu
770 775 780

Pro Asp Gly Leu Lys Glu Ile Lys Cys Leu Glu Glu Leu His Ala Asn
785 790 795 800

Asp Thr Ala Ile Asp Glu Leu Pro Ser Ser Ile Phe Tyr Leu Asp Ser
805 810 815

Leu Lys Val Leu Ser Phe Ala Gly Cys Gln Gly Pro Ser Thr Thr Ser
820 825 830

Met Asn Trp Phe Leu Pro Phe Asn Leu Met Phe Gly Ser Gln Pro Ala
835 840 845

Ser Asn Gly Phe Arg Leu Pro Ser Ser Val Met Gly Leu Pro Ser Leu
850 855 860

Glu Tyr Leu Asn Leu Ser Tyr Cys Asn Leu Ser Glu Glu Ser Phe Pro
865 870 875 880

Asn Tyr Phe His His Leu Ser Ser Leu Lys Ser Leu Asp Leu Thr Gly
885 890 895

Asn Asn Phe Val Ile Ile Pro Ser Ser Ile Ser Lys Leu Ser Arg Leu
900 905 910

Arg Phe Leu Cys Leu Asn Trp Cys Gln Lys Leu Gln Leu Leu Pro Glu
915 920 925

Leu Pro Leu Thr Met Thr Gln Leu Asn Ala Ser Asn Cys Asp Ser Leu
930 935 940

Asp Thr Met Lys Phe Asn Pro Ala Lys Leu Cys Ser Leu Phe Ala Ser
945 950 955 960

Pro Arg Lys Leu Ser Tyr Val Gln Glu Leu Tyr Lys Arg Phe Glu Asp
965 970 975

Arg Cys Leu Pro Thr Thr Arg Phe Asp Met Leu Ile Pro Gly Asp Glu
980 985 990

Ile Pro Ser Trp Phe Val Pro Gln Arg Ser Val Ser Trp Ala Lys Val
995 1000 1005

His Ile Pro Asn Asn Phe Pro Gln Asp Glu Trp Val Gly Phe Ala
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Leu Cys Phe Leu Leu Val Ser Tyr Ala Asp Pro Pro Glu Leu Cys
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Lys His Glu Ile Asp Cys Tyr Leu Phe Ala Ser Asn Gly Lys Lys
1040 1045 1050

Leu Ile Thr Thr Arg Ser Leu Pro Pro Met Asp Pro Cys Tyr Pro
1055 1060 1065

His Leu Tyr Ile Leu Tyr Met Ser Ile Asp Glu Phe Arg Asp Glu
1070 1075 1080

Ile Leu Lys Asp Asp Tyr Trp Ser Glu Ser Gly Ile Glu Phe Val
1085 1090 1095

Leu Lys Cys Tyr Cys Cys Gln Ser Leu Gln Val Val Ser Cys Gly
1100 1105 1110

Ser Arg Leu Val Cys Lys Gln Asp Val Glu Asp Trp Ser Lys Met
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Ser His Phe Asn Glu Ser
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Gln Asp Gly Val Ser Ser Ile Lys Val Val Tyr Ala Lys Asp Ser Gln
35 40 45

Asp Ile Glu Gly Ser Glu His Gly Lys Lys Thr Leu Leu Gly Phe Glu
50 55 60

Thr Phe Glu Val Asp Ala Asp Asp Tyr Ile Val Ala Val Gln Val Thr
65 70 75 80

Tyr Asp Asn Val Phe Gly Gln Asp Ser Asp Ile Ile Thr Ser Ile Thr
85 90 95

Phe Asn Thr Phe Lys Gly Lys Thr Ser Pro Pro Tyr Gly Leu Glu Thr
100 105 110

Gln Lys Lys Phe Val Leu Lys Asp Lys Asn Gly Gly Lys Leu Val Gly
115 120 125

Phe His Gly Arg Ala Gly Glu Ala Leu Tyr Ala Leu Gly Ala Tyr Phe

130 135 140

Ala Thr Thr Thr Thr Pro Val Thr Pro Ala Lys Lys Leu Ser Ala Ile
145 150 155 160

Gly Gly Asp Glu Gly Thr Ala Trp Asp Asp Gly Ala Tyr Asp Gly Val
165 170 175

Lys Lys Val Tyr Val Gly Gln Gly Gln Asp Gly Ile Ser Ala Val Lys
180 185 190

Phe Glu Tyr Asn Lys Gly Ala Glu Asn Ile Val Gly Gly Glu His Gly
195 200 205

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

Glu Tyr Ile Thr Ala Val Glu Gly Thr Tyr Asp Lys Ile Phe Gly Ser
225 230 235 240

Asp Gly Leu Ile Ile Thr Met Leu Arg Phe Lys Thr Asn Lys Gln Thr
245 250 255

Ser Ala Pro Phe Gly Leu Glu Ala Gly Thr Ala Phe Glu Leu Lys Glu
260 265 270

Glu Gly His Lys Ile Val Gly Phe His Gly Lys Ala Ser Glu Leu Leu

275 280 285

His Gln Phe Gly Val His Val Met Pro Leu Thr Asn
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Ser Asp Glu Glu Arg Asp Lys Leu Leu Leu Gln Ile Glu Glu Glu Cys
35 40 45

Leu Asn Val Tyr Lys Lys Lys Val Glu Leu Ala Ala Lys Ser Arg Ala
50 55 60

Glu Leu Leu Gln Thr Leu Ser Asp Ala Thr Val Glu Leu Ser Asn Leu
65 70 75 80

Thr Thr Ala Leu Gly Glu Lys Ser Tyr Ile Asp Ile Pro Asp Lys Thr
85 90 95

Ser Gly Thr Ile Lys Glu Gln Leu Ser Ala Ile Ala Pro Ala Leu Glu
100 105 110

Gln Leu Trp Gln Gln Lys Glu Glu Arg Val Arg Ala Phe Ser Asp Val
115 120 125

Gln Ser Gln Ile Gln Lys Ile Cys Glu Glu Ile Ala Gly Gly Leu Asn
130 135 140

Asn Gly Pro His Val Val Asp Glu Thr Asp Leu Ser Leu Lys Arg Leu
145 150 155 160

Asp Asp Phe Gln Arg Lys Leu Gln Glu Leu Gln Lys Glu Lys Ser Asp
165 170 175

Arg Leu Gln Lys Val Leu Glu Phe Val Ser Thr Val His Asp Leu Cys
180 185 190

Ala Val Leu Arg Leu Asp Phe Leu Ser Thr Val Thr Glu Val His Pro
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Ser Leu Asp Glu Ala Asn Gly Val Gln Thr Lys Ser Ile Ser Asn Glu
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Thr Leu Ala Arg Leu Ala Lys Thr Val Leu Thr Leu Lys Glu Asp Lys
225 230 235 240

Met Gln Arg Leu Lys Lys Leu Gln Glu Leu Ala Thr Gln Leu Thr Asp
245 250 255

Leu Trp Asn Leu Met Asp Thr Ser Asp Glu Glu Arg Glu Leu Phe Asp
260 265 270

His Val Thr Ser Asn Ile Ser Ala Ser Val His Glu Val Thr Ala Ser
275 280 285

Gly Ala Leu Ala Leu Asp Leu Ile Glu Gln Ala Glu Val Glu Val Asp
290 295 300

Arg Leu Asp Gln Leu Lys Ser Ser Arg Met Lys Glu Ile Ala Phe Lys
305 310 315 320

Lys Gln Ser Glu Leu Glu Glu Ile Tyr Ala Arg Ala His Ile Glu Ile
325 330 335

Lys Pro Glu Val Val Arg Glu Arg Ile Met Ser Leu Ile Asp Ala Gly
340 345 350

Asn Thr Glu Pro Thr Glu Leu Leu Ala Asp Met Asp Ser Gln Ile Ala
355 360 365

Lys Ala Lys Glu Glu Ala Phe Ser Arg Lys Glu Ile Leu Asp Arg Val
370 375 380

Glu Lys Trp Met Ser Ala Cys Glu Glu Glu Ser Trp Leu Glu Asp Tyr
385 390 395 400

Asn Arg Asp Gln Asn Arg Tyr Ser Ala Ser Arg Gly Ala His Leu Asn
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Leu Lys Arg Ala Glu Lys Ala Arg Ile Leu Val Ser Lys Ile Thr Ala
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Met Val Asp Thr Leu Ile Ala Lys Thr Arg Ala Trp Glu Glu Glu Asn
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Ser Met Ser Phe Glu Tyr Asp Gly Val Pro Leu Leu Ala Met Leu Asp
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Glu Tyr Thr Met Leu Arg Gln Glu Arg Glu Asp Glu Lys Arg Arg Leu
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485 490 495

Ala Phe Gly Ser Lys Pro Ser Pro Ala Arg Pro Val Ser Ala Lys Lys
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Pro Val Gly Thr Arg Val Asn Gly Gly Gly Leu Asn Glu Thr Pro Met
515 520 525

Arg Arg Leu Ser Met Asn Ser Asn Gln Asn Gly Ser Lys Ser Lys Arg
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545 550 555 560

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Ser Pro

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Pro Val Val Arg Cys Ser Ser Thr Arg Asp Val Pro Lys Leu Glu Leu
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Phe Ser Arg Gly Lys Phe Asp Arg Ile Leu Gln Asp Pro Pro Leu Ile
50 55 60

Glu Lys Ala Glu Ser Glu Leu Ser Asp Tyr Cys Ser Thr Leu Glu Gly
65 70 75 80

Asp Asp Ser Tyr Ser Cys Trp Arg Ala Tyr Phe Glu Leu Lys Asp Leu
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Glu Arg Glu Lys Pro Lys Val Glu Val Glu Asn Leu Ile Leu Gln Thr
100 105 110

Gly Gly Leu Lys Ser Leu Ile Gly Cys Leu His Gly Val Ala Ser Met
115 120 125

Glu Lys Asp Asn Lys Thr Lys Asn Gly Leu His Val Gly Glu Glu Ser
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Asp Arg Glu Lys Gly Met Asn Leu His Ile His Ile Pro Asp Gly Leu
145 150 155 160

Pro Lys Ser Glu Gln Glu Leu Glu Glu Glu Glu Lys Ser Lys Met Pro
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gagtttcacg gcaagcctca gttcgtcgaa ccgtcgaagt cttgttttgc ggtggtcagg 180

tgttcaagca cgagagacgt tcctaagctt gagctcttca gccgcggaaa attcgaccgt 240

gtacttcaag atccgccatt aatagaaaag gccgagaccg aactctcaga ttactgttct 300

acactcgaag gtgatgcttc ttacagctgc tggagagctt actttgaact caaagacctt 360

gagaaggaga agccaaaggt ggaagttgag aatctaatct tgcaaacagg cggtttgaaa 420

ttgctaatcg ggtgtttaca tggacttgct tcgatgaaga aggaaagcaa aaccaagaat 480

ggtttagagg ttacagagga aacggattca gataagatga aaccgcacgt tcacgtcccc 540

gatggtttac caaaatctca agaagaattg gaagaagaag agaaatcaag aatgccagat 600

tctgctttca caagattgct tagagccaaa ggaaccatcc ctgcttggtt ctctcacgct 660

ccggaccacg aaacagactg agagaatcca tctcacagag ttttacttct atgtacatat 720

agcaacaagt ggtttcttga tattttgctt tataacatat aattattata ataccttttc 780

ataataccta taaaatatgg tttgtcaatg tgtgatgatc ttgaatggtt taatgataaa 840

gttgttttga agccgtgtgc ttattt 866

<210> 134
<211> 910
<212> ADN
<213> Raphanus sativus

<400> 134
gaagcagtgg tatcacatta cggccgggga ctcttctgca taatctccaa cttcaaaaac 60

caaccttctt tcttgctact tgctaacaat tatatctttc agtgaagatg ataaagtctg 120

ttactcttcg accgtttcct ctccctatag agtttcacgg caagcctaag ttcgtccaaa 180

cgtcgaagtc ttgtttcccg gtggtcaggt gttcaagcac gagagacgtt cctaagcttg 240

agctcttcag ccgcggacag ttcgaccgtg ttcttcaaga tcccccatta atagaaaaaa 300

ccgagaccga actctcagat tactgttgta aactcgaagg tgatgactca tacagctgct 360

ggagagctta ctttgaactc aaagaccttg agaaagagaa gccaaaggtg gaagttgaga 420

acctaatctt gcaaacagac ggtgtgaaat cgctaatcgg gtgtttacat ggaatcgctt 480

caatggagaa ggaaagcaaa accaagaatg gtttagaggt tagagaggaa tcagattcag 540

acaagatgaa actgcacgtt catgttcctg atggtttacc aaaatctcaa caagaattgg 600

aggaagaaga gaaatcaaga atgccagatt ctgctttcac aagattgctt agagccaaag 660

gaaccatccc tgcttggttc tctcaccctc ctgaccacaa aacagactga agaatccatc 720

tcacacagtt ttacttctat gtacatataa ctattgtaat atatctgttt ttttaatata 780

tcttcataat gcctataaaa tatagctgtc aatgtgtgat gatcttgaat ggttcgatga 840

taaagttgtt tccgagccgt gtgcttattt tagtacttgg ttttggttac aaagatattt 900

ctattcttga 910

<210> 135
<211> 331
<212> PRT
<213> Arabidopsis lyrata

<400> 135

Met Ala Arg Leu Lys Ser Phe Leu Leu Leu Leu Ser Leu Leu Cys Phe
1 5 10 15

Val Pro Leu Cys Leu Cys Asp Thr Ser Asn Gly Gly Lys Leu Cys Ser
20 25 30

Gly Phe Tyr Ala Arg Ser Cys Pro Gln Ala Glu Glu Ile Val Arg Ser
35 40 45

Val Val Ala Lys Ala Val Val Arg Glu Thr Arg Met Ala Ala Ser Leu
50 55 60

Leu Arg Leu His Phe His Asp Cys Phe Val Gln Gly Cys Asp Gly Ser
65 70 75 80

Leu Leu Leu Asp Ser Ser Gly Arg Ile Val Ser Glu Lys Asn Ser Asn
85 90 95

Pro Asn Ser Arg Ser Ala Arg Gly Phe Asp Val Val Asp Gln Ile Lys
100 105 110

Ala Glu Leu Glu Lys Gln Cys Pro Gly Thr Val Ser Cys Ala Asp Val
115 120 125

Leu Thr Leu Ala Ala Arg Asp Ser Ser Val Val Thr Gly Gly Pro Ser
130 135 140

Trp Val Val Pro Leu Gly Arg Arg Asp Ser Arg Ser Ala Ser Leu Ser
145 150 155 160

Gly Ser Asn Asn Asn Ile Pro Ala Pro Asn Asn Thr Phe Gln Thr Ile
165 170 175

Leu Ser Lys Phe Asn Arg Gln Gly Leu Asp Val Thr Asp Leu Val Ala
180 185 190

Leu Ser Gly Ser His Thr Ile Gly Phe Ser Arg Cys Thr Ser Phe Arg
195 200 205

Gln Arg Leu Tyr Asn Gln Ser Gly Asn Gly Arg Pro Asp Met Thr Leu
210 215 220

Glu Gln Ser Phe Ala Ala Asn Leu Arg Gln Arg Cys Pro Arg Ser Gly
225 230 235 240

Gly Asp Gln Ile Leu Ser Val Leu Asp Ile Ile Ser Ala Ala Lys Phe
245 250 255

Asp Asn Ser Tyr Phe Lys Asn Leu Leu Glu Asn Met Gly Leu Leu Asn
260 265 270

Ser Asp Gln Val Leu Phe Ser Ser Asn Glu Lys Ser Arg Glu Leu Val
275 280 285

Lys Lys Tyr Ala Glu Asp Gln Gly Glu Phe Phe Glu Gln Phe Ala Glu
290 295 300

Ser Met Ile Lys Met Gly Asn Ile Ser Pro Leu Thr Gly Ser Ser Gly
305 310 315 320

Glu Ile Arg Lys Asn Cys Arg Lys Ile Asn Ser
325 330

<210> 136
<211> 331
<212> PRT
<213> Brassica rapa

<400> 136

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

Leu Pro Ile Tyr Leu Cys Gln Gln Ser Tyr Gly Gly Lys Leu Asn Pro
20 25 30

Gly Tyr Tyr Ala His Ser Cys Pro Gln Ala Gly Glu Ile Val Arg Ser
35 40 45

Val Val Ala Gln Ala Val Ala Arg Glu Thr Arg Met Ala Ala Ser Leu
50 55 60

Met Arg Leu His Phe His Asp Cys Phe Val Gln Gly Cys Asp Gly Ser
65 70 75 80

Leu Leu Leu Asp Ser Ser Gly Arg Ile Val Ser Glu Lys Ser Ser Asn
85 90 95

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

Ala Gln Leu Glu Lys Gln Cys Pro Gly Thr Val Ser Cys Ala Asp Ile
115 120 125

Leu Thr Leu Ala Ala Arg Asp Ser Ser Val Leu Thr Gly Gly Pro Ser
130 135 140

Trp Met Val Pro Leu Gly Arg Arg Asp Ser Arg Ser Ala Ser Leu Ser
145 150 155 160

Gly Ser Asn Asn Asn Ile Pro Ala Pro Asn Asn Thr Phe Gln Thr Ile
165 170 175

Leu Ser Lys Phe Asn Arg Gln Gly Leu Asp Val Thr Asp Leu Val Ala
180 185 190

Leu Ser Gly Ser His Thr Ile Gly Phe Ser Arg Cys Thr Ser Phe Arg
195 200 205

Gln Arg Leu Tyr Asn Gln Ser Gly Asn Gly Arg Pro Asp Met Thr Leu
210 215 220

Glu Gln Ser Phe Ala Ala Asn Leu Arg Gln Arg Cys Pro Arg Ser Gly
225 230 235 240

Gly Asp Gln Asn Leu Ser Val Leu Asp Ile Val Ser Ala Ala Lys Phe
245 250 255

Asp Asn Ser Tyr Phe Lys Asn Leu Ile Glu Asn Met Gly Leu Leu Asn
260 265 270

Ser Asp Gln Val Leu Phe Ser Ser Asn Asp Lys Ser Arg Asp Leu Val
275 280 285

Lys Lys Tyr Ala Glu Asp Gln Glu Glu Phe Phe Glu Gln Phe Ala Glu
290 295 300

Ser Met Ile Lys Met Gly Asn Ile Ser Pro Leu Thr Gly Ser Ser Gly
305 310 315 320

Glu Ile Arg Lys Asp Cys Arg Lys Ile Asn Ser
325 330

<210> 137
<211> 331
<212> PRT
<213> Raphanus sativus

<220>
<221> misc_feature
<222> (178)..(178)
<223> Xaa puede ser cualquier aminoácido de origen natural

<220>
<221> misc_feature
<222> (181)..(181)
<223> Xaa puede ser cualquier aminoácido de origen natural

<400> 137

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

Leu Pro Leu Cys Leu Cys His Lys Thr Ser Gly Gly Lys Leu Ser Pro
20 25 30

Tyr Tyr Tyr Ala His Ser Cys Pro Gln Ala Gly Glu Ile Val Arg Ser
35 40 45

Val Val Ala Lys Ala Val Ala Arg Glu Thr Arg Met Ala Ala Ser Leu

50 55 60

Met Arg Leu His Phe His Asp Cys Phe Val Lys Gly Cys Asp Gly Ser
65 70 75 80

Leu Leu Leu Asp Ser Ser Gly Arg Ile Val Ser Glu Lys Asn Ser Asn
85 90 95

Pro Asn Arg Lys Ser Ala Arg Gly Phe Asp Val Val Asp Gln Ile Lys
100 105 110

Ala Gln Leu Glu Lys Glu Cys Pro Gly Thr Val Ser Cys Ala Asp Ala
115 120 125

Leu Thr Leu Ala Ala Arg Asp Ser Ser Val Leu Thr Gly Gly Pro Ser
130 135 140

Trp Met Val Pro Leu Gly Arg Arg Asp Ser Arg Ser Ala Ser Leu Ser
145 150 155 160

Gly Ser Asn Asn Asn Ile Pro Ala Pro Asn Asn Thr Phe Gln Thr Ile
165 170 175

Leu Xaa Lys Phe Xaa Arg Gln Gly Leu Asp Ile Thr Asp Leu Val Ala
180 185 190

Leu Ser Gly Ser His Thr Ile Gly Phe Ser Arg Cys Thr Ser Phe Arg

195 200 205

Gln Arg Leu Tyr Asn Gln Ser Gly Asn Gly Arg Pro Asp Met Thr Leu
210 215 220

Glu Gln Ser Phe Ala Ala Asn Leu Arg Gln Arg Cys Pro Arg Ser Gly
225 230 235 240

Gly Asp Gln Asn Leu Ser Val Leu Asp Lys Val Ser Pro Ala Asn Phe
245 250 255

Asp Asn Ser Tyr Phe Lys Asn Leu Val Glu Asn Met Gly Leu Leu Ser
260 265 270

Ser Asp Gln Val Leu Phe Ser Ser Asn Asp Lys Ser Arg Glu Leu Val
275 280 285

Lys Lys Tyr Ala Glu Asp Gln Gly Glu Phe Phe Lys Gln Phe Ala Glu
290 295 300

Ser Met Ile Lys Met Gly Asn Ile Ser Pro Leu Thr Gly Ser Ser Gly
305 310 315 320

Glu Ile Arg Lys Asn Cys Arg Lys Ile Asn Ser
325 330

<210> 138

<211> 338
<212> PRT
<213> Arabidopsis

<400> 138

Met Ala Arg Ile Gly Ser Phe Leu Ile Ile Leu Tyr Leu Ile Tyr Ala
1 5 10 15

Leu Thr Leu Cys Ile Cys Asp Asp Asp Glu Ser Asn Tyr Gly Gly Asp
20 25 30

Lys Gly Asn Leu Phe Pro Gly Phe Tyr Arg Ser Ser Cys Pro Arg Ala
35 40 45

Glu Glu Ile Val Arg Ser Val Val Ala Lys Ala Val Ala Arg Glu Thr
50 55 60

Arg Met Ala Ala Ser Leu Met Arg Leu His Phe His Asp Cys Phe Val
65 70 75 80

Gln Gly Cys Asp Gly Ser Leu Leu Leu Asp Thr Ser Gly Ser Ile Val
85 90 95

Thr Glu Lys Asn Ser Asn Pro Asn Ser Arg Ser Ala Arg Gly Phe Glu
100 105 110

Val Val Asp Glu Ile Lys Ala Ala Leu Glu Asn Glu Cys Pro Asn Thr
115 120 125

Val Ser Cys Ala Asp Ala Leu Thr Leu Ala Ala Arg Asp Ser Ser Val
130 135 140

Leu Thr Gly Gly Pro Ser Trp Met Val Pro Leu Gly Arg Arg Asp Ser
145 150 155 160

Thr Ser Ala Ser Leu Ser Gly Ser Asn Asn Asn Ile Pro Ala Pro Asn
165 170 175

Asn Thr Phe Asn Thr Ile Val Thr Arg Phe Asn Asn Gln Gly Leu Asp
180 185 190

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

Arg Cys Thr Ser Phe Arg Gln Arg Leu Tyr Asn Gln Ser Gly Asn Gly
210 215 220

Ser Pro Asp Arg Thr Leu Glu Gln Ser Tyr Ala Ala Asn Leu Arg Gln
225 230 235 240

Arg Cys Pro Arg Ser Gly Gly Asp Gln Asn Leu Ser Glu Leu Asp Ile
245 250 255

Asn Ser Ala Gly Arg Phe Asp Asn Ser Tyr Phe Lys Asn Leu Ile Glu
260 265 270

Asn Met Gly Leu Leu Asn Ser Asp Glu Val Leu Phe Ser Ser Asn Glu
275 280 285

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

Phe Glu Gln Phe Ala Glu Ser Met Ile Lys Met Gly Asn Ile Ser Pro
305 310 315 320

Leu Thr Gly Ser Ser Gly Glu Ile Arg Lys Asn Cys Arg Lys Ile Asn
325 330 335

Asn Ser

<210> 139
<211> 339
<212> PRT
<213> Arabidopsis lyrata

<400> 139

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

Leu Thr Leu Cys Ile Cys Asp Asp Asp Glu Ser Met Tyr Tyr Gly Gly
20 25 30

Asn Lys Gly Asn Leu Phe Pro Gly Phe Tyr Arg Ser Ser Cys Pro Arg
35 40 45

Ala Glu Glu Ile Val Arg Ser Val Val Ala Lys Ala Val Ala Arg Glu
50 55 60

Thr Arg Met Ala Ala Ser Leu Met Arg Leu His Phe His Asp Cys Phe
65 70 75 80

Val Gln Gly Cys Asp Gly Ser Leu Leu Leu Asp Thr Ser Gly Ser Ile
85 90 95

Val Thr Glu Lys Asn Ser Asn Pro Asn Ser Arg Ser Ala Arg Gly Phe
100 105 110

Glu Val Val Asp Glu Ile Lys Ala Ala Leu Glu Asn Glu Cys Pro Asn
115 120 125

Thr Val Ser Cys Ala Asp Ala Leu Thr Leu Ala Ala Arg Asp Ser Ser
130 135 140

Ile Leu Thr Gly Gly Pro Ser Trp Met Val Pro Leu Gly Arg Arg Asp
145 150 155 160

Ser Arg Ser Ala Ser Leu Ser Gly Ser Asn Asn Asn Ile Pro Ala Pro
165 170 175

Asn Asn Thr Phe Asn Thr Ile Val Ser Arg Phe Asn Asn Gln Gly Leu
180 185 190

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

Ser Arg Cys Thr Ser Phe Arg Gln Arg Leu Tyr Asn Gln Phe Gly Asn
210 215 220

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

Gln Arg Cys Pro Arg Ser Gly Gly Asp Gln Asn Leu Ser Glu Leu Asp
245 250 255

Ile Asn Ser Ala Gly Arg Phe Asp Asn Ser Tyr Phe Lys Asn Leu Ile
260 265 270

Glu Lys Met Gly Leu Leu Asn Ser Asp Glu Val Leu Phe Ser Ser Asn
275 280 285

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

Phe Phe Glu Gln Phe Ala Glu Ser Met Ile Lys Met Gly Asn Ile Ser
305 310 315 320

Pro Leu Thr Gly Ser Ser Gly Glu Ile Arg Lys Asn Cys Arg Lys Ile
325 330 335

Asn Asn Ser

<210> 140
<211> 771
<212> PRT
<213> Arabidopsis lyrata

<400> 140

Met Val Lys Glu Ile Ser Tyr Gly Phe Leu Ile Leu Ser Met Val Met
1 5 10 15

Phe Val Ser Pro Val Ile Ala Ile Asn Gly Gly Gly Tyr Pro Arg Cys
20 25 30

Asn Cys Glu Tyr Glu Gly Thr Ser Phe Trp Thr Thr Glu Asn Ile Leu
35 40 45

Glu Thr Gln Arg Val Ser Asp Phe Leu Ile Ala Val Ala Tyr Phe Ser
50 55 60

Ile Pro Ile Glu Leu Leu Tyr Phe Val Ser Cys Ser Asn Val Pro Phe
65 70 75 80

Lys Trp Val Leu Phe Glu Phe Ile Ala Phe Ile Val Leu Cys Gly Met
85 90 95

Thr His Leu Leu His Gly Trp Thr Tyr Ser Ala His Pro Phe Arg Leu
100 105 110

Met Met Ala Leu Thr Val Phe Lys Met Leu Thr Ala Leu Val Ser Cys
115 120 125

Ala Thr Ala Ile Thr Leu Ile Thr Leu Ile Pro Leu Leu Leu Lys Val
130 135 140

Lys Val Arg Glu Phe Met Leu Lys Lys Lys Ala His Glu Leu Gly Arg
145 150 155 160

Glu Val Gly Leu Ile Leu Ile Lys Lys Glu Thr Gly Phe His Val Arg
165 170 175

Met Leu Thr Gln Glu Ile Arg Lys Ser Leu Asp Arg His Thr Ile Leu
180 185 190

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

Ala Val Trp Met Pro Asn Asp Gly Glu Thr Glu Met Asn Leu Thr His
210 215 220

Glu Leu Arg Gly Arg Val Gly Tyr Gly Gly Cys Ser Val Ser Met Glu
225 230 235 240

Asp Leu Asp Val Val Arg Ile Arg Glu Ser Asp Glu Val Asn Val Leu
245 250 255

Ser Val Glu Ser Ser Ile Ala Arg Ala Ser Gly Gly Asp Val Ser Glu
260 265 270

Ile Gly Pro Val Ala Ala Ile Arg Met Pro Met Leu Arg Val Ser Asp
275 280 285

Phe Asn Gly Glu Pro Ser Tyr Ala Ile Leu Val Cys Val Leu Pro Ser
290 295 300

Gly Gln Pro Arg Asp Trp Thr Tyr Gln Glu Ile Glu Ile Val Lys Val
305 310 315 320

Val Ala Asp Gln Val Thr Val Ala Leu Asp His Ala Ala Val Leu Glu
325 330 335

Glu Ser Gln Leu Met Arg Glu Lys Leu Ala Glu Arg Asn Arg Ala Leu
340 345 350

Gln Met Ala Lys Arg Asp Ala Leu Arg Ala Ser Gln Ala Arg Asn Ala
355 360 365

Phe Gln Lys Thr Met Ser Glu Gly Met Arg Arg Pro Met His Ser Ile
370 375 380

Leu Gly Leu Leu Ser Met Ile Gln Asp Glu Lys Leu Ser Asp Glu Gln
385 390 395 400

Lys Met Ile Val Asp Thr Met Val Lys Thr Gly Asn Val Met Ser Asn
405 410 415

Leu Val Gly Asp Ser Met Asp Met Ser Asp Gly Arg Phe Val Thr Glu
420 425 430

Met Lys Pro Phe Ser Leu His Arg Thr Val His Glu Ala Ala Cys Ile
435 440 445

Ala Arg Cys Leu Cys Leu Cys Asn Gly Ile Arg Phe Leu Val Asp Ala
450 455 460

Glu Lys Ser Leu Pro Asp Asn Val Val Gly Asp Glu Arg Arg Val Phe
465 470 475 480

Gln Val Ile Leu His Met Val Gly Ser Leu Val Lys Pro Arg Lys Arg
485 490 495

Gln Glu Gly Ser Ser Leu Met Leu Lys Ile Leu Lys Glu Arg Gly Ser
500 505 510

Leu Asp Arg Ser Asp Gln Arg Trp Ala Ala Trp Arg Ser Pro Ala Ser
515 520 525

Ser Ala Asp Gly Asp Val Tyr Ile Arg Phe Glu Met Asn Val Glu Asn
530 535 540

Asp Asp Ser Ser Ser Gln Ser Phe Ala Ser Val Ser Ser Arg Asp Gln
545 550 555 560

Glu Val Gly Asp Val Arg Phe Ser Gly Gly Tyr Gly Leu Gly Gln Asp
565 570 575

Leu Ser Phe Gly Val Cys Lys Lys Val Val Gln Leu Ile His Gly Asn
580 585 590

Ile Ser Val Val Pro Gly Ser Asp Gly Ser Pro Glu Thr Met Ser Leu
595 600 605

Leu Leu Arg Phe Arg Arg Arg Pro Ser Ile Ser Val His Gly Ser Ser
610 615 620

Glu Ser Pro Ala Pro Asp His His Ala His Pro His Ser Asn Ser Leu
625 630 635 640

Leu Arg Gly Leu Gln Val Leu Leu Val Asp Thr Asn Asp Ser Asn Arg
645 650 655

Ala Val Thr Arg Lys Leu Leu Gln Lys Leu Gly Cys Asp Val Thr Thr
660 665 670

Val Ser Ser Gly Phe Asp Cys Leu Ser Ala Val Ala Pro Gly Ser Ser
675 680 685

Ser Ser Ser Thr Ser Phe Gln Val Val Val Leu Asp Leu Gln Met Val
690 695 700

Glu Met Asp Gly Tyr Glu Val Ala Met Arg Ile Arg Ser Arg Ser Trp
705 710 715 720

Pro Leu Ile Val Ala Thr Thr Val Ser Leu Asp Glu Glu Met Trp Asp
725 730 735

Lys Cys Ala Gln Ile Gly Ile Asn Gly Val Val Arg Lys Pro Val Val
740 745 750

Leu Arg Ala Met Glu Ser Glu Leu Arg Arg Val Leu Leu Gln Ala Asp
755 760 765

Gln Leu Leu
770

<210> 141
<211> 775
<212> PRT
<213> Brassica oleracea

<400> 141

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

Ile Trp Val Ser Pro Ala Ala Ala Gly Asn Gly Gly Gly Cys Asn Cys
20 25 30

Glu Asp Glu Gly Val Ser Phe Trp Ser Thr Glu Asn Ile Leu Glu Thr
35 40 45

Gln Arg Val Ser Asp Phe Leu Ile Ala Val Ala Tyr Phe Ser Ile Pro
50 55 60

Ile Glu Leu Leu Tyr Phe Val Ser Cys Ser Asn Val Pro Phe Lys Trp
65 70 75 80

Val Leu Phe Glu Phe Ile Ala Phe Ile Val Leu Cys Gly Met Thr His
85 90 95

Leu Leu His Gly Trp Thr Tyr Gly Pro His Pro Phe Lys Leu Met Val
100 105 110

Ala Leu Thr Val Phe Lys Met Leu Thr Ala Leu Val Ser Cys Ala Thr
115 120 125

Ala Ile Thr Leu Ile Thr Leu Ile Pro Leu Leu Leu Lys Val Lys Val

130 135 140

Arg Glu Phe Met Leu Lys Lys Lys Ala His Glu Leu Gly Arg Glu Val
145 150 155 160

Gly Leu Ile Met Ile Gln Lys Glu Thr Gly Val His Val Arg Met Leu
165 170 175

Thr Gln Glu Ile Arg Lys Ser Leu Asp Arg His Thr Ile Leu Tyr Thr
180 185 190

Thr Leu Val Glu Leu Ser Lys Thr Leu Ala Leu Gln Asn Cys Ala Val
195 200 205

Trp Met Glu Asn Glu Gly Lys Ser Glu Met Asn Leu Thr His Glu Leu
210 215 220

Arg Gly Ser Ser Gly Arg Ser Gly Tyr Gly Tyr Ser Val Ser Met His
225 230 235 240

Asp Val Asp Val Val Arg Val Arg Glu Ser Asn Asp Val Asn Ile Leu
245 250 255

Ser Val Asp Ser Leu Ile Ala Arg Ala Ser Gly Gly Asp Val Ser Glu
260 265 270

Ile Gly Pro Val Ala Ala Ile Arg Met Pro Met Leu Arg Val Ser Asp

275 280 285

Phe Lys Gly Gly Thr Pro Glu Leu Ile Gln Thr Cys Tyr Ala Ile Leu
290 295 300

Val Cys Val Leu Pro Ser Gly Gln Pro Arg Asp Trp Ser Tyr Gln Glu
305 310 315 320

Ile Glu Ile Val Lys Val Val Ala Asp Gln Val Ala Val Ala Leu Ser
325 330 335

His Ala Ala Val Leu Glu Glu Ser Gln Met Met Arg Asp Lys Leu Ala
340 345 350

Asp Gln Asn Arg Ala Leu Gln Ile Ala Lys Arg Asp Ala Met Arg Ala
355 360 365

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

Arg Pro Met His Ser Ile Leu Gly Leu Leu Ser Met Ile Gln Asp Glu
385 390 395 400

Lys Leu Ser Asn Glu Gln Lys Met Ile Val Asp Thr Met Val Lys Thr
405 410 415

Gly Asn Val Met Ser Asn Leu Val Gly Asp Ala Met Asp Val Ser Asp

420 425 430

Gly Arg Phe Val Thr Glu Met Lys Pro Phe Ser Leu His Arg Thr Val
435 440 445

Arg Glu Ala Ala Cys Leu Ala Arg Cys Leu Cys Leu Tyr Asn Gly Phe
450 455 460

Arg Phe Thr Val Asp Ala Glu Met Ser Leu Pro Asp Asn Val Val Gly
465 470 475 480

Asp Glu Arg Arg Val Phe Gln Val Ile Leu His Met Val Gly Ser Leu
485 490 495

Val Lys Pro Arg Lys Cys Arg Glu Gly Ser Leu Ser Ser Ser Val Ile
500 505 510

Phe Lys Val Phe Lys Glu Arg Gly Ser Leu Asp Arg Ser Asp Gln Arg
515 520 525

Trp Ala Ala Trp Arg Ser Pro Thr Cys Ser Ala Asp Gly Asp Val Tyr
530 535 540

Ile Arg Phe Glu Met Ser Val Glu Asn Asp Gly Ser Gly Ser Gln Ser
545 550 555 560

Phe Ala Ser Val Ser Ser Arg Asp Gln Glu Val Gly Glu Val Arg Leu

565 570 575

Ser Gly Tyr Gly Leu Gly Gln Asp Leu Ser Phe Asp Val Cys Lys Lys
580 585 590

Val Val Gln Leu Ile Gln Gly Asn Ile Ser Val Val Pro Gly Ser Asp
595 600 605

Gly Ser Pro Glu Thr Met Ser Leu Leu Leu Arg Phe Arg Arg Arg Pro
610 615 620

Ser Ile Ser Val His Gly Thr Gly Glu Ala Pro Ala Pro Asp His His
625 630 635 640

Leu His Pro His Ser Asp Ser Leu Leu Arg Gly Leu Gln Val Leu Leu
645 650 655

Val Asp Thr Asn Asp Ser Asn Arg Ala Val Thr Arg Lys Leu Leu Glu
660 665 670

Lys Leu Gly Cys Ile Val Thr Ala Val Ser Ser Gly Phe Asp Cys Leu
675 680 685

Thr Ala Ile Ala Pro Ser Ser Ser Ser Ser Ser Ser Thr Phe Gln Val
690 695 700

Val Val Leu Asp Leu Gln Met Ala Glu Met Asp Gly Tyr Glu Val Ala

705 710 715 720

Met Arg Ile Arg Ser Arg Ser Trp Pro Leu Met Val Ala Met Thr Val
725 730 735

Ser Leu Asp Glu Glu Met Trp Asp Lys Cys Met Gln Ile Gly Ile Asn
740 745 750

Gly Val Val Arg Lys Pro Val Met Leu Arg Ala Met Glu Ser Glu Leu
755 760 765

Arg Arg Val Leu Leu Gln Ala
770 775

<210> 142
<211> 253
<212> PRT
<213> Arabidopsis lyrata

<400> 142

Met Ala Ile Ser Gln Gln Phe Leu Asn Pro Thr Leu Phe Lys Ser Leu
1 5 10 15

Ala Ser Thr Asn Lys Asn Ser Pro Ser Pro Phe Phe Arg Leu Lys Ser
20 25 30

Thr Ser Thr Thr Phe Asn Phe Lys Pro Leu Thr Ser Ser Ser Ser Ala
35 40 45

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

Lys Ser Arg Glu Thr Phe His Gly Leu Cys Phe Val Leu Lys Asp Asn
65 70 75 80

Ile Asp Thr Asp Gln Ile Ile Pro Ala Glu Tyr Gly Thr Leu Ile Pro
85 90 95

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

Leu Pro Lys Phe Tyr Asn Glu Arg Phe Val Val Pro Gly Glu Ile Lys
115 120 125

Ser Lys Tyr Ser Val Ile Ile Gly Gly Asp Asn Phe Gly Cys Gly Ser
130 135 140

Ser Arg Glu His Ala Pro Val Cys Leu Gly Ala Ala Gly Ala Lys Ala
145 150 155 160

Val Val Ala Glu Ser Tyr Ala Arg Ile Phe Phe Arg Asn Cys Val Ala
165 170 175

Thr Gly Glu Ile Phe Pro Leu Glu Ser Glu Val Arg Ile Cys Asp Glu
180 185 190

Cys Lys Thr Gly Asp Val Val Thr Ile Glu His Lys Glu Asp Gly Ser
195 200 205

Ser Leu Leu Ile Asn His Thr Thr Arg Lys Glu Tyr Lys Leu Lys Pro
210 215 220

Leu Gly Asp Ala Gly Pro Val Ile Asp Ala Gly Gly Ile Phe Ala Tyr
225 230 235 240

Ala Arg Lys Ala Gly Met Ile Pro Ser Ala Ser Ser Ala
245 250

<210> 143
<211> 450
<212> PRT
<213> Arabidopsis lyrata

<400> 143

Met Cys Arg Lys Gly Asn Ser His Ile Tyr Leu Leu Ile Ile Gly Lys
1 5 10 15

Val Ala Leu Val Ser Ala Tyr Gly Ile His Gln Leu His Ile Phe Ile
20 25 30

Phe Val Leu Ala Val Phe His Val Leu Tyr Cys Ile Ile Thr Tyr Ala
35 40 45

Leu Gly Lys Thr Lys Met Lys Lys Trp Lys Ser Trp Glu Arg Glu Thr
50 55 60

Lys Thr Ile Glu Tyr Gln Tyr Ala Asn Asp Pro Glu Arg Phe Arg Phe
65 70 75 80

Ala Arg Asp Thr Ser Phe Gly Arg Arg His Leu Asn Ile Trp Ser Lys
85 90 95

Ser Thr Phe Thr Leu Trp Ile Thr Cys Phe Phe Arg Gln Phe Phe Gly
100 105 110

Ser Val Thr Lys Val Asp Tyr Leu Thr Leu Arg His Gly Phe Ile Met
115 120 125

Ala His Leu Pro Ala Gly Ser Ala Ala Arg Phe Asp Phe Gln Lys Tyr
130 135 140

Ile Glu Arg Ser Leu Glu Gln Asp Phe Thr Val Val Val Gly Ile Ser
145 150 155 160

Pro Leu Ile Trp Cys Ile Ala Val Leu Phe Ile Leu Thr Asn Thr His
165 170 175

Gly Trp Asp Ser Tyr Leu Trp Leu Pro Phe Ile Pro Leu Ile Val Ile
180 185 190

Leu Ile Val Gly Ala Lys Leu Gln Met Ile Ile Ser Lys Leu Gly Leu
195 200 205

Arg Ile Gln Glu Lys Gly Asp Val Val Lys Gly Ala Pro Val Val Glu
210 215 220

Pro Gly Asp Asp Leu Phe Trp Phe Gly Arg Pro Arg Phe Ile Leu Phe
225 230 235 240

Leu Ile His Leu Val Leu Phe Thr Asn Ala Phe Gln Leu Ala Phe Phe
245 250 255

Val Trp Ser Thr Tyr Glu Phe Thr Leu Lys Asn Cys Phe His His Lys
260 265 270

Thr Glu Asp Ile Ala Ile Arg Ile Thr Met Gly Val Leu Ile Gln Val
275 280 285

Leu Cys Ser Tyr Ile Thr Leu Pro Leu Tyr Ala Leu Val Thr Gln Met
290 295 300

Gly Thr Ser Met Arg Pro Thr Ile Phe Asn Asp Arg Val Ala Asn Ala
305 310 315 320

Leu Lys Lys Trp His His Thr Ala Lys Lys Gln Thr Lys His Gly His
325 330 335

Ser Gly Ser Asn Thr Pro His Ser Ser Arg Pro Thr Thr Pro Thr His
340 345 350

Gly Met Ser Pro Val His Leu Leu His Asn Tyr Asn Asn Arg Ser Leu
355 360 365

Asp Gln Gln Thr Ser Phe Thr Ala Ser Pro Ser Pro Pro Arg Phe Ser
370 375 380

Asp Tyr Ser Gly Gln Gly His Gly His Gln His Phe Phe Asp Pro Glu
385 390 395 400

Ser Gln Asn His Ser Tyr Gln Arg Glu Ile Thr Asp Ser Glu Phe Ser
405 410 415

Asn Ser His His Pro Gln Val Asp Met Ala Ser Pro Val Arg Glu Glu
420 425 430

Lys Glu Ile Ile Glu His Val Lys Val Asp Leu Ser Glu Phe Thr Phe
435 440 445

Lys Lys
450

<210> 144
<211> 427
<212> PRT

<213> Arabidopsis lyrata

<400> 144

Met Ala Ile Pro Arg Phe Ser Ser Leu Leu Arg Cys Arg Lys Trp Ala
1 5 10 15

Lys Ser Asp Trp Leu Val Ala Ser Ile Gly Phe Val Leu Ile Val Phe
20 25 30

Phe Leu Ser Phe Phe Ile Asp Pro Thr Ser Asp Ser Val Pro Ser Val
35 40 45

Asp Arg Ser Arg Pro Ile Ile Phe Pro Ser Asp Leu Val Lys Leu Lys
50 55 60

Leu Ser Ser Ile Ala Lys Glu Arg Gly Ala Phe Cys Leu Asp Gly Ser
65 70 75 80

Leu Pro Gly Tyr His Phe His Glu Gly Ser Gly Ser Gly Ser Gln Ser
85 90 95

Trp Leu Val His Leu Glu Gly Gly Gly Trp Cys Asn Thr Val Ala Ser
100 105 110

Cys Ser Ala Arg Ala Leu Thr Lys Leu Gly Ser Ser Asn Tyr Phe Glu
115 120 125

Gln Glu Val Ala Phe Gln Gly Val Leu Ser Ser Asp Pro Ser Gln Asn
130 135 140

Pro Glu Phe Phe Asn Trp Asn Lys Val Ala Ile Arg Tyr Cys Asp Gly
145 150 155 160

Ala Ser Phe Ala Gly His Pro Glu Ala Glu Phe Lys Asn Glu Thr Arg
165 170 175

Leu Phe Phe Arg Gly Gln Leu Ile Trp Glu Ala Ile Ile Asp Glu Leu
180 185 190

Leu Ser Met Gly Met Ser Asp Ala Lys Gln Ala Ile Leu Thr Gly Cys
195 200 205

Ser Ala Gly Gly Leu Ala Ser Leu Ile His Cys Asp Tyr Phe Arg Asp
210 215 220

His Leu Pro Lys Asp Ala Ala Val Lys Cys Val Ser Asp Gly Gly Tyr
225 230 235 240

Phe Leu Asn Val Pro Asp Val Leu Gly Asn Pro Thr Met Arg Ser Phe
245 250 255

Tyr His Asp Val Ala Asn Leu Gln Gly Val Asp Lys Ser Leu Asp Gln
260 265 270

Lys Cys Glu Ala Lys Thr Lys Pro Ser Lys Cys Met Phe Pro Gln Glu
275 280 285

Phe Leu Lys Asn Ile Arg Thr Pro Val Phe Leu Val Asn Pro Ala Tyr
290 295 300

Asp Phe Trp Gln Ile Gln Asn Val Leu Val Pro Thr Ser Ala Asp Pro
305 310 315 320

Asp Lys Ser Trp Ala Lys Cys Arg Leu Asn Ile Lys Glu Cys Asp Ala
325 330 335

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

Ile Gly Glu Phe His Gln Ser Lys Asp Gly Gly Met Phe Ile Asp Ser
355 360 365

Cys Tyr Ala His Cys Gln Thr Val Met Ser Val Thr Trp His Ser Pro
370 375 380

Thr Ser Pro Arg Ile Glu Asn Lys Thr Ile Ala Glu Ser Val Gly Asp
385 390 395 400

Trp Tyr Phe Asn Arg Lys Pro Val Lys Leu Ile Asp Cys Pro Tyr Pro
405 410 415

Cys Asn Pro Ser Cys Tyr Asn Met Asn Phe Thr
420 425

<210> 145
<211> 498
<212> PRT
<213> Arabidopsis lyrata

<400> 145

Met Val Gln Tyr Gln Arg Leu Ile Ile His His Gly Arg Lys Glu Glu
1 5 10 15

Lys Phe Arg Val Ser Ala Glu Glu Ser Gly Gly Gly Gly Cys Tyr Ser
20 25 30

Lys Arg Ala Lys Gln Lys Phe Arg Cys Leu Leu Phe Leu Ser Ile Leu
35 40 45

Ser Cys Cys Phe Val Met Ser Pro Tyr Tyr Leu Phe Gly Phe Ser Thr
50 55 60

Leu Ser Leu Leu Asp Ser Phe Arg Arg Glu Ile Glu Gly Leu Ser Ser
65 70 75 80

Tyr Glu Pro Phe Ile Thr Pro Leu Cys Ser Glu Ile Ser Asn Gly Thr
85 90 95

Ile Cys Cys Asp Arg Thr Gly Leu Arg Ser Asp Ile Cys Glu Met Lys

100 105 110

Gly Asp Ile Arg Thr Asn Ser Ala Ser Ser Ser Ile Phe Leu Phe Thr
115 120 125

Ser Ser Thr Lys Asn Asn Thr Lys Pro Glu Lys Ile Lys Pro Tyr Thr
130 135 140

Arg Lys Trp Glu Thr Ser Val Met Asp Thr Val Gln Glu Leu Asn Leu
145 150 155 160

Ile Thr Lys Asp Ser Asn Ser Ser Ser Asp Arg Val Cys Asp Val Tyr
165 170 175

His Asp Val Pro Ala Val Phe Phe Ser Thr Gly Gly Tyr Thr Gly Asn
180 185 190

Val Tyr His Glu Phe Asn Asp Gly Ile Ile Pro Leu Phe Ile Thr Ser
195 200 205

Gln His Tyr Asn Lys Lys Val Val Phe Val Ile Val Glu Tyr His Asp
210 215 220

Trp Trp Glu Met Lys Tyr Gly Asp Ile Val Ser Gln Leu Ser Asp Tyr
225 230 235 240

Pro Leu Val Asp Phe Ser Gly Asp Ala Arg Thr His Cys Phe Lys Glu

245 250 255

Ala Thr Val Gly Leu Arg Ile His Asp Glu Leu Thr Val Asn Ser Ser
260 265 270

Leu Val Ile Gly Asn Gln Thr Ile Val Asp Phe Arg Asn Val Leu Asp
275 280 285

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

Ala Asn Val Thr Ala Leu Asp Phe Lys Lys Lys Pro Lys Leu Val Ile
305 310 315 320

Leu Ser Arg Asn Gly Ser Ser Arg Ala Ile Leu Asn Glu Asn Leu Leu
325 330 335

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

Gln Lys Thr Thr Glu Met Ala Lys Ile Tyr Arg Ser Leu Asn Thr Ser
355 360 365

Asp Val Met Ile Gly Val His Gly Ala Ala Met Thr His Phe Leu Phe
370 375 380

Leu Lys Pro Lys Thr Val Phe Ile Gln Ile Ile Pro Leu Gly Thr Asp

385 390 395 400

Trp Ala Ala Glu Thr Tyr Tyr Gly Glu Pro Ala Lys Lys Leu Gly Leu
405 410 415

Lys Tyr Ile Gly Tyr Lys Ile Ala Pro Lys Glu Ser Ser Leu Tyr Glu
420 425 430

Glu Tyr Gly Lys Asp Asp Pro Ile Ile Arg Asp Pro Asp Ser Leu Asn
435 440 445

Asp Lys Gly Trp Glu Tyr Thr Lys Lys Ile Tyr Leu Gln Gly Gln Asn
450 455 460

Val Lys Leu Asp Leu Arg Arg Phe Arg Glu Thr Leu Thr Arg Ser Tyr
465 470 475 480

Asp Phe Ser Ile Arg Arg Arg Phe Arg Glu Asp Tyr Leu Leu His Arg
485 490 495

Glu Asp

<210> 146
<211> 309
<212> PRT
<213> Canola

<400> 146

Met Val Gln Tyr His Arg Leu Ile Ile His His Gly Arg Lys Glu Glu
1 5 10 15

Arg Phe Arg Val Ser Val Glu Glu Val Gly Ser Leu Lys Lys Ala Lys
20 25 30

Gln Lys Phe Leu Ser Phe Leu Phe Leu Thr Ile Leu Ser Cys Cys Phe
35 40 45

Ile Val Ser Pro Tyr Leu Phe Gly Phe Ser Thr Leu Ser Leu Leu Asp
50 55 60

Ser Phe Ser Arg Glu Asn Glu Ala Leu Ser Ser Tyr Glu Pro Ala Pro
65 70 75 80

Ala Pro Val Cys Leu Glu Val Ser Asn Gly Thr Ile Cys Cys Asp Arg
85 90 95

Thr Gly Leu Arg Ser Asp Ile Cys Val Met Lys Gly Asp Ile Arg Thr
100 105 110

Asp Ser Ala Ser Ser Ser Leu Phe Leu Leu Thr Ser Thr Asn Asn Thr
115 120 125

Thr Thr Pro Gln Lys Ile Lys Pro Tyr Thr Arg Lys Trp Glu Thr Ser
130 135 140

Val Met Asp Thr Val Gln Glu Leu Asn Leu Ile Thr Lys His Ser Asn
145 150 155 160

Lys Ser Ser Asp His Val Cys Asp Val Tyr His Asp Val Pro Ala Val
165 170 175

Phe Phe Ser Thr Gly Gly Tyr Thr Gly Asn Val Tyr His Glu Phe Asn
180 185 190

Asp Gly Ile Ile Pro Leu Phe Ile Thr Ser Gln His Tyr Asn Lys Lys
195 200 205

Val Val Phe Val Ile Val Glu Tyr His Asp Trp Trp Glu Met Lys Tyr
210 215 220

Gly Asp Ile Val Ser Gln Leu Ser Asp Tyr Pro Leu Val Asp Phe Asn
225 230 235 240

Gly Asp Ser Arg Thr His Cys Phe Lys Glu Ala Thr Val Gly Leu Arg
245 250 255

Ile His Asp Glu Leu Thr Val Asn Ser Thr Leu Met Ser His Gly Asn
260 265 270

Lys Thr Ile Val Asp Phe Arg Asn Val Trp Thr Val Leu Thr Arg Met
275 280 285

Val Ser Lys Ala Trp Phe Lys Arg Lys Gln Lys Gln Arg Leu Thr Ser
290 295 300

Arg Ser Arg Ser Trp
305

<210> 147
<211> 541
<212> PRT
<213> Glycine max

<400> 147

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

Gly Ile Ala Val Val Ala Glu Asp Pro Tyr Arg Phe Phe Thr Trp Asn
20 25 30

Val Thr Tyr Gly Asp Ile Tyr Pro Leu Gly Val Arg Gln Gln Gly Ile
35 40 45

Leu Ile Asn Gly Gln Phe Pro Gly Pro Asp Ile His Ser Val Thr Asn
50 55 60

Asp Asn Leu Ile Ile Asn Val Phe Asn Ser Leu Asp Gln Pro Phe Leu
65 70 75 80

Leu Ser Trp Asn Gly Val Gln Gln Arg Arg Asn Ser Phe Glu Asp Gly
85 90 95

Val Leu Gly Thr Thr Cys Pro Ile Pro Ala Gly Gly Asn Phe Thr Tyr
100 105 110

Ile Leu Gln Val Lys Asp Gln Ile Gly Ser Phe Tyr Tyr Phe Pro Ser
115 120 125

Leu Ala Phe His Lys Ala Ala Gly Gly Phe Gly Gly Ile Arg Ile Leu
130 135 140

Ser Arg Pro Arg Ile Pro Val Pro Phe Asp Asp Pro Ala Gly Asp Tyr
145 150 155 160

Thr Val Leu Ile Gly Asp Trp Tyr Lys Leu Asn His Thr Asp Leu Lys
165 170 175

Ser Gln Leu Asp Ser Gly Arg Lys Leu Pro Leu Pro Asp Gly Ile Leu
180 185 190

Ile Asn Gly Arg Gly Ser Asn Gly Ala Tyr Leu Asn Val Glu Gln Gly
195 200 205

Lys Thr Tyr Arg Leu Arg Ile Ser Asn Val Gly Leu Glu Asn Ser Leu
210 215 220

Asn Leu Arg Ile Gln Asn His Lys Leu Lys Leu Val Glu Val Glu Gly
225 230 235 240

Thr His Thr Leu Gln Thr Thr Tyr Ser Ser Leu Asp Val His Val Gly
245 250 255

Gln Ser Tyr Ser Val Leu Val Thr Ala Asp Gln Pro Ala Gln Asp Tyr
260 265 270

Tyr Ile Val Val Ser Ser Arg Phe Thr Ser Thr Val Leu Thr Thr Thr
275 280 285

Gly Ile Leu Arg Tyr Ser Asn Ser Ala Gly Pro Val Ser Gly Pro Pro
290 295 300

Pro Gly Gly Pro Thr Ile Gln Ile Asp Trp Ser Leu Asn Gln Ala Arg
305 310 315 320

Ser Ile Arg Thr Asn Leu Thr Ala Ser Gly Pro Arg Pro Asn Pro Gln
325 330 335

Gly Ser Tyr His Tyr Gly Leu Ile Asn Thr Thr Arg Thr Ile Ile Leu
340 345 350

Ser Gly Ser Pro Gly Ile Val Asn Gly Lys Gln Arg Tyr Ala Ile Asn
355 360 365

Ser Val Ser Tyr Val Ala Pro Asp Thr Pro Leu Lys Leu Ala Asp Tyr
370 375 380

Phe Lys Ile Pro Gly Val Phe Arg Val Gly Ser Ile Ser Asp Arg Pro
385 390 395 400

Thr Gly Gly Gly Ile Tyr Leu Asp Thr Ser Val Leu Gln Thr Asp Tyr
405 410 415

Arg Thr Phe Val Glu Phe Val Phe Gln Asn Asp Glu Asp Ile Ile Gln
420 425 430

Ser Tyr His Leu Asp Gly Tyr Ser Phe Phe Val Val Gly Met Asp Gly
435 440 445

Gly Gln Trp Thr Pro Ala Ser Arg Asn Thr Tyr Asn Leu Arg Asp Ala
450 455 460

Val Ser Arg Ser Thr Thr Gln Val Tyr Pro Lys Ser Trp Thr Ala Ile
465 470 475 480

Tyr Ile Ala Leu Asp Asn Val Gly Met Trp Asn Leu Arg Ser Glu Phe
485 490 495

Trp Ala Arg Gln Tyr Leu Gly Gln Gln Phe Tyr Met Arg Val Tyr Thr
500 505 510

Thr Ser Thr Ser Ile Arg Asp Glu Tyr Pro Val Pro Lys Asn Ala Leu
515 520 525

Leu Cys Gly Arg Ala Ser Gly Arg His Thr Arg Pro Leu
530 535 540

<210> 148
<211> 543
<212> PRT
<213> Glycine max

<400> 148

Met Thr Leu Lys Thr Ala Ala Val Ala Val Ala Ile Val Cys Ile Ser
1 5 10 15

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

Trp Asn Val Thr Tyr Gly Asp Ile Tyr Pro Leu Gly Val Arg Gln Gln
35 40 45

Gly Ile Leu Ile Asn Gly Gln Phe Pro Gly Pro Asp Ile His Ser Val
50 55 60

Thr Asn Asp Asn Leu Ile Ile Asn Val Phe Asn Ser Leu Asp Gln Pro
65 70 75 80

Phe Leu Leu Ser Trp Asn Gly Val Gln Gln Arg Arg Asn Ser Phe Glu
85 90 95

Asp Gly Val Leu Gly Thr Thr Cys Pro Ile Pro Pro Gly Gly Asn Phe
100 105 110

Thr Tyr Ile Leu Gln Val Lys Asp Gln Ile Gly Ser Phe Tyr Tyr Phe
115 120 125

Pro Ser Leu Ala Phe His Lys Ala Ala Gly Gly Phe Gly Gly Ile Arg
130 135 140

Ile Leu Ser Arg Pro Arg Ile Pro Val Pro Phe Asp Asp Pro Ala Gly
145 150 155 160

Asp Tyr Thr Val Leu Ile Gly Asp Trp Tyr Lys Leu Asn His Thr Asp
165 170 175

Leu Met Ser Leu Leu Asp Ser Gly Arg Lys Leu Pro Phe Pro Asn Gly
180 185 190

Ile Leu Ile Asn Gly Arg Gly Ser Asn Gly Ala Tyr Phe Asn Val Glu
195 200 205

Gln Gly Lys Thr Tyr Arg Leu Arg Ile Ser Asn Val Gly Leu Glu Asn
210 215 220

Ser Leu Asn Phe Arg Ile Gln Asn His Lys Leu Lys Leu Val Glu Val
225 230 235 240

Glu Gly Thr His Thr Leu Gln Thr Thr Tyr Ser Ser Leu Asp Val His
245 250 255

Val Gly Gln Ser Tyr Ser Val Leu Val Thr Ala Asp Gln Pro Ala Gln
260 265 270

Asp Tyr Tyr Ile Val Val Ser Thr Arg Phe Thr Ser Thr Val Leu Thr
275 280 285

Ser Thr Gly Val Leu Arg Tyr Ser Asn Ser Ala Gly Pro Val Ser Gly
290 295 300

Pro Pro Pro Gly Gly Pro Thr Ile Gln Ile Asp Trp Ser Leu Asn Gln
305 310 315 320

Ala Arg Ser Ile Arg Thr Asn Leu Thr Ala Ser Gly Pro Arg Pro Asn
325 330 335

Pro Gln Gly Ser Tyr His Tyr Gly Leu Ile Asn Thr Thr Arg Thr Ile
340 345 350

Ile Leu Ser Ser Ser Pro Gly Ile Val Asn Gly Lys Gln Arg Tyr Ala
355 360 365

Ile Asn Ser Val Ser Tyr Val Ala Pro Asp Thr Pro Leu Lys Leu Ala
370 375 380

Asp Tyr Phe Lys Ile Pro Gly Val Phe Arg Val Gly Ser Phe Ser Asp
385 390 395 400

Arg Pro Thr Gly Gly Gly Ile Tyr Leu Asp Thr Ser Val Leu Gln Thr
405 410 415

Asp Tyr Arg Thr Phe Val Glu Phe Val Phe Gln Asn Asp Glu Asp Ile
420 425 430

Ile Gln Ser Tyr His Leu Asp Gly Tyr Ser Phe Phe Val Val Gly Met
435 440 445

Asp Gly Gly Gln Trp Thr Pro Ala Ser Arg Asn Thr Tyr Asn Leu Arg
450 455 460

Asp Ala Val Ser Arg Cys Thr Thr Gln Val Tyr Pro Lys Ser Trp Thr
465 470 475 480

Ala Ile Tyr Ile Ala Leu Asp Asn Val Gly Met Trp Asn Leu Arg Ser
485 490 495

Glu Phe Trp Ala Arg Gln Tyr Leu Gly Gln Gln Phe Tyr Met Arg Val
500 505 510

Tyr Thr Thr Ser Thr Ser Ile Arg Asp Glu Tyr Pro Val Pro Lys Asn
515 520 525

Ala Leu Leu Cys Gly Arg Ala Ser Gly Arg His Thr Arg Pro Leu
530 535 540

<210> 149
<211> 541
<212> PRT
<213> Cacao

<400> 149

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

Phe Ala Ile Ala Gly Ala Asp Asp Pro Tyr Arg Phe Phe Asn Trp Asn
20 25 30

Val Thr Tyr Gly Asp Ile Tyr Pro Leu Gly Val Arg Gln Thr Gly Ile
35 40 45

Leu Ile Asn Gly Gln Phe Pro Gly Pro Asp Ile His Ser Val Thr Asn
50 55 60

Asp Asn Leu Ile Ile Asn Val Phe Asn Ser Leu Asp Glu Pro Phe Leu
65 70 75 80

Leu Ser Trp Asn Gly Ile Gln Gln Arg Arg Asn Ser Tyr Glu Asp Gly

85 90 95

Val Tyr Gly Thr Thr Cys Pro Ile Pro Pro Gly Lys Asn Phe Thr Tyr
100 105 110

Ile Leu Gln Val Lys Asp Gln Ile Gly Ser Phe Tyr Tyr Phe Pro Ser
115 120 125

Leu Ala Phe His Lys Ala Ala Gly Gly Phe Gly Gly Ile Arg Ile Leu
130 135 140

Ser Arg Pro Arg Ile Pro Val Pro Phe Pro Asp Pro Ala Gly Asp Tyr
145 150 155 160

Thr Val Leu Ile Gly Asp Trp Tyr Lys Ser Asn His Thr Asp Leu Arg
165 170 175

Ala His Leu Asp Leu Gly Lys Lys Leu Pro Phe Pro Asp Gly Ile Leu
180 185 190

Ile Asn Gly Arg Gly Pro Gly Gly Ala Ser Phe Asn Val Glu Gln Gly
195 200 205

Lys Thr Tyr Arg Leu Arg Ile Ser Asn Val Gly Leu Gln Asn Ser Leu
210 215 220

Asn Phe Arg Ile Gln Asn His Lys Leu Lys Leu Val Glu Val Glu Gly

225 230 235 240

Thr His Thr Leu Gln Thr Thr Tyr Ser Ser Ile Asp Ile His Val Gly
245 250 255

Gln Ser Ser Ser Val Leu Phe Thr Ala Asp Gln Pro Ala Gln Asp Tyr
260 265 270

Tyr Ile Val Val Ser Thr Arg Phe Thr Asn Pro Val Leu Thr Thr Thr
275 280 285

Ala Thr Leu Arg Tyr Ser Asn Ser Ala Gly Pro Val Ser Gly Pro Pro
290 295 300

Pro Gly Gly Pro Thr Ile Gln Ile Asp Trp Ser Leu Asn Gln Ala Arg
305 310 315 320

Ser Ile Arg Thr Asn Leu Thr Ala Ser Gly Pro Arg Pro Asn Pro Gln
325 330 335

Gly Ser Tyr His Tyr Gly Leu Ile Asn Thr Thr Arg Thr Ile Arg Leu
340 345 350

Ala Asn Ser Ala Gly Gln Val Asn Gly Lys Gln Arg Tyr Ala Val Asn
355 360 365

Ser Val Ser Phe Val Pro Ala Asp Thr Pro Leu Lys Leu Ala Asp Tyr

370 375 380

Phe Lys Ile Gly Gly Val Phe Arg Val Gly Ser Ile Ser Asp Asn Pro
385 390 395 400

Tyr Gly Gly Gly Ile Tyr Leu Asp Thr Ser Val Met Asn Ala Asp Tyr
405 410 415

Arg Ala Phe Ile Glu Ile Val Phe Gln Asn Asp Glu Asp Ile Val Gln
420 425 430

Ser Trp His Leu Asp Gly Tyr Ser Phe Phe Val Val Gly Met Asp Gly
435 440 445

Gly Gln Trp Thr Ala Ala Ser Arg Asn Gln Tyr Asn Leu Arg Asp Ala
450 455 460

Ile Ser Arg Cys Thr Thr Gln Val Tyr Pro Lys Ser Trp Thr Ala Ile
465 470 475 480

Tyr Val Ala Leu Asp Asn Val Gly Met Trp Asn Leu Arg Ser Glu Phe
485 490 495

Trp Ala Arg Gln Tyr Leu Gly Gln Gln Phe Tyr Leu Arg Val Tyr Thr
500 505 510

Asp Ser Ser Ser Leu Arg Asp Glu Tyr Pro Ile Pro Lys Asn Ala Leu

515 520 525

Leu Cys Gly Arg Ala Ser Gly Arg Ser Thr Arg Pro Leu
530 535 540

<210> 150
<211> 547
<212> PRT
<213> Glycine max

<400> 150

Met Pro Leu Lys Leu Ala Gly Gly Ala Thr Val Gly Ser Leu Leu Leu
1 5 10 15

Cys Val Ala Ile Ser Leu Phe His Ile Ala Gly Ala Glu Asp Pro Tyr
20 25 30

Arg Phe Phe Asn Trp Asn Val Thr Tyr Gly Asp Ile Tyr Pro Leu Gly
35 40 45

Val Arg Gln Thr Gly Ile Leu Ile Asn Gly Gln Phe Pro Gly Pro Asp
50 55 60

Ile His Ser Val Thr Asn Asp Asn Leu Ile Ile Asn Val Phe Asn Ser
65 70 75 80

Leu Asp Glu Pro Phe Leu Leu Ser Trp Asn Gly Ile Gln Gln Arg Arg
85 90 95

Asn Ser Phe Glu Asp Gly Val Phe Gly Thr Thr Cys Pro Ile Pro Pro
100 105 110

Gly Lys Asn Phe Thr Tyr Ile Leu Gln Val Lys Asp Gln Ile Gly Ser
115 120 125

Phe Tyr Tyr Phe Pro Ser Leu Ala Phe His Lys Ala Ala Gly Gly Phe
130 135 140

Gly Gly Ile Arg Ile Leu Ser Arg Pro Arg Ile Pro Val Pro Phe Pro
145 150 155 160

Asp Pro Ala Gly Asp Tyr Thr Val Leu Ile Gly Asp Trp Tyr Lys Ser
165 170 175

Asn His Thr Thr Leu Lys Ala Arg Leu Asp Arg Gly Lys Lys Leu Pro
180 185 190

Phe Pro Asp Gly Ile Leu Ile Asn Gly Arg Gly Pro Asn Gly Val Ser
195 200 205

Leu Asn Val Glu Gln Gly Lys Thr Tyr Arg Leu Arg Ile Ser Asn Val
210 215 220

Gly Leu Gln His Ser Leu Asn Phe Arg Ile Gln Asn His Lys Met Lys
225 230 235 240

Leu Val Glu Val Glu Gly Thr His Thr Leu Gln Thr Thr Tyr Ser Ser
245 250 255

Leu Asp Val His Val Gly Gln Ser Tyr Ser Val Leu Val Thr Ala Asp
260 265 270

Gln Pro Ala Gln Asp Tyr Tyr Ile Val Phe Ser Ser Arg Phe Ser Tyr
275 280 285

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

Pro Val Ser Gly Pro Pro Pro Gly Gly Pro Thr Ile Gln Ile Asp Trp
305 310 315 320

Ser Leu Asn Gln Ala Arg Ser Ile Arg Thr Asn Leu Thr Ala Ser Gly
325 330 335

Pro Arg Pro Asn Pro Gln Gly Ser Tyr His Tyr Gly Met Ile Asn Thr
340 345 350

Thr Lys Thr Ile Ile Leu Ala Ser Ser Ala Gly Gln Val Asn Gly Lys
355 360 365

Gln Arg Tyr Ala Ile Asn Ser Val Ser Tyr Val Ala Pro Asp Thr Pro
370 375 380

Leu Lys Leu Ala Asp Tyr Phe Lys Ile Ser Gly Val Phe Arg Pro Gly
385 390 395 400

Ser Ile Ser Asp Arg Pro Thr Gly Gly Gly Ile Tyr Leu Asp Thr Ser
405 410 415

Val Leu Gln Ala Asp Tyr Arg Thr Phe Val Glu Ile Val Phe Gln Asn
420 425 430

Asn Glu Lys Ile Val Gln Ser Tyr His Leu Asp Gly Tyr Ser Phe Phe
435 440 445

Val Val Gly Met Asp Gly Gly Gln Trp Thr Pro Ala Ser Arg Asn Gln
450 455 460

Tyr Asn Leu Arg Asp Ala Val Ala Arg Cys Thr Thr Gln Val Tyr Pro
465 470 475 480

Phe Ser Trp Thr Ala Ile Tyr Ile Ala Leu Asp Asn Val Gly Met Trp
485 490 495

Asn Leu Arg Ser Glu Phe Trp Ala Arg Gln Tyr Leu Gly Gln Gln Leu
500 505 510

Tyr Leu Arg Val Tyr Thr Ala Ser Thr Ser Ile Arg Asp Glu Phe Pro
515 520 525

Val Pro Lys Asn Ala Ile Leu Cys Gly Arg Ala Ser Gly Arg His Thr
530 535 540

Arg Pro Leu
545

<210> 151
<211> 541
<212> PRT
<213> Gossypium hirsutum

<400> 151

Met Gln Leu His Ser Ala Val Ala Leu Ile Cys Ala Thr Val Ser Leu
1 5 10 15

Phe Val Ile Ala Gly Ala Glu Asp Pro Tyr Arg Phe Phe Asn Trp Asn
20 25 30

Val Thr Tyr Gly Asp Ile Phe Pro Leu Gly Val His Gln Thr Gly Ile
35 40 45

Leu Ile Asn Gly Gln Phe Pro Gly Pro Asp Ile His Ser Val Thr Asn
50 55 60

Asp Asn Leu Ile Ile Asn Val Phe Asn Ser Leu Asn Glu Pro Phe Leu
65 70 75 80

Leu Ser Trp Asn Gly Val Gln Asn Arg Arg Asn Ser Tyr Glu Asp Gly
85 90 95

Val Tyr Gly Thr Thr Cys Pro Ile Pro Pro Gly Lys Asn Phe Thr Tyr
100 105 110

Ile Leu Gln Val Lys Asp Gln Ile Gly Ser Phe Tyr Tyr Phe Pro Ser
115 120 125

Leu Gly Phe His Lys Ala Ala Gly Gly Phe Gly Gly Ile Arg Ile Leu
130 135 140

Ser Arg Pro Arg Ile Pro Val Pro Phe Pro Asp Pro Ala Gly Asp Tyr
145 150 155 160

Thr Val Leu Ile Gly Asp Trp Tyr Lys Ala Asn His Thr Asp Leu Arg
165 170 175

Ala Gln Leu Asp Ser Gly Arg Lys Leu Pro Phe Pro Asp Gly Ile Leu
180 185 190

Ile Asn Gly Arg Gly Pro Gly Gly Ala Ser Phe Asn Val Glu Gln Gly
195 200 205

Lys Thr Tyr Arg Leu Arg Ile Ser Asn Val Gly Leu Gln Asn Ser Leu
210 215 220

Asn Phe Arg Ile Gln Asn His Lys Leu Lys Leu Val Glu Val Glu Gly
225 230 235 240

Thr His Thr Leu Gln Thr Thr Tyr Ser Ser Ile Asp Leu His Leu Gly
245 250 255

Gln Ser Met Ser Val Leu Phe Thr Ala Asp Gln Pro Ala Gln Asp Tyr
260 265 270

Tyr Ile Val Val Ser Ser Arg Phe Thr Asn Pro Val Leu Thr Ser Thr
275 280 285

Ala Thr Leu Arg Tyr Ser Asn Ser Ala Gly Pro Val Ser Gly Pro Pro
290 295 300

Pro Gly Gly Pro Thr Ile Gln Val Asp Trp Ser Leu Asn Gln Ala Arg
305 310 315 320

Ser Ile Arg Thr Asn Leu Thr Ala Ser Gly Pro Arg Pro Asn Pro Gln
325 330 335

Gly Ser Tyr His Tyr Gly Leu Ile Asn Thr Thr Arg Thr Ile Arg Leu
340 345 350

Ala Asn Ser Ala Gly Gln Val Asn Gly Lys Gln Arg Tyr Ala Val Asn
355 360 365

Ser Val Ser Phe Val Pro Ala Asp Thr Pro Leu Lys Leu Ala Asp Phe
370 375 380

Phe Lys Ile Asp Gly Val Tyr Arg Ile Gly Ser Ile Ser Asp Asn Pro
385 390 395 400

Thr Gly Gly Gly Ile Tyr Leu Asp Thr Ser Val Met Asn Ser Asp Tyr
405 410 415

Arg Ser Phe Ile Glu Ile Val Phe Gln Asn Asp Glu Asp Ile Val Gln
420 425 430

Ser Trp His Leu Asp Gly Tyr Ser Phe Phe Val Val Gly Met Asp Gly
435 440 445

Gly Gln Trp Thr Ala Ala Ser Arg Asn Gly Tyr Asn Leu Arg Asp Ala
450 455 460

Val Ser Arg Cys Thr Thr Gln Val Tyr Pro Lys Ser Trp Thr Ala Ile
465 470 475 480

Tyr Val Ala Leu Asp Asn Val Gly Met Trp Asn Leu Arg Ser Glu Tyr
485 490 495

Trp Ala Arg Gln Tyr Leu Gly Gln Gln Phe Tyr Leu Arg Val Phe Thr
500 505 510

Thr Ser Thr Ser Leu Arg Asp Glu Tyr Pro Ile Pro Lys Asn Ala Leu
515 520 525

Leu Cys Gly Arg Ala Ser Gly Arg Arg Thr Arg Pro Leu
530 535 540

<210> 152
<211> 548
<212> PRT
<213> Vigna unguiculata

<400> 152

Met His Leu Lys Leu Ala Glu Lys Ala Ser Val Ala Val Leu Leu Phe
1 5 10 15

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

Tyr Arg Phe Phe Asn Trp Asn Val Thr Tyr Gly Asp Ile Phe Pro Leu
35 40 45

Gly Val Arg Gln Arg Gly Ile Leu Ile Asn Gly Gln Phe Pro Gly Pro
50 55 60

Asp Ile His Ser Val Thr Asn Asp Asn Leu Ile Ile Asn Val Phe Asn
65 70 75 80

Ser Leu Asp Glu Pro Phe Leu Leu Ser Trp Asn Gly Ile Gln Gln Arg
85 90 95

Arg Asn Ser Phe Glu Asp Gly Val Phe Gly Thr Thr Cys Pro Ile Pro
100 105 110

Pro Gly Lys Asn Phe Thr Tyr Ile Leu Gln Val Lys Asp Gln Ile Gly
115 120 125

Ser Phe Tyr Tyr Phe Pro Ser Leu Ala Phe His Lys Ala Ala Gly Gly
130 135 140

Phe Gly Gly Ile Arg Ile Leu Ser Arg Pro Arg Ile Pro Val Pro Phe
145 150 155 160

Pro Asp Pro Ala Gly Asp Tyr Thr Val Leu Ile Gly Asp Trp Tyr Lys
165 170 175

Ser Asn His Thr Thr Leu Lys Ala His Val Asp Asn Gly Lys Lys Leu
180 185 190

Pro Phe Pro Asp Gly Ile Leu Ile Asn Gly Arg Gly Pro Asn Gly Val
195 200 205

Ala Phe Asn Val Glu Gln Gly Lys Thr Tyr Arg Leu Arg Ile Ser Asn
210 215 220

Val Gly Leu Gln His Ser Leu Asn Phe Arg Ile Gln Asn His Lys Met
225 230 235 240

Lys Leu Val Glu Val Glu Gly Thr His Thr Val Gln Thr Thr Tyr Ser
245 250 255

Ser Leu Asp Val His Val Gly Gln Ser Tyr Ser Val Leu Val Thr Ala
260 265 270

Asp Gln Pro Ala Gln Asp Tyr Tyr Ile Val Ala Ser Ser Arg Phe Ser
275 280 285

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

Gly Pro Val Ser Gly Pro Pro Pro Gly Gly Pro Thr Ile Gln Ile Asp
305 310 315 320

Trp Ser Leu Asn Gln Ala Arg Ser Ile Arg Thr Asn Leu Thr Ala Ser
325 330 335

Gly Pro Arg Pro Asn Pro Gln Gly Ser Tyr His Tyr Gly Leu Ile Asn
340 345 350

Thr Ser Arg Thr Ile Val Leu Ala Ser Ser Ala Gly Gln Val Asn Gly
355 360 365

Lys Gln Arg Tyr Ala Leu Asn Ser Val Ser Tyr Val Ala Pro Asp Thr
370 375 380

Pro Leu Lys Leu Ala Asp Tyr Phe Lys Ile Ser Gly Val Phe Arg Pro
385 390 395 400

Gly Ser Ile Ser Asp Arg Pro Thr Gly Gly Gly Ile Tyr Leu Asp Thr
405 410 415

Ser Val Leu Gln Thr Asp Tyr Arg Ser Phe Val Glu Phe Val Phe Gln
420 425 430

Asn Asn Glu Asn Ile Val Gln Ser Tyr His Leu Asp Gly Tyr Ser Phe
435 440 445

Phe Val Val Gly Met Asp Gly Gly Gln Trp Thr Pro Ala Ser Arg Asn
450 455 460

Gln Tyr Asn Leu His Asp Ala Val Ser Arg Cys Thr Thr Gln Val Tyr
465 470 475 480

Pro Met Ser Trp Thr Ala Ile Tyr Val Ala Leu Asp Asn Val Gly Met
485 490 495

Trp Asn Leu Arg Ser Glu Phe Trp Ala Arg Gln Tyr Leu Gly Gln Gln
500 505 510

Leu Tyr Leu Arg Val Phe Thr Thr Ser Thr Ser Ile Arg Asp Glu Phe
515 520 525

Pro Val Pro Lys Asn Ala Ile Leu Cys Gly Arg Ala Ser Gly Arg His
530 535 540

Thr Arg Pro Leu
545

<210> 153
<211> 546
<212> PRT
<213> Manihot esculenta

<400> 153

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

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

Phe Phe Asn Trp Asn Val Thr Tyr Gly Asp Ile Tyr Pro Leu Gly Val
35 40 45

Arg Gln Thr Gly Ile Leu Ile Asn Gly Gln Phe Pro Gly Pro Asp Ile
50 55 60

His Ser Val Thr Asn Asp Asn Leu Ile Ile Asn Val Phe Asn Ser Leu

65 70 75 80

Asp Glu Pro Phe Leu Leu Ser Trp Asn Gly Ile Gln Gln Arg Arg Asn
85 90 95

Ser Tyr Glu Asp Gly Val Ile Gly Thr Thr Cys Pro Ile Pro Pro Gly
100 105 110

Lys Asn Phe Thr Tyr Ile Leu Gln Val Lys Asp Gln Ile Gly Ser Phe
115 120 125

Tyr Tyr Phe Pro Ser Leu Ala Phe His Lys Ala Ala Gly Gly Phe Gly
130 135 140

Gly Ile Arg Ile Leu Ser Arg Pro Arg Ile Pro Val Pro Phe Pro Asp
145 150 155 160

Pro Asp Gly Asp Tyr Thr Val Leu Ile Gly Asp Trp Tyr Lys Ser Asn
165 170 175

His Thr Val Leu Arg Ala His Leu Asp Arg Gly Lys Lys Leu Pro Phe
180 185 190

Pro Asp Gly Ile Leu Ile Asn Gly Arg Gly Pro Asn Gly Tyr Ala Leu
195 200 205

Thr Val Glu Gln Gly Lys Thr Tyr Arg Leu Arg Ile Ser Asn Val Gly

210 215 220

Leu Gln His Ser Leu Asn Phe Arg Ile Gln Asn His Lys Met Lys Leu
225 230 235 240

Val Glu Val Glu Gly Thr His Thr Leu Gln Thr Thr Tyr Ser Ser Leu
245 250 255

Asp Val His Val Gly Gln Ser Tyr Ser Val Leu Val Thr Ala Asp Gln
260 265 270

Pro Gly Gln Asp Tyr Tyr Ile Val Val Ser Ser Arg Phe Thr Thr Pro
275 280 285

Ile Leu Thr Thr Thr Gly Val Leu His Tyr Ser Asn Ser Ala Gly Pro
290 295 300

Val Ser Gly Pro Pro Pro Gly Gly Pro Thr Ile Gln Ile Asp Trp Ser
305 310 315 320

Leu Asn Gln Ala Arg Ser Ile Arg Thr Asn Leu Thr Ala Ser Gly Pro
325 330 335

Arg Pro Asn Pro Gln Gly Ser Tyr His Tyr Gly Met Ile Asn Thr Thr
340 345 350

Arg Thr Ile Arg Phe Ala Ser Ser Ala Gly Gln Val Asn Gly Lys Gln

355 360 365

Arg Tyr Ala Val Asn Ser Val Ser Phe Val Ala Pro Asp Thr Pro Leu
370 375 380

Lys Leu Ala Asp Tyr Phe Lys Ile Gln Gly Val Phe Arg Glu Asn Ser
385 390 395 400

Ile Ser Asp Lys Pro Tyr Gly Gly Gly Ile Tyr Leu Asp Thr Ser Val
405 410 415

Leu Thr Val Asn Tyr Arg Glu Phe Val Glu Ile Val Phe Glu Asn Ser
420 425 430

Glu Asn Ile Val Gln Ser Trp His Leu Asp Gly Tyr Ser Phe Phe Val
435 440 445

Val Gly Met Asp Gly Gly Gln Trp Thr Ser Asp Ser Arg Asn Gln Tyr
450 455 460

Asn Leu Arg Asp Ala Val Ala Arg Cys Thr Thr Gln Val Tyr Pro Met
465 470 475 480

Ser Trp Thr Ala Ile Tyr Val Pro Leu Asp Asn Val Gly Met Trp Asn
485 490 495

Leu Arg Ser Glu Phe Trp Ala Arg Gln Tyr Leu Gly Gln Gln Leu Tyr

500 505 510

Leu Arg Val Tyr Thr Ala Ser Thr Ser Leu Arg Asp Glu Phe Pro Ile
515 520 525

Pro Lys Asn Ala Leu Leu Cys Gly Arg Ala Ser Ser Arg Ser Thr Arg
530 535 540

Pro Leu
545

<210> 154
<211> 542
<212> PRT
<213> Citrus, Citrus reticulata, Citrus sinensis

<400> 154

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

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

Trp Asn Val Thr Tyr Gly Asp Ile Tyr Pro Leu Gly Val Arg Gln Arg
35 40 45

Gly Ile Leu Ile Asn Trp Gln Phe Pro Gly Pro Asp Ile His Ser Val
50 55 60

Thr Asn Asp Asn Leu Ile Ile Asn Val Phe Asn Ser Leu Asp Glu Pro
65 70 75 80

Phe Leu Leu Ser Trp Asn Gly Ile Gln Asn Arg Arg Asn Ser Phe Glu
85 90 95

Asp Gly Val Tyr Gly Thr Thr Cys Pro Ile Pro Pro Gly Lys Asn Phe
100 105 110

Thr Tyr Ile Leu Gln Val Lys Asp Gln Ile Gly Ser Phe Tyr Tyr Phe
115 120 125

Pro Ser Leu Ala Phe His Lys Ala Ala Gly Gly Phe Gly Gly Ile Arg
130 135 140

Ile Leu Ser Arg Pro Arg Ile Pro Val Pro Phe Pro Asp Pro Ala Gly
145 150 155 160

Asp Tyr Thr Val Leu Ile Gly Asp Trp Tyr Lys Ser Asn His Thr Asp
165 170 175

Leu Arg Ala His Leu Asp Lys Gly Lys Lys Leu Pro Leu Pro Asp Gly
180 185 190

Ile Leu Ile Asn Gly Arg Gly Ser Gly Ala Ala Phe Asn Val Glu Gln
195 200 205

Gly Lys Thr Tyr Arg Leu Arg Ile Ser Asn Val Gly Leu Gln Asn Ser
210 215 220

Leu Asn Phe Arg Ile Gln Asn His Lys Met Lys Leu Val Glu Val Glu
225 230 235 240

Gly Thr His Thr Leu Gln Thr Thr Tyr Ser Ser Leu Asp Val His Val
245 250 255

Gly Gln Ser Tyr Ser Val Leu Val Thr Ala Asp Gln Pro Ala Arg Asp
260 265 270

Tyr Tyr Ile Val Val Ser Ser Arg Phe Thr Ser Thr Val Leu Thr Thr
275 280 285

Thr Gly Ile Leu His Tyr Ser Asn Ser Ala Gly Pro Val Ser Gly Pro
290 295 300

Ile Pro Gly Gly Pro Thr Val Gln Ile Asp Trp Ser Leu Asn Gln Ala
305 310 315 320

Arg Ser Ile Arg Ser Asn Leu Thr Ala Ser Gly Pro Arg Pro Asn Pro
325 330 335

Gln Gly Ser Tyr His Tyr Gly Leu Ile Asn Thr Thr Lys Thr Ile Arg
340 345 350

Leu Ser Ser Ser Ala Gly Gln Val Asn Gly Lys Gln Arg Tyr Ala Ile
355 360 365

Asn Ser Val Ser Phe Ile Pro Ala Asp Thr Pro Leu Lys Leu Ala Asp
370 375 380

Tyr Phe Lys Ile Gly Gly Val Phe Arg Ile Gly Ser Ile Ser Asp Asn
385 390 395 400

Pro Thr Gly Gly Gly Ile Tyr Gln Asp Thr Ala Val Met Gly Ala Asp
405 410 415

Tyr Arg Ala Phe Ile Glu Ile Val Phe Gln Asn Asp Glu Asp Ile Ile
420 425 430

Gln Ser Tyr His Leu Asn Gly Tyr Gln Phe Trp Val Val Gly Met Asp
435 440 445

Gly Gly Gln Trp Thr Ser Ala Ser Arg Asn Gln Tyr Asn Leu Arg Asp
450 455 460

Ala Val Ala Arg Val Thr Val Gln Val Tyr Pro Lys Ser Trp Ser Ala
465 470 475 480

Ile Tyr Ile Ala Leu Asp Asn Val Gly Met Trp Asn Leu Arg Ser Glu
485 490 495

Ser Trp Ala Arg Gln Tyr Leu Gly Gln Gln Phe Tyr Leu Arg Val Tyr
500 505 510

Thr Ala Ser Thr Ser Leu Arg Asp Glu Tyr Pro Ile Pro Lys Asn Ala
515 520 525

Arg Leu Cys Gly Lys Ala Ala Gly Arg His Thr Arg Pro Leu
530 535 540

<210> 155
<211> 546
<212> PRT
<213> Ricinus communis

<400> 155

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

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

Phe Phe Asn Trp Asn Val Thr Tyr Gly Asp Ile Tyr Pro Leu Gly Ile
35 40 45

Arg Gln Gln Gly Ile Leu Ile Asn Gly Gln Phe Pro Gly Pro Asp Ile
50 55 60

His Ser Val Thr Asn Asp Asn Leu Ile Ile Asn Val Phe Asn Ser Leu
65 70 75 80

Asp Glu Pro Phe Leu Leu Ser Trp Asn Gly Ile Gln Gln Arg Arg Asn
85 90 95

Ser Tyr Glu Asp Gly Val Tyr Gly Thr Thr Cys Pro Ile Pro Pro Gly
100 105 110

Lys Asn Phe Thr Tyr Ile Leu Gln Val Lys Asp Gln Ile Gly Ser Phe
115 120 125

Tyr Tyr Phe Pro Ser Leu Ala Phe His Lys Ala Ala Gly Gly Phe Gly
130 135 140

Gly Ile Arg Ile Leu Ser Arg Pro Arg Ile Pro Val Pro Phe Ala Asp
145 150 155 160

Pro Asp Gly Asp Tyr Thr Ile Leu Ile Gly Asp Trp Tyr Lys Ser Asn
165 170 175

His Thr Asp Leu Lys Ala His Leu Asp Asn Gly Lys Lys Leu Pro Phe
180 185 190

Pro Asp Gly Ile Leu Ile Asn Gly Arg Gly Pro Ser Gly Tyr Tyr Leu
195 200 205

Thr Val Glu Gln Gly Lys Thr Tyr Arg Leu Arg Ile Ser Asn Ile Gly
210 215 220

Leu Gln Asn Ser Leu Asn Phe Arg Ile Gln Asn His Lys Met Lys Leu
225 230 235 240

Val Glu Val Glu Gly Thr His Thr Leu Gln Thr Thr Tyr Ser Ser Leu
245 250 255

Asp Val His Val Gly Gln Ser Tyr Ser Val Leu Phe Thr Ala Asp Gln
260 265 270

Pro Gly Gln Asp Tyr Tyr Ile Val Val Ser Ser Arg Phe Thr Thr Gln
275 280 285

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

Val Ser Gly Pro Pro Pro Gly Gly Pro Thr Ile Gln Ile Asp Trp Ser
305 310 315 320

Leu Asn Gln Ala Arg Ser Ile Arg Thr Asn Leu Thr Ala Ser Gly Pro
325 330 335

Arg Pro Asn Pro Gln Gly Ser Tyr His Tyr Gly Met Ile Asn Thr Ser
340 345 350

Arg Thr Ile Ile Leu Ala Ser Ser Ala Gly Gln Val Asn Gly Lys Gln
355 360 365

Arg Tyr Ala Val Asn Ser Val Ser Phe Ile Pro Gln Asp Thr Pro Leu
370 375 380

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

Ile Ser Asp Arg Pro Tyr Gly Gly Gly Ile Tyr Leu Asp Thr Ser Val
405 410 415

Leu Thr Val Asp Tyr Arg Ala Phe Val Glu Ile Val Phe Gln Asn Asn
420 425 430

Glu Asp Ile Val Gln Ser Trp His Leu Asp Gly Tyr Ser Phe Phe Val
435 440 445

Val Gly Met Asp Gly Gly Gln Trp Thr Ser Ala Ser Arg Asp Gln Tyr
450 455 460

Asn Leu Arg Asp Ala Val Ala Arg Cys Thr Ala Gln Val Tyr Pro Met
465 470 475 480

Ser Trp Thr Ala Ile Tyr Val Pro Leu Asp Asn Val Gly Met Trp Asn
485 490 495

Leu Arg Thr Glu Phe Trp Ala Arg Gln Tyr Leu Gly Gln Gln Leu Tyr
500 505 510

Leu Arg Val Tyr Thr Thr Ser Thr Ser Leu Arg Asp Glu Tyr Pro Ile
515 520 525

Pro Lys Asn Ala Leu Thr Cys Gly Lys Ala Ser Gly Arg Arg Thr Arg
530 535 540

Pro Leu
545

<210> 156
<211> 541
<212> PRT
<213> Canola

<400> 156

Met Ala Ala Asn Ala Ser Phe Ala Ala Ala Leu Ile Val Gly Phe Ala
1 5 10 15

Leu Leu Phe Ala Val Thr Ala Glu Ser Pro Tyr Arg Phe Phe Glu Trp
20 25 30

Asn Val Thr Tyr Gly Asp Ile Tyr Pro Leu Gly Val Arg Gln Gln Gly
35 40 45

Ile Leu Ile Asn Gly Gln Phe Pro Gly Pro Asp Ile His Ser Val Thr
50 55 60

Asn Asp Asn Leu Ile Ile Asn Val Tyr Asn Ser Leu Asp Glu Pro Phe
65 70 75 80

Leu Leu Ser Trp Asn Gly Val Gln Gln Arg Arg Asn Ser Tyr Val Asp
85 90 95

Gly Val Tyr Gly Thr Thr Cys Pro Ile Pro Pro Gly Lys Asn Tyr Thr
100 105 110

Tyr Ile Leu Gln Val Lys Asp Gln Ile Gly Ser Phe Tyr Tyr Phe Pro
115 120 125

Ser Leu Ala Phe His Lys Ala Ala Gly Gly Phe Gly Gly Leu Arg Ile
130 135 140

Leu Ser Arg Pro Gly Ile Pro Val Pro Phe Ala Asp Pro Ala Gly Asp
145 150 155 160

Asn Thr Val Leu Ile Gly Asp Trp Tyr Lys Ser Asn His Thr Asp Leu
165 170 175

Lys Ala Gln Leu Asp Ser Gly Arg Lys Leu Pro Leu Pro Asp Gly Ile
180 185 190

Leu Ile Asn Gly Arg Gly Ser Gly Ala Thr Leu Asn Val Glu Gln Gly
195 200 205

Lys Thr Tyr Arg Leu Arg Ile Ser Asn Ile Gly Leu Gln His Ser Leu
210 215 220

Asn Phe Arg Ile Gln Asn His Lys Met Lys Val Val Glu Val Glu Gly
225 230 235 240

Thr His Thr Leu Gln Thr Thr Phe Ser Ser Leu Asp Val His Val Gly
245 250 255

Gln Ser Tyr Ser Val Leu Val Thr Ala Asp Gln Pro Ala Gln Asp Tyr
260 265 270

Tyr Val Val Val Ser Ser Arg Phe Thr Ser Asp Val Leu Thr Thr Thr
275 280 285

Gly Val Leu Arg Tyr Ser Gly Ser Ala Gly Gly Val Ser Gly Pro Ile
290 295 300

Pro Gly Gly Pro Thr Ile Gln Ile Asp Trp Ser Leu Asn Gln Ala Arg
305 310 315 320

Ala Ile Arg Thr Asn Leu Thr Ala Ser Gly Pro Arg Pro Asn Pro Gln
325 330 335

Gly Ser Tyr His Tyr Gly Met Ile Asn Thr Thr Arg Thr Ile Arg Leu
340 345 350

Ala Ser Ser Ala Gly Gln Val Asn Gly Lys Gln Arg Tyr Ala Val Asn
355 360 365

Ser Val Ser Phe Asn Pro Ala Asp Thr Pro Leu Lys Leu Ala Asp Tyr
370 375 380

Phe Lys Ile Asp Gly Val Tyr Arg Val Gly Ser Ile Gln Ser Gln Pro
385 390 395 400

Thr Gly Gly Gly Ile Tyr Leu Asp Thr Ser Val Met Gln Thr Asp Tyr
405 410 415

Arg Thr Phe Ile Glu Ile Val Phe Glu Asn Ser Glu Asp Ile Val Gln
420 425 430

Ser Trp His Leu Asp Gly Tyr Ser Phe Trp Val Val Gly Met Asp Gly
435 440 445

Gly Gln Trp Thr Pro Asp Ser Arg Asn Glu Tyr Asn Leu Arg Asp Ala
450 455 460

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

Tyr Ile Ala Leu Asp Asn Val Gly Met Trp Asn Leu Arg Ser Glu Phe
485 490 495

Trp Ala Arg Gln Tyr Leu Gly Gln Gln Phe Tyr Leu Arg Val Tyr Thr
500 505 510

Thr Ser Thr Ser Leu Arg Asp Glu Tyr Pro Ile Pro Lys Asn Ala Leu
515 520 525

Leu Cys Gly Arg Ala Ser Gly Arg Arg Thr Arg Pro Leu
530 535 540

<210> 157
<211> 544
<212> PRT
<213> Prunus

<400> 157

Met Ser Leu Asn Phe Ala Gly Ala Ala Val Ser Ala Leu Leu Phe Leu
1 5 10 15

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

Glu Trp Asn Val Thr Tyr Gly Asp Ile Tyr Pro Leu Gly Val Arg Gln
35 40 45

Lys Gly Ile Leu Ile Asn Gly Gln Phe Pro Gly Pro Asp Ile His Ser

50 55 60

Val Thr Asn Asp Asn Leu Ile Ile Asn Val Phe Asn Ser Leu Asp Glu
65 70 75 80

Pro Phe Leu Ile Ser Trp Asn Gly Ile Gln Gln Arg Arg Asn Ser Phe
85 90 95

Glu Asp Gly Val Tyr Gly Thr Thr Cys Pro Ile Pro Pro Gly Arg Asn
100 105 110

Phe Thr Tyr Ile Leu Gln Val Lys Asp Gln Ile Gly Ser Phe Tyr Tyr
115 120 125

Phe Pro Ser Leu Ala Phe His Lys Ala Ala Gly Gly Phe Gly Gly Ile
130 135 140

Arg Ile Leu Ser Arg Pro Arg Ile Pro Val Pro Phe Pro Asp Pro Ala
145 150 155 160

Gly Asp Tyr Thr Val Leu Ile Gly Asp Trp Tyr Lys Ser Asn His Thr
165 170 175

Ser Leu Lys Ala His Leu Asp Ala Gly Lys Lys Leu Pro Phe Pro Asp
180 185 190

Gly Ile Leu Ile Asn Gly Arg Gly Pro Gly Gly Phe Ser Phe Asn Phe

195 200 205

Glu Gln Gly Lys Thr Tyr Arg Leu Arg Ile Ser Asn Val Gly Leu Gln
210 215 220

His Ser Leu Asn Phe Arg Ile Gln Asn His Lys Leu Lys Leu Val Glu
225 230 235 240

Val Glu Gly Thr His Thr Leu Gln Thr Thr Tyr Ser Ser Leu Asp Val
245 250 255

His Val Gly Gln Ser Tyr Ser Val Leu Val Thr Ala Asp Gln Pro Gly
260 265 270

Gln Asp Tyr Tyr Ile Val Ala Ser Ser Arg Phe Thr Thr Pro Ile Leu
275 280 285

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

Gly Pro Pro Pro Gly Gly Pro Thr Ile Gln Val Asp Trp Ser Leu Asn
305 310 315 320

Gln Ala Arg Ser Ile Arg Thr Asn Leu Thr Ala Ser Gly Pro Arg Pro
325 330 335

Asn Pro Gln Gly Ser Tyr His Tyr Gly Leu Ile Asn Thr Thr Lys Thr

340 345 350

Tyr Val Leu Glu Asn Ser Ala Gly Gln Val Asn Gly Lys Gln Arg Tyr
355 360 365

Gly Val Asn Ser Val Ser Phe Val Pro Ala Asp Thr Pro Leu Lys Leu
370 375 380

Ala Asp Tyr Phe Lys Ile Gly Gly Val Phe Arg Val Gly Ser Ile Ser
385 390 395 400

Asp Arg Pro Thr Gly Gly Gly Leu Tyr Leu Asp Thr Ser Val Leu Gly
405 410 415

Ala Asp Tyr Arg Thr Phe Val Glu Phe Val Phe Gln Asn Asn Glu Asp
420 425 430

Ile Ile Gln Ser Trp His Leu Asp Gly Tyr Ser Phe Phe Val Val Gly
435 440 445

Leu Asp Gly Gly Gln Trp Thr Pro Ala Ser Arg Lys Glu Tyr Asn Leu
450 455 460

Arg Asp Ala Val Ser Arg Cys Thr Val Gln Val Tyr Pro Lys Ser Trp
465 470 475 480

Thr Ala Ile Tyr Val Ala Leu Asp Asn Val Gly Met Trp Asn Leu Arg

485 490 495

Thr Glu Phe Trp Ala Arg Gln Tyr Leu Gly Gln Gln Leu Tyr Leu Arg
500 505 510

Val Tyr Thr Pro Ser Thr Ser Ile Arg Asp Glu Tyr Pro Ile Pro Lys
515 520 525

Asn Ala Leu Leu Cys Gly Arg Ala Thr Gly Arg Arg Thr Arg Pro Leu
530 535 540

<210> 158
<211> 541
<212> PRT
<213> Gossypium hirsutum

<400> 158

Met Gln Leu His Leu Ala Val Val Leu Leu Cys Ala Thr Ala Gly Leu
1 5 10 15

Phe Ala Ile Ala Gly Ala Glu Asp Pro Tyr Arg Phe Phe Asp Trp Asn
20 25 30

Val Thr Phe Gly Asp Ile Tyr Pro Leu Gly Val Arg Gln Thr Gly Ile
35 40 45

Leu Ile Asn Gly Gln Phe Pro Gly Pro Asp Ile His Ser Val Thr Asn
50 55 60

Asp Asn Leu Ile Ile Asn Val His Asn Ser Leu Asn Glu Pro Phe Leu
65 70 75 80

Ile Ser Trp Ser Gly Ile Gln Gln Arg Arg Asn Ser Tyr Glu Asp Gly
85 90 95

Val Tyr Gly Thr Thr Cys Pro Ile Pro Pro Gly Lys Asn Phe Thr Tyr
100 105 110

Ile Leu Gln Val Lys Asp Gln Ile Gly Ser Phe Phe Tyr Phe Pro Ser
115 120 125

Leu Ala Phe His Lys Ala Ser Gly Gly Phe Gly Gly Ile Arg Ile Leu
130 135 140

Ser Arg Pro Arg Ile Pro Val Pro Phe Pro Asp Pro Ala Gly Asp Tyr
145 150 155 160

Thr Val Leu Val Gly Asp Trp Tyr Lys Ser Asn His Thr Asn Leu Lys
165 170 175

Ala Arg Leu Asp Arg Gly Lys Lys Leu Pro Phe Pro Asp Gly Ile Leu
180 185 190

Ile Asn Gly Arg Gly Pro Gly Gly Ala Ser Phe Asn Val Glu Gln Gly
195 200 205

Lys Thr Tyr Arg Leu Arg Ile Ser Asn Val Gly Leu Gln Asn Ser Leu
210 215 220

Asn Phe Arg Ile Gln Asn His Arg Leu Thr Leu Val Glu Val Glu Gly
225 230 235 240

Thr His Thr Leu Gln Thr Thr Tyr Ser Ser Ile Asp Leu His Leu Gly
245 250 255

Gln Ser Cys Ser Val Leu Phe Lys Ala Asp Gln Pro Ala Lys Asp Tyr
260 265 270

Tyr Ile Ala Val Ser Thr Arg Phe Thr Ser Arg Val Leu Thr Ser Thr
275 280 285

Ala Ile Leu Arg Tyr Ser Asn Ser Ala Gly Pro Val Ser Gly Pro Pro
290 295 300

Pro Gly Gly Pro Thr Ile Gln Ile Asp Trp Ser Leu Asn Gln Ala Arg
305 310 315 320

Ser Ile Arg Thr Asn Leu Thr Ala Ser Gly Pro Arg Pro Asn Pro Gln
325 330 335

Gly Ser Tyr His Tyr Gly Leu Ile Asn Thr Thr Arg Thr Ile Arg Leu
340 345 350

Ala Asn Ser Ala Gly Gln Val Asn Gly Lys Gln Arg Tyr Ala Val Asn
355 360 365

Ser Val Ser Phe Val Pro Ala Asp Thr Pro Leu Lys Leu Ala Asp Tyr
370 375 380

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

Tyr Gly Gly Lys Ile Tyr Leu Asp Thr Ser Val Met Gln Ala Asp Tyr
405 410 415

Arg Ala Phe Ile Glu Ile Val Phe Gln Asn Asn Glu Asn Ile Val Gln
420 425 430

Ser Trp His Leu Asp Gly Tyr Ser Phe Phe Val Val Gly Met Asp Gly
435 440 445

Gly Gln Trp Thr Thr Ala Ser Arg Arg Gly Tyr Asn Leu Arg Asp Ala
450 455 460

Val Ser Arg Cys Thr Thr Gln Val Tyr Pro Lys Ser Trp Thr Ala Ile
465 470 475 480

Tyr Val Ala Leu Asp Asn Val Gly Met Trp Asn Leu Arg Ser Glu Phe
485 490 495

Trp Ala Arg Gln Tyr Leu Gly Gln Gln Phe Tyr Leu Arg Val Tyr Thr
500 505 510

Thr Ser Thr Ser Leu Arg Asp Glu Tyr Pro Ile Pro Lys Asn Ala Leu
515 520 525

Leu Cys Gly Arg Ala Ser Gly Arg His Thr Arg Pro Leu
530 535 540

<210> 159
<211> 544
<212> PRT
<213> Medicago

<400> 159

Met Thr Leu Asn Leu Ala Ala Val Gly Ala Leu Leu Leu Cys Val Ser
1 5 10 15

Thr Ser Leu Phe His Ile Thr Ser Ala Glu Asp Pro Tyr Lys Phe Phe
20 25 30

Asn Trp Asn Val Thr Tyr Gly Asp Ile Tyr Pro Leu Gly Val Arg Gln
35 40 45

Arg Gly Ile Leu Ile Asn Gly Gln Phe Pro Gly Pro Asp Ile His Ser
50 55 60

Val Thr Asn Asp Asn Leu Ile Ile Asn Val Phe Asn Ser Leu Asn Glu
65 70 75 80

Pro Phe Leu Ile Ser Trp Asn Gly Ile Gln Gln Arg Arg Asn Ser Phe
85 90 95

Glu Asp Gly Val Ser Gly Thr Thr Cys Pro Ile Pro Pro Gly Arg Asn
100 105 110

Phe Thr Tyr Ile Leu Gln Val Lys Asp Gln Ile Gly Ser Phe Tyr Tyr
115 120 125

Phe Pro Ser Leu Ala Phe Gln Lys Ala Ala Gly Gly Phe Gly Gly Ile
130 135 140

Arg Ile Leu Ser Arg Pro Arg Ile Pro Val Pro Phe Pro Glu Pro Ala
145 150 155 160

Gly Asp Tyr Thr Val Leu Ile Gly Asp Trp Tyr Lys Ser Asn His Thr
165 170 175

Thr Leu Lys Ala His Leu Asp Lys Gly Lys Lys Leu Pro Ile Pro Asp
180 185 190

Gly Val Leu Ile Asn Gly Arg Gly Pro Asn Gly Leu Ser Phe Asn Val
195 200 205

Glu Gln Gly Lys Thr Tyr Arg Leu Arg Ile Ser Asn Val Gly Leu Gln
210 215 220

His Ser Leu Asn Phe Arg Ile Gln Asn His Lys Leu Lys Leu Val Glu
225 230 235 240

Val Glu Gly Thr His Thr Leu Gln Thr Thr Tyr Ser Ser Leu Asp Val
245 250 255

His Val Gly Gln Ser Tyr Ser Val Leu Val Thr Ala Asp Gln Pro Ser
260 265 270

Gln Asp Tyr Tyr Val Val Ala Ser Thr Arg Phe Ser Ser Lys Ile Leu
275 280 285

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

Gly Pro Pro Pro Gly Gly Pro Thr Ile Gln Val Asp Trp Ser Leu Asn
305 310 315 320

Gln Ala Arg Ser Ile Arg Thr Asn Leu Thr Ala Ser Gly Pro Arg Pro
325 330 335

Asn Pro Gln Gly Ser Tyr His Tyr Gly Leu Ile Asn Thr Thr Lys Thr
340 345 350

Ile Ile Leu Ala Ser Ser Pro Gly Gln Val Asn Gly Lys Gln Arg Tyr
355 360 365

Gly Ile Asn Ser Val Ser Tyr Val Val Pro Asp Thr Pro Leu Lys Leu
370 375 380

Ala Asp Tyr Phe Lys Ile Ser Gly Val Phe Arg Val Gly Ser Ile Ser
385 390 395 400

Glu Arg Pro Thr Gly Gly Gly Leu Tyr Leu Asp Thr Ser Val Met Gln
405 410 415

Ala Asp Tyr Arg Ser Phe Val Glu Ile Val Phe Gln Asn Asn Glu Asn
420 425 430

Ile Val Gln Ser Tyr His Leu Asp Gly Tyr Ser Phe Phe Val Val Gly
435 440 445

Met Asp Gly Gly Gln Trp Thr Thr Ser Ser Arg Asn Gly Tyr Asn Leu
450 455 460

Arg Asp Ala Val Ala Arg Cys Thr Thr Gln Val Tyr Pro Tyr Ser Trp
465 470 475 480

Thr Ala Ile Tyr Val Ala Leu Asp Asn Val Gly Met Trp Asn Leu Arg
485 490 495

Thr Glu Phe Trp Ala Arg Gln Tyr Leu Gly Gln Gln Phe Tyr Leu Arg
500 505 510

Val Tyr Thr Ala Ser Thr Ser Ile Arg Asp Glu Phe Pro Ile Pro Lys
515 520 525

Asn Ala Arg Leu Cys Gly Arg Ala Ser Gly Arg His Thr Arg Pro Leu
530 535 540

<210> 160
<211> 544
<212> PRT
<213> Malus

<400> 160

Met Pro Leu Asn Gly Ala Glu Gly Ala Ile Trp Ala Leu Leu Cys Leu
1 5 10 15

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

Glu Trp Asn Val Thr Tyr Gly Asp Ile Tyr Pro Leu Gly Val Arg Gln
35 40 45

Lys Gly Ile Leu Ile Asn Gly Gln Phe Pro Gly Pro Asp Ile His Ser
50 55 60

Val Thr Asn Asp Asn Leu Ile Ile Asn Val Phe Asn Ser Leu Asp Glu
65 70 75 80

Pro Phe Leu Leu Ser Trp Asn Gly Ile Gln Gln Arg Arg Asn Ser Phe
85 90 95

Glu Asp Gly Val Tyr Gly Thr Thr Cys Pro Ile Pro Pro Gly Lys Asn
100 105 110

Phe Thr Tyr Ile Leu Gln Val Lys Asp Gln Ile Gly Ser Phe Tyr Tyr
115 120 125

Phe Pro Ser Leu Ala Phe His Lys Ala Ala Gly Gly Phe Gly Gly Ile
130 135 140

Arg Ile Leu Ser Arg Pro Arg Ile Pro Val Pro Phe Pro Asp Pro Ala
145 150 155 160

Gly Asp Tyr Thr Val Leu Ile Gly Asp Trp Tyr Lys Ala Asn His Thr
165 170 175

Thr Leu Lys Ala His Leu Asp Arg Gly Lys Lys Leu Pro Phe Pro Asp
180 185 190

Gly Ile Leu Ile Asn Gly Arg Gly Pro Gly Gly Phe Ser Leu Asn Phe
195 200 205

Glu Gln Gly Lys Thr Tyr Arg Leu Arg Ile Ser Asn Ile Gly Leu Gln
210 215 220

Asn Ser Leu Asn Phe Arg Ile Gln Asn His Lys Met Lys Leu Val Glu
225 230 235 240

Val Glu Gly Thr His Thr Leu Gln Thr Thr Tyr Ser Ser Leu Asp Val
245 250 255

His Val Gly Gln Ser Tyr Ser Val Leu Val Thr Ala Asp Gln Pro Gly
260 265 270

Gln Asp Tyr Tyr Leu Val Ala Ser Ser Arg Phe Thr Ser Pro Ile Leu
275 280 285

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

Gly Pro Pro Pro Gly Gly Pro Thr Ile Gln Val Asp Trp Ser Leu Asn
305 310 315 320

Gln Ala Arg Ser Ile Arg Thr Asn Leu Thr Ala Ser Gly Pro Arg Pro
325 330 335

Asn Pro Gln Gly Ser Tyr His Tyr Gly Leu Ile Asn Leu Thr Lys Thr
340 345 350

Tyr Val Leu Gln Asn Ser Ala Gly Gln Val Asn Gly Lys Gln Arg Tyr
355 360 365

Gly Val Asn Ser Val Ser Phe Val Pro Ala Asp Thr Pro Leu Lys Leu
370 375 380

Ala Asp Tyr Phe Lys Ile Gly Gly Val Phe Arg Val Gly Ser Ile Ser
385 390 395 400

Asp Arg Pro Thr Gly Gly Gly Leu Tyr Leu Asp Thr Ser Val Leu Gly
405 410 415

Ala Asp Tyr Arg Ala Phe Val Glu Ile Val Phe Gln Asn Asn Glu Asp
420 425 430

Ile Ile Gln Ser Trp His Leu Asp Gly Tyr Ser Phe Phe Val Val Gly
435 440 445

Met Asp Gly Gly Gln Trp Thr Thr Ala Ser Arg Asn Ala Tyr Asn Leu
450 455 460

Arg Asp Ala Val Ser Arg Cys Thr Thr Gln Val Tyr Pro Lys Ser Trp
465 470 475 480

Thr Ala Ile Tyr Ile Pro Leu Asp Asn Val Gly Met Trp Asn Leu Arg
485 490 495

Thr Glu Phe Trp Ala Arg Gln Tyr Leu Gly Gln Gln Leu Tyr Leu Arg
500 505 510

Val Tyr Thr Pro Ser Thr Ser Ile Arg Asp Glu Tyr Pro Ile Pro Arg
515 520 525

Asn Ala Arg Leu Cys Gly Arg Ala Ser Gly Arg Arg Thr Arg Pro Leu
530 535 540

<210> 161
<211> 548
<212> PRT
<213> Populus

<400> 161

Met Pro Leu Asn Leu Ala Cys Lys Pro Ala Val Leu Cys Thr Phe Leu
1 5 10 15

Cys Leu Thr Val Ser Ile Leu Ser Val Val Lys Ala Glu Asp Pro Tyr
20 25 30

Arg Phe Phe Asp Trp Asn Val Thr Tyr Gly Phe Ile Tyr Pro Leu Gly
35 40 45

Val Arg Gln Gln Gly Ile Leu Ile Asn Gly Gln Phe Pro Gly Pro Asp
50 55 60

Ile His Ser Val Thr Asn Asp Asn Leu Ile Ile Asn Val Tyr Asn Ser

65 70 75 80

Leu Asp Glu Pro Phe Leu Leu Ser Trp Asn Gly Ile Gln Gln Arg Arg
85 90 95

Asn Ser Tyr Glu Asp Gly Val Phe Gly Thr Thr Cys Pro Ile Pro Pro
100 105 110

Gly Lys Asn Phe Thr Tyr Ile Leu Gln Val Lys Asp Gln Ile Gly Ser
115 120 125

Phe Tyr Tyr Phe Pro Ser Leu Gly Phe His Lys Ala Ala Gly Gly Phe
130 135 140

Gly Gly Ile Arg Ile Leu Ser Arg Pro Arg Ile Pro Val Pro Phe Asp
145 150 155 160

Asp Pro Ala Gly Asp Tyr Thr Ile Leu Ile Gly Asp Trp Tyr Met Ser
165 170 175

Asn His Thr Lys Leu Lys Ala Ile Leu Asp Ser Gly Arg Lys Leu Pro
180 185 190

Phe Pro Asn Gly Ile Leu Ile Asn Gly Arg Gly Arg Asn Gly Tyr Ser
195 200 205

Leu Thr Val Glu Gln Gly Lys Thr Tyr Arg Leu Arg Ile Ser Asn Val

210 215 220

Gly Leu Gln Asn Ser Leu Asn Phe Arg Ile Gln Asn His Lys Met Lys
225 230 235 240

Leu Val Glu Val Glu Gly Thr His Thr Leu Gln Thr Thr Tyr Ser Ser
245 250 255

Leu Asp Val His Val Gly Gln Ser Tyr Ser Val Leu Phe Thr Ala Asp
260 265 270

Gln Pro Gly Gln Asp Tyr Tyr Ile Val Val Thr Ser Arg Phe Thr Ala
275 280 285

Pro Val Val Leu Asn Thr Thr Gly Ile Leu His Tyr Ser Asn Ser Ala
290 295 300

Gly Pro Val Ser Gly Pro Phe Pro Gly Gly Pro Thr Thr Gln Ile Asp
305 310 315 320

Trp Ser Leu Asn Gln Ala Arg Ser Ile Arg Thr Asn Leu Thr Ala Ser
325 330 335

Gly Pro Arg Pro Asn Pro Gln Gly Ser Tyr His Tyr Gly Met Ile Asn
340 345 350

Thr Thr Arg Thr Ile Ile Val Ala Asn Ser Ala Gly Gln Val Asn Gly

355 360 365

Lys Gln Arg Tyr Gly Val Asn Ser Val Ser Phe Ile Ala Pro Asp Thr
370 375 380

Pro Met Lys Leu Ala Asp Tyr Phe Lys Ile Gln Gly Val Phe Lys Glu
385 390 395 400

Asn Ser Ile Ser Asp Arg Pro Tyr Gly Gly Gly Leu Tyr Leu Asp Thr
405 410 415

Ser Val Leu Thr Leu Pro Tyr Arg Ala Phe Val Glu Ile Val Phe Gln
420 425 430

Asn Asn Glu Asp Ile Val Gln Ser Trp His Leu Asp Gly Tyr Ser Phe
435 440 445

Phe Val Val Gly Met Asp Gly Gly Gln Trp Thr Thr Ala Ser Arg Asn
450 455 460

Gln Tyr Asn Leu Arg Asp Gly Val Ser Arg Cys Thr Ile Gln Val Tyr
465 470 475 480

Pro Lys Ala Trp Thr Ala Ile Tyr Ile Pro Leu Asp Asn Val Gly Met
485 490 495

Trp Asn Leu Arg Thr Glu Phe Trp Ala Arg Gln Tyr Leu Gly Gln Gln

500 505 510

Phe Tyr Leu Arg Val Tyr Thr Asp Ser Thr Ser Leu Arg Asp Glu Tyr
515 520 525

Pro Ile Pro Lys Asn Ala Leu Leu Cys Gly Arg Ala Ser Gly Arg His
530 535 540

Thr Arg Pro Leu
545

<210> 162
<211> 540
<212> PRT
<213> Vitis

<400> 162

Ala Leu Asn Ser Phe Arg Ala Phe Leu Ser Ile Phe Ser Leu Leu Phe
1 5 10 15

Thr Ile Val Ala Ala Glu Asp Pro Tyr Arg Phe Phe Thr Trp Asn Val
20 25 30

Thr Phe Gly Asp Ile Tyr Pro Leu Gly Val Arg Gln Gln Gly Ile Leu
35 40 45

Ile Asn Gly Gln Phe Pro Gly Pro Asp Ile Tyr Ser Val Thr Asn Asp
50 55 60

Asn Leu Ile Ile Asn Val Tyr Asn Ser Leu Thr Glu Pro Phe Leu Leu
65 70 75 80

Ser Trp Ser Gly Val Gln Gln Arg Arg Asn Ser Tyr Glu Asp Gly Val
85 90 95

Tyr Gly Thr Thr Cys Pro Ile Pro Pro Gly Arg Asn Phe Thr Tyr Ile
100 105 110

Leu Gln Val Lys Asp Gln Ile Gly Ser Phe Phe Tyr Phe Pro Ser Leu
115 120 125

Asp Phe His Lys Ala Ala Gly Gly Phe Gly Gly Ile Arg Ile Leu Ser
130 135 140

Arg Pro Arg Ile Pro Val Pro Phe Pro Asp Pro Ala Gly Asp Ile Thr
145 150 155 160

Val Leu Ile Gly Asp Trp Tyr Lys Ala Asn His Thr Thr Leu Lys Ala
165 170 175

Ile Leu Asp Arg Gly Lys Lys Leu His Phe Pro Asp Gly Ile Leu Ile
180 185 190

Asn Gly Arg Gly Pro Asn Gly Val Ser Phe Thr Val Glu Gln Gly Lys
195 200 205

Thr Tyr Arg Phe Arg Ile Ser Asn Val Gly Leu Gln Asn Ser Leu Asn
210 215 220

Phe Arg Ile Gln Asp His Lys Met Val Leu Val Glu Val Glu Gly Thr
225 230 235 240

His Thr Leu Gln Thr Thr Tyr Ser Ser Leu Asp Val His Val Gly Gln
245 250 255

Ser Tyr Ser Val Leu Val Thr Ala Asp Gln Pro Ala Gln Asp Phe Tyr
260 265 270

Ile Val Val Ser Thr Arg Phe Thr Ser Gln Val Leu Thr Thr Thr Gly
275 280 285

Ile Leu Arg Tyr Ser Asn Ser Ala Gly Pro Val Ser Gly Pro Pro Pro
290 295 300

Gly Gly Pro Thr Ile Gln Ile Asp Trp Ser Leu Asn Gln Ala Arg Ser
305 310 315 320

Ile Arg Thr Asn Leu Thr Ala Ser Gly Pro Arg Pro Asn Pro Gln Gly
325 330 335

Ser Tyr His Tyr Gly Met Ile Thr Thr Ser Arg Thr Ile Arg Leu Ala
340 345 350

Ser Ser Ala Gly Gln Val Asn Gly Lys Gln Arg Tyr Ala Val Asn Ser
355 360 365

Val Ser Tyr Val Pro Gly Asp Thr Pro Leu Lys Val Ala Asp Phe Phe
370 375 380

Lys Ile Gly Gly Val Phe Arg Val Gly Ser Ile Ser Asp Asn Pro Thr
385 390 395 400

Gly Gly Gly Val Tyr Leu Asp Thr Ser Val Met Gly Ala Asp Phe Arg
405 410 415

Ala Phe Val Glu Ile Val Phe Glu Asn Pro Glu Asp Ile Ile Gln Ser
420 425 430

Trp His Ile Asp Gly Tyr Ser Phe Phe Val Val Gly Met Asp Gly Gly
435 440 445

Leu Trp Thr Ala Asn Ser Arg Asn Gln Tyr Asn Leu Arg Asp Ala Val
450 455 460

Ala Arg Ser Thr Thr Gln Val Tyr Pro Lys Ser Trp Thr Ala Ile Tyr
465 470 475 480

Val Ala Leu Asp Asn Val Gly Met Trp Asn Val Arg Ser Glu Phe Trp
485 490 495

Ala Arg Gln Tyr Leu Gly Gln Gln Phe Tyr Leu Arg Val Tyr Ser Pro
500 505 510

Val Glu Ser Ile Arg Asp Glu Phe Pro Ile Pro Lys Asn Ala Leu Leu
515 520 525

Cys Gly Lys Ala Ser Gly Arg Arg Thr Arg Pro Leu
530 535 540

<210> 163
<211> 549
<212> PRT
<213> Arachis hypogaea

<400> 163

Met Pro Leu Lys Leu Gly Gly Gly Ala Ala Ala Phe Gly Ala Phe Leu
1 5 10 15

Val Leu Cys Val Gly Phe Ser Leu Phe Ala Val Thr Leu Ala Glu Asp
20 25 30

Pro Tyr Arg Phe Phe Asn Trp Asn Val Thr Tyr Gly Asp Ile Tyr Pro
35 40 45

Leu Gly Val Arg Gln Arg Gly Ile Leu Ile Asn Gly Gln Phe Pro Gly
50 55 60

Pro Asp Ile His Ser Val Thr Asn Asp Asn Leu Ile Ile Asn Val Phe
65 70 75 80

Asn Ser Leu Asp Glu Pro Phe Leu Leu Ser Trp Asn Gly Ile Gln Gln
85 90 95

Arg Arg Asn Ser Phe Glu Asp Gly Val Leu Gly Thr Thr Cys Pro Ile
100 105 110

Pro Pro Gly Arg Asn Phe Thr Tyr Ile Leu Gln Val Lys Asp Gln Ile
115 120 125

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

Gly Phe Gly Gly Ile Arg Ile Leu Ser Arg Pro Arg Ile Pro Val Pro
145 150 155 160

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

Lys Ser Asn His Thr Thr Leu Lys Ala His Leu Asp Arg Gly Lys Lys
180 185 190

Leu Pro Leu Pro Asp Gly Ile Leu Ile Asn Gly Arg Gly Pro Asn Gly
195 200 205

Ala Tyr Leu Asn Val Glu Gln Gly Lys Thr Tyr Arg Leu Arg Ile Ser
210 215 220

Asn Val Gly Leu Gln His Ser Leu Asn Phe Arg Ile Gln Asn His Lys
225 230 235 240

Leu Lys Leu Val Glu Val Glu Gly Thr His Ser Leu Gln Thr Thr Tyr
245 250 255

Ser Ser Leu Asp Val His Val Gly Gln Ser Tyr Ser Val Leu Val Thr
260 265 270

Ala Asp Gln Pro Ala His Asp Tyr Tyr Ile Val Val Ser Thr Arg Phe
275 280 285

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

Gly Gly Gln Val Ser Gly Pro Ile Pro Gly Gly Pro Thr Ile Gln Ile
305 310 315 320

Asp Trp Ser Leu Asn Gln Ala Arg Ser Ile Arg Thr Asn Leu Thr Ala
325 330 335

Ser Gly Pro Arg Pro Asn Pro Gln Gly Ser Tyr His Tyr Gly Leu Ile
340 345 350

Asn Thr Thr Lys Thr Ile Ile Leu Ala Ser Ser Ala Gly Gln Val Asn
355 360 365

Arg Lys Gln Arg Tyr Ala Ile Asn Ser Val Ser Tyr Val Ala Pro Asp
370 375 380

Thr Pro Leu Lys Leu Ala Asp Tyr Phe Lys Ile Ser Gly Val Phe Arg
385 390 395 400

Ala Gly Ser Ile Ser Asp Arg Pro Tyr Gly Gly Gly Ile Tyr Leu Asp
405 410 415

Thr Ser Val Leu Gln Ala Asp Tyr Arg Ser Phe Val Glu Ile Val Phe
420 425 430

Gln Asn Asn Glu Asn Ile Val Gln Ser Tyr His Leu Asp Gly Tyr Ser
435 440 445

Phe Phe Val Val Gly Met Asp Gly Gly Gln Trp Thr Thr Ala Ser Arg
450 455 460

Asn Ser Tyr Asn Leu Arg Asp Ala Ile Ala Arg Cys Thr Thr Gln Val
465 470 475 480

Tyr Pro Tyr Ser Trp Thr Ala Ile Tyr Val Ala Leu Asp Asn Val Gly
485 490 495

Met Trp Asn Leu Arg Ser Glu Phe Trp Ala Arg Gln Tyr Leu Gly Gln
500 505 510

Gln Phe Tyr Leu Arg Val Tyr Thr Asp Ser Asn Ser Ile Arg Asp Glu
515 520 525

Phe Pro Val Pro Lys Asn Ala Leu Leu Cys Gly Lys Ala Ser Gly Arg
530 535 540

His Thr Arg Pro Leu
545

<210> 164
<211> 541
<212> PRT
<213> Gossypium hirsutum

<400> 164

Met Pro Leu His Ser Ala Val Ala Leu Phe Tyr Ala Ala Ala Ser Leu
1 5 10 15

Phe Ala Ile Ala Gly Ala Glu Asp Pro Tyr Arg Phe Tyr Ser Trp Asn
20 25 30

Val Thr Tyr Gly Asp Ile Tyr Pro Leu Gly Val Arg Gln Thr Gly Leu
35 40 45

Leu Ile Asn Gly Gln Phe Pro Gly Pro Asp Ile His Ser Val Thr Asn
50 55 60

Asp Asn Leu Ile Ile Asn Val Tyr Asn Asn Leu Asn Glu Ser Phe Leu
65 70 75 80

Leu Ser Trp Asn Gly Val Gln Gln Arg Arg Asn Ser Tyr Glu Asp Gly
85 90 95

Val Phe Gly Thr Thr Cys Pro Ile Pro Pro Gly Lys Asn Phe Thr Tyr
100 105 110

Met Leu Gln Val Lys Asp Gln Ile Gly Ser Phe Tyr Tyr Tyr Pro Ser
115 120 125

Leu Gly Phe His Lys Ala Ala Gly Gly Phe Gly Gly Ile Arg Ile Leu
130 135 140

Ser Arg Pro Arg Ile Pro Val Pro Phe Pro Asp Pro Ala Gly Asp Tyr
145 150 155 160

Thr Val Leu Ile Gly Asp Trp Tyr Lys Ser Asn His Thr Val Leu Gln
165 170 175

Ala His Leu Asp Gly Gly Lys Lys Leu Pro Phe Pro Asp Gly Val Leu
180 185 190

Ile Asn Gly Arg Gly Pro Gly Gly Ala Ser Phe Asn Val Glu Gln Gly
195 200 205

Lys Thr Tyr Arg Leu Arg Ile Ser Asn Val Gly Leu Gln Asn Ser Leu
210 215 220

Asn Phe Arg Ile Gln Asn His Arg Leu Thr Leu Val Glu Val Glu Gly
225 230 235 240

Thr His Thr Leu Gln Thr Thr Tyr Ser Ser Ile Asp Leu His Leu Gly
245 250 255

Gln Ser Cys Ser Val Leu Phe Thr Ala Asp Gln Pro Ala Gln Asp Tyr
260 265 270

Tyr Ile Val Ala Ser Thr Arg Phe Thr Asn Pro Val Leu Thr Thr Thr
275 280 285

Ala Thr Leu Arg Tyr Ser Asn Ser Ala Gly Pro Val Ser Gly Pro Pro
290 295 300

Pro Gly Gly Pro Thr Ile Gln Ile Asp Trp Ser Leu Asn Gln Ala Arg
305 310 315 320

Ser Ile Arg Thr Asn Leu Thr Ala Ser Gly Pro Arg Pro Asn Pro Gln
325 330 335

Gly Ser Tyr His Tyr Gly Leu Ile Asn Thr Thr Arg Thr Ile Arg Leu
340 345 350

Ala Asn Ser Ala Gly Gln Val Asn Gly Lys Gln Arg Tyr Ala Val Asn
355 360 365

Ser Val Ser Phe Val Leu Pro Asp Thr Pro Leu Lys Leu Ala Asp Tyr
370 375 380

Phe Lys Ile Gly Gly Val Phe Arg Pro Gly Ser Ile Ser Asp Asn Pro
385 390 395 400

Tyr Gly Gly Gly Ile Tyr Leu Asp Thr Ser Val Leu Asn Ala Asp Tyr
405 410 415

Arg Ala Phe Val Glu Ile Val Phe Glu Asn Thr Glu Asn Ile Ile Gln
420 425 430

Ser Trp His Leu Asn Gly Tyr Ser Phe Phe Val Val Gly Met Asp Gly
435 440 445

Gly Gln Trp Thr Ala Ala Ser Arg Asn Gly Tyr Asn Leu Arg Asp Ala
450 455 460

Val Ala Arg Cys Thr Thr Gln Val Tyr Pro Lys Ser Trp Thr Ala Ile
465 470 475 480

Tyr Val Ala Leu Asp Asn Val Gly Ile Trp Asn Leu Arg Ser Glu Tyr
485 490 495

Trp Ala Arg Gln Tyr Leu Gly Gln Gln Leu Tyr Leu Arg Val Tyr Thr
500 505 510

Asp Ser Thr Ser Leu Arg Asp Glu Tyr Pro Ile Pro Lys Asn Ala Leu
515 520 525

Leu Cys Gly Arg Ala Ala Gly Arg Ser Thr Arg Pro Leu
530 535 540

<210> 165
<211> 212
<212> PRT
<213> Raphanus sativus

<400> 165

Met Ala Ala Asn Ala Ser Phe Ala Ala Ala Leu Leu Ile Gly Phe Ser
1 5 10 15

Leu Leu Phe Ala Val Met Ala Glu Ser Pro Tyr Arg Phe Phe Asp Trp
20 25 30

Asn Val Thr Tyr Gly Asp Ile Tyr Pro Leu Gly Val Arg Gln Gln Gly
35 40 45

Ile Leu Ile Asn Gly Gln Phe Pro Gly Pro Asp Ile His Ser Val Thr

50 55 60

Asn Asp Asn Val Ile Ile Asn Val Tyr Asn Ser Leu Asp Glu Pro Phe
65 70 75 80

Leu Leu Ser Trp Asn Gly Ile Gln Gln Arg Arg Asn Ser Tyr Val Asp
85 90 95

Gly Val Tyr Gly Thr Thr Cys Pro Ile Pro Pro Gly Lys Asn Tyr Thr
100 105 110

Tyr Ile Leu Gln Val Lys Asp Gln Ile Gly Ser Phe Tyr Tyr Phe Pro
115 120 125

Ser Leu Ala Phe His Lys Ala Ala Gly Ala Phe Gly Gly Phe Arg Ile
130 135 140

Leu Ser Arg Pro Gly Ile Pro Val Pro Phe Ala Asp Pro Ala Gly Asp
145 150 155 160

Tyr Thr Val Leu Ile Gly Asp Trp Tyr Lys Ser Asn His Thr Asp Leu
165 170 175

Lys Ala Gln Leu Asp Ser Gly Arg Lys Leu Pro Leu Pro Asp Gly Ile
180 185 190

Leu Ile Asn Gly Arg Gly Ser Gly Ala Thr Leu Asn Val Glu Gln Val

195 200 205

Arg His Thr Gly
210

<210> 166
<211> 545
<212> PRT
<213> Fragaria ananassa

<400> 166

Met Pro Leu Asn Leu Gly Ala Ile Ser Ala Leu Leu Cys Leu Ser Leu
1 5 10 15

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

Phe Gln Trp Asn Val Thr Tyr Gly Asp Ile Tyr Pro Leu Gly Val Arg
35 40 45

Gln Arg Gly Ile Leu Ile Asn Gly Gln Phe Pro Gly Pro Asp Ile Asn
50 55 60

Ser Val Thr Asn Asp Asn Leu Ile Ile Asn Val Phe Asn Ser Leu Asp
65 70 75 80

Glu Pro Phe Leu Leu Ser Trp Asn Gly Ile Gln Gln Arg His Asn Ser
85 90 95

Phe Gln Asp Gly Val Tyr Gly Thr Thr Cys Pro Ile Pro Pro Gly Arg
100 105 110

Asn Leu Thr Tyr Ile Leu Gln Val Lys Asp Gln Ile Gly Ser Phe Tyr
115 120 125

Tyr Phe Pro Ser Leu Ala Phe His Lys Ala Ala Gly Gly Phe Gly Gly
130 135 140

Ile Arg Ile Leu Ser Arg Pro Arg Ile Pro Val Pro Phe Pro Asp Pro
145 150 155 160

Ser Gly Asp Tyr Thr Val Leu Ile Gly Asp Trp Tyr Lys Ser Asn His
165 170 175

Thr Thr Leu Lys Ala His Leu Asp Arg Gly Lys Lys Leu Pro Phe Pro
180 185 190

Asp Gly Ile Leu Ile Asn Gly Arg Gly Pro Asn Gln Phe Ser Leu Thr
195 200 205

Phe Glu Gln Gly Lys Thr Tyr Arg Leu Arg Ile Ser Asn Val Gly Leu
210 215 220

Gln His Ser Leu Asn Phe Arg Ile Gln Asp His Lys Met Lys Leu Val
225 230 235 240

Glu Val Glu Gly Thr His Thr Leu Gln Thr Thr Tyr Ser Ser Leu Asp
245 250 255

Val His Val Gly Gln Ser Tyr Ser Val Leu Val Thr Ala Asp Gln Pro
260 265 270

Gly His Asp Tyr Tyr Ile Val Val Ser Ser Arg Phe Ser Thr Pro Ile
275 280 285

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

Ser Gly Pro Ile Pro Gly Gly Pro Thr Ile Gln Ile Asp Trp Ser Leu
305 310 315 320

Asn Gln Ala Arg Ser Ile Arg Thr Asn Leu Thr Ala Ser Gly Pro Arg
325 330 335

Pro Asn Pro Gln Gly Ser Tyr His Tyr Gly Leu Ile Asn Leu Thr Lys
340 345 350

Thr Tyr Ile Leu Ala Ser Ala Ala Gly Gln Val Asn Gly Lys Gln Arg
355 360 365

Tyr Gly Ile Asn Ser Val Ser Phe Val Pro Ala Asp Thr Pro Leu Lys
370 375 380

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

Ser Asp Arg Pro Thr Gly Gly Asn Leu Tyr Leu Asp Thr Ser Val Leu
405 410 415

Gly Ala Asp Tyr Arg Thr Phe Val Glu Ile Val Phe Gln Asn Asp Glu
420 425 430

Asp Ile Val Gln Ser Tyr His Leu Asp Gly Tyr Gln Phe Phe Val Val
435 440 445

Gly Met Asp Gly Gly Lys Trp Thr Thr Ala Ser Arg Asn Gly Tyr Asn
450 455 460

Leu Arg Asp Ala Val Ala Arg Ser Thr Thr Gln Val Tyr Pro Phe Ser
465 470 475 480

Trp Thr Ala Ile Tyr Leu Ser Leu Asp Asn Val Gly Met Trp Asn Leu
485 490 495

Arg Thr Glu Phe Trp Ala Arg Gln Tyr Leu Gly Gln Gln Leu Tyr Leu
500 505 510

Arg Val Tyr Thr Ser Ser Thr Ser Ile Arg Asp Glu Tyr Pro Ile Pro
515 520 525

Arg Asn Ala Arg Leu Cys Gly Arg Ala Ser Gly Arg His Thr Arg Pro
530 535 540

Leu
545

<210> 167
<211> 385
<212> PRT
<213> Manihot esculenta

<400> 167

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

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

Arg Phe Phe Asn Trp Asn Val Thr Tyr Gly Asp Ile Tyr Pro Leu Gly
35 40 45

Val Arg Gln Arg Gly Ile Leu Ile Asn Gly Gln Phe Pro Gly Pro Asp
50 55 60

Ile His Ser His Leu Ser Ala Leu Thr Ile Gly Phe Asn Leu Val Ala
65 70 75 80

Ser Leu Met Asn Ser Val Glu Ile Leu Gln Asn Gly Ile Gln Gln Arg
85 90 95

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

Pro Gly Lys Asn Phe Thr Tyr Ile Leu Gln Val Lys Asp Gln Ile Gly
115 120 125

Ser Phe Tyr Tyr Phe Pro Ser Leu Ala Phe His Lys Ala Ala Gly Gly
130 135 140

Phe Gly Gly Ile Arg Ile Leu Ser Arg Pro Arg Ile Pro Val Pro Phe
145 150 155 160

Ser Asp Pro Asp Gly Asp Tyr Thr Ile Leu Ile Gly Asp Trp Tyr Lys
165 170 175

Ser Asn His Thr Asp Leu Lys Ala Gln Leu Asp Gly Gly Asn Lys Leu
180 185 190

Pro Phe Pro Asp Gly Ile Leu Ile Asn Gly Arg Gly Pro Asn Gly Tyr
195 200 205

Ala Leu Thr Val Glu Gln Gly Lys Thr Tyr Arg Leu Arg Ile Ser Asn
210 215 220

Val Gly Leu Gln His Ser Leu Asn Phe Arg Ile Gln Asn His Lys Met
225 230 235 240

Lys Leu Val Glu Val Glu Gly Thr His Thr Leu Gln Asn Thr Tyr Ser
245 250 255

Ser Leu Asp Val His Val Gly Gln Ser Tyr Ser Val Leu Val Thr Ala
260 265 270

Asp Gln Pro Gly Gln Asp Tyr Tyr Ile Val Val Ser Ser Arg Phe Thr
275 280 285

Thr Pro Ile Leu Thr Thr Thr Gly Val Leu His Tyr Ser Asn Ser Ala
290 295 300

Gly Pro Val Ser Gly Pro Pro Pro Gly Gly Pro Thr Ile Gln Ile Asp
305 310 315 320

Trp Ser Leu Asn Gln Ala Arg Ser Ile Arg Thr Asn Leu Thr Ala Ser
325 330 335

Gly Pro Arg Pro Asn Pro Gln Gly Ser Tyr His Tyr Gly Met Ile Asn
340 345 350

Thr Thr Arg Thr Ile Arg Phe Ala Asn Ser Ala Gly Gln Val Asn Gly
355 360 365

Lys Gln Arg Tyr Ala Val Asn Ser Val Ser Leu Phe Gln Gln Ile Pro
370 375 380

His
385

<210> 168
<211> 544
<212> PRT
<213> Malus

<400> 168

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

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

Glu Trp Asn Val Thr Tyr Gly Asp Ile Tyr Pro Leu Gly Val Arg Gln
35 40 45

Lys Gly Ile Leu Ile Asn Gly Gln Phe Pro Gly Pro Asp Ile His Ser
50 55 60

Val Thr Asn Asp Asn Leu Ile Ile Asn Val Phe Asn Ser Leu Asp Glu
65 70 75 80

Pro Phe Leu Leu Ser Trp Asn Gly Ile Gln Gln Arg Arg Asn Ser Phe
85 90 95

Val Asp Gly Val Tyr Gly Thr Thr Cys Pro Ile Pro Pro Gly Arg Asn
100 105 110

Phe Thr Tyr Ile Leu Gln Val Lys Asp Gln Ile Gly Ser Phe Tyr Tyr
115 120 125

Phe Pro Ser Leu Asp Phe His Lys Ala Ala Gly Gly Phe Gly Gly Ile
130 135 140

Arg Ile Leu Ser Arg Pro Arg Ile Pro Val Pro Phe Pro Asp Pro Asp
145 150 155 160

Gly Asp Tyr Thr Val Leu Ile Gly Asp Trp Tyr Lys Ser Asn His Thr
165 170 175

Thr Leu Lys Ala His Leu Asp Ser Gly Lys Lys Leu Pro Ser Pro Asp
180 185 190

Gly Ile Leu Ile Asn Gly Arg Gly Pro Gly Gly Phe Ser Leu Asn Phe
195 200 205

Glu Gln Gly Lys Thr Tyr Arg Leu Arg Ile Ser Asn Val Gly Leu Gln
210 215 220

Asn Ser Leu Asn Phe Arg Ile Gln Asn His Lys Met Lys Leu Val Glu
225 230 235 240

Val Glu Gly Thr His Thr Leu Gln Thr Ser Tyr Ser Ser Leu Asp Val
245 250 255

His Val Gly Gln Ser Tyr Ser Val Leu Val Thr Ala Asp Gln Pro Gly
260 265 270

Gln Asp Tyr Tyr Val Val Ala Ser Ser Arg Phe Thr Ser Pro Ile Leu
275 280 285

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

Gly Pro Pro Pro Gly Gly Pro Thr Ile Gln Val Asp Trp Ser Leu Asn
305 310 315 320

Gln Ala Arg Ser Ile Arg Thr Asn Leu Thr Ala Ser Gly Pro Arg Pro
325 330 335

Asn Pro Gln Gly Ser Tyr His Tyr Gly Leu Ile Asn Leu Thr Lys Thr
340 345 350

Tyr Val Leu Glu Asn Ser Ala Gly Gln Val Asn Gly Lys Gln Arg Tyr
355 360 365

Gly Val Asn Ser Val Ser Phe Val Pro Ala Asp Thr Pro Leu Lys Leu
370 375 380

Ala Asp Tyr Phe Lys Ile Gly Gly Val Phe Arg Val Gly Ser Ile Ser
385 390 395 400

Asp Lys Pro Thr Gly Gly Gly Leu Tyr Leu Asp Thr Ser Val Leu Gly
405 410 415

Ala Asp Tyr Arg Thr Phe Val Glu Ile Val Phe Gln Asn Asn Glu Asp
420 425 430

Ile Ile Gln Ser Trp His Leu Asp Gly Tyr Ser Phe Phe Val Val Gly
435 440 445

Met Asp Gly Gly Gln Trp Thr Thr Ala Ser Arg Asp Ala Tyr Asn Leu
450 455 460

Arg Asp Ala Val Ser Arg Cys Thr Thr Gln Val Tyr Pro Lys Ser Trp
465 470 475 480

Thr Ala Ile His Ile Ala Leu Asp Asn Val Gly Met Trp Asn Leu Arg
485 490 495

Thr Glu Phe Trp Ala Arg Gln Tyr Leu Gly Gln Gln Leu Tyr Leu Arg
500 505 510

Val Tyr Thr Ser Ser Thr Ser Leu Arg Asp Glu Phe Pro Ile Pro Arg
515 520 525

Asn Ala Arg Leu Cys Gly Arg Ala Ser Gly Gln Arg Thr Arg Pro Leu
530 535 540

<210> 169
<211> 541
<212> PRT
<213> Arabidopsis lyrata

<400> 169

Met Ala Ala Asn Ala Ser Phe Ala Ala Ala Leu Leu Ile Gly Leu Ser
1 5 10 15

Leu Leu Phe Ala Val Val Ala Glu Asp Pro Tyr Arg Phe Phe Glu Trp
20 25 30

Asn Ile Thr Tyr Gly Asp Ile Tyr Pro Leu Gly Val Arg Gln Gln Gly
35 40 45

Ile Leu Ile Asn Gly Gln Phe Pro Gly Pro Asp Ile His Ser Val Thr
50 55 60

Asn Asp Asn Leu Ile Ile Asn Val Tyr Asn Ser Leu Asp Glu Pro Phe
65 70 75 80

Leu Leu Ser Trp Asn Gly Ile Gln Gln Arg Arg Asn Ser Phe Val Asp

85 90 95

Gly Val Tyr Gly Thr Thr Cys Pro Ile Pro Pro Gly Lys Asn Tyr Thr
100 105 110

Tyr Ile Leu Gln Met Lys Asp Gln Ile Gly Ser Phe Tyr Tyr Phe Pro
115 120 125

Ser Leu Gly Phe His Lys Ala Ala Gly Gly Phe Gly Gly Ile Arg Ile
130 135 140

Leu Ser Arg Pro Arg Ile Pro Val Pro Phe Pro Asp Pro Ala Gly Asp
145 150 155 160

Thr Thr Val Leu Ile Gly Asp Trp Tyr Lys Ser Asn His Thr Asp Leu
165 170 175

Arg Ala Gln Leu Asp Ser Gly Lys Lys Leu Pro Leu Pro Asp Gly Ile
180 185 190

Leu Ile Asn Gly Arg Ser Ser Gly Ala Thr Leu Asn Val Glu Gln Gly
195 200 205

Lys Thr Tyr Arg Leu Arg Ile Ser Asn Val Gly Leu Gln Asp Ser Leu
210 215 220

Asn Phe Arg Ile Gln Asp His Lys Met Lys Val Ile Glu Val Glu Gly

225 230 235 240

Thr His Thr Leu Gln Thr Thr Phe Ser Ser Leu Asp Val His Val Gly
245 250 255

Gln Ser Tyr Ser Val Leu Val Thr Ala Asp Gln Thr Pro Arg Asp Tyr
260 265 270

Tyr Val Val Val Ser Ser Arg Phe Thr Ser Asn Val Leu Thr Thr Thr
275 280 285

Gly Ile Leu Arg Tyr Ser Asn Ser Ala Gly Ala Val Ser Gly Pro Ile
290 295 300

Pro Gly Gly Pro Thr Ile Gln Ile Asp Trp Ser Leu Asn Gln Ala Arg
305 310 315 320

Ala Ile Arg Thr Asn Leu Thr Ala Ser Gly Pro Arg Pro Asn Pro Gln
325 330 335

Gly Ser Tyr His Tyr Gly Met Ile Asn Thr Thr Arg Thr Ile Arg Leu
340 345 350

Ala Ser Ser Ala Gly Gln Val Asp Gly Lys Gln Arg Tyr Ala Val Asn
355 360 365

Ser Val Ser Phe Lys Pro Ala Asp Thr Pro Leu Lys Ile Ala Asp Tyr

370 375 380

Phe Lys Ile Asp Gly Val Phe Arg Ser Gly Ser Ile Gln Tyr Gln Pro
385 390 395 400

Thr Gly Gly Gly Ile Tyr Leu Asp Thr Ser Val Met Gln Val Asp Tyr
405 410 415

Arg Thr Phe Val Glu Ile Val Phe Glu Asn Ser Glu Asp Ile Val Gln
420 425 430

Ser Trp His Leu Asp Gly Tyr Ser Phe Trp Val Val Gly Met Asp Gly
435 440 445

Gly Gln Trp Ser Pro Asp Ser Arg Asn Val Tyr Asn Leu Arg Asp Ala
450 455 460

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

Leu Ile Ala Leu Asp Asn Val Gly Met Trp Asn Leu Arg Ser Glu Phe
485 490 495

Trp Ala Arg Gln Tyr Leu Gly Gln Gln Leu Tyr Leu Arg Val Tyr Thr
500 505 510

Pro Ser Thr Ser Leu Arg Asp Glu Tyr Pro Ile Pro Lys Asn Ala Leu

515 520 525

Leu Cys Gly Arg Ala Ser Gly Arg Arg Thr Arg Pro Leu
530 535 540

<210> 170
<211> 540
<212> PRT
<213> Tragopogon

<400> 170

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

Ala Ile Ala Gly Ala Glu Asp Pro Tyr Arg Phe Phe Asn Trp Asn Val
20 25 30

Thr Tyr Gly Asp Ile Tyr Pro Leu Gly Val Arg Gln Gln Gly Ile Leu
35 40 45

Ile Asn Gly Gln Phe Pro Gly Pro Asp Ile His Ser Val Thr Asn Asp
50 55 60

Asn Leu Ile Ile Asn Val Phe Asn Ser Leu Pro Glu Pro Phe Leu Ile
65 70 75 80

Ser Trp Asn Gly Val Gln Gln Arg Arg Asn Ser Phe Glu Asp Gly Val
85 90 95

Tyr Gly Thr Thr Cys Pro Ile Pro Pro Gly Lys Asn Phe Thr Tyr Ile
100 105 110

Leu Gln Val Lys Asp Gln Ile Gly Ser Phe Tyr Tyr Phe Pro Ser Leu
115 120 125

Ala Phe His Lys Ala Ala Gly Gly Phe Gly Gly Ile Arg Ile Leu Ser
130 135 140

Arg Pro Arg Ile Pro Val Pro Phe Asp Glu Pro Ala Gly Asp Phe Thr
145 150 155 160

Val Leu Ile Gly Asp Trp Tyr Lys Ala Asn His Thr Thr Leu Lys Arg
165 170 175

Val Leu Asp Asn Gly His Lys Ile Pro Phe Pro Asp Gly Ile Leu Ile
180 185 190

Asn Gly Arg Gly Pro Asn Gly Ala Tyr Phe Thr Val Glu Gln Gly Lys
195 200 205

Thr Tyr Arg Leu Arg Ile Ser Asn Val Gly Leu Gln Asn Ser Leu Asn
210 215 220

Phe Arg Ile Gln Asn His Lys Met Lys Leu Val Glu Val Glu Gly Thr
225 230 235 240

His Thr Val Gln Gln Thr Tyr Ser Ser Leu Asp Val His Cys Gly Gln
245 250 255

Ser Tyr Ser Val Leu Phe Thr Ala Asp Gln Pro Gly His Asp Tyr Tyr
260 265 270

Ile Val Val Ser Ser Arg Phe Thr Thr Pro Val Leu Thr Thr Thr Gly
275 280 285

Val Leu His Tyr Ser Asn Ser Gly Gly Gln Val Ser Gly Pro Ile Pro
290 295 300

Gly Gly Pro Thr Ile Gln Val Asp Trp Ser Leu Asn Gln Ala Arg Ser
305 310 315 320

Ile Arg Thr Asn Leu Thr Ala Ser Gly Pro Arg Pro Asn Pro Gln Gly
325 330 335

Ser Tyr His Tyr Gly Met Ile Asn Thr Ser Arg Thr Ile Ile Leu Gln
340 345 350

Ser Ser Ala Gly Gln Val Gly Gly Lys Gln Arg Tyr Gly Ile Asn Ser
355 360 365

Val Ser Phe Lys Pro Ala Asp Thr Pro Leu Lys Leu Ala Asp Tyr Phe
370 375 380

Asn Ile Gly Gly Val Phe Arg Val Gly Ser Ile Ser Asp Arg Pro Thr
385 390 395 400

Gly Gly Gly Leu Tyr Gln Asp Thr Ser Val Met Gly Ala Asp Tyr Arg
405 410 415

Ala Phe Val Glu Ile Val Phe Glu Asn Pro Ala Asp Ile Val Leu Ser
420 425 430

Tyr His Leu Asp Gly Tyr Gln Phe Phe Val Val Gly Met Asp Gly Gly
435 440 445

Gln Trp Thr Gln Ala Ser Arg Asn Gly Tyr Asn Leu Arg Asp Gly Val
450 455 460

Ala Arg Ser Thr Ile Gln Val Tyr Pro Lys Ser Trp Ser Ala Ile Tyr
465 470 475 480

Leu Gly Leu Asp Asn Val Gly Met Trp Asn Leu Arg Thr Glu Phe Trp
485 490 495

Ala Arg Gln Tyr Leu Gly Glu Gln Phe Tyr Leu Arg Val Tyr Thr Asn
500 505 510

Ser Gly Ser Ile Arg Asp Glu Phe Pro Ile Pro Lys Asn Ala Arg Leu
515 520 525

Cys Gly Arg Ala Thr Gly Phe His Thr Arg Pro Leu
530 535 540

<210> 171
<211> 541
<212> PRT
<213> Cucumis sativus

<400> 171

Met Leu Pro Leu Thr Ser Pro Phe Phe Ala Leu Cys Ala Phe Phe Cys
1 5 10 15

Phe Phe Ser Thr Leu Ser Ala Glu Asn Pro Tyr Arg Phe Phe Thr Trp
20 25 30

Asn Val Ser Tyr Ala Asn Ile Tyr Pro Leu Gly Val Arg Gln Gln Gly
35 40 45

Ile Leu Ile Asn Gly Gln Phe Pro Gly Pro Asp Val His Cys Val Thr
50 55 60

Asn Asp Asn Leu Ile Ile Asn Val Phe Asn Ser Leu Asp Glu Pro Phe
65 70 75 80

Leu Ile Ser Trp Asn Gly Ile Gln Gln Arg Arg Asn Ser Tyr Glu Asp
85 90 95

Gly Val Tyr Gly Thr Thr Cys Pro Ile Pro Pro Gly Lys Asn Phe Thr
100 105 110

Tyr Ile Leu Gln Val Lys Asp Gln Ile Gly Ser Phe Tyr Tyr Phe Pro
115 120 125

Ser Leu Ala Phe His Lys Ala Ala Gly Gly Phe Gly Gly Ile Arg Ile
130 135 140

Leu Ser Arg Pro Arg Ile Pro Val Pro Phe Pro Asp Pro Ala Gly Asp
145 150 155 160

Tyr Thr Val Leu Ile Gly Asp Trp Tyr Lys Ser Asn His Thr Thr Leu
165 170 175

Lys Ala His Leu Asp Arg Gly Lys Lys Leu Pro Phe Pro Asp Gly Ile
180 185 190

Leu Ile Asn Gly Arg Ala Asn Asp Thr Ser Phe Gly Val Glu Gln Gly
195 200 205

Lys Thr Tyr Arg Leu Arg Ile Ser Asn Val Gly Leu Gln His Ser Leu
210 215 220

Asn Phe Arg Ile Gln Gly His Lys Met Lys Leu Val Glu Val Glu Gly
225 230 235 240

Thr His Thr Leu Gln Thr Thr Tyr Ser Ser Leu Asp Val His Val Gly
245 250 255

Gln Ser Tyr Ser Val Leu Ile Thr Ala Asp Gln Pro Ala Gln Asp Tyr
260 265 270

Tyr Ile Val Val Ser Thr Arg Phe Thr Ser Arg Val Leu Ala Thr Thr
275 280 285

Gly Ile Leu Arg Tyr Ser Asn Ser Ala Gly Pro Val Lys Gly Pro Pro
290 295 300

Pro Gly Gly Pro Thr Ile Gln Ile Asp Trp Ser Leu Asn Gln Ala Arg
305 310 315 320

Ser Ile Arg Thr Asn Leu Thr Ala Ser Gly Pro Arg Pro Asn Pro Gln
325 330 335

Gly Ser Tyr His Tyr Gly Leu Ile Asn Thr Thr Lys Thr Ile Ile Leu
340 345 350

Ala Asn Ser Ala Gly Gln Val Asn Arg Lys Gln Arg Tyr Ala Val Asn
355 360 365

Ser Val Ser Phe Val Pro Ala Asp Thr Pro Leu Lys Leu Ala Asp Phe
370 375 380

Phe Lys Ile Gly Gly Val Phe Arg Val Gly Ser Ile Ser Asp Arg Pro
385 390 395 400

Thr Gly Gly Gly Ile Tyr Leu Asp Thr Ser Val Met Gly Val Asp Tyr
405 410 415

Arg Ala Phe Val Glu Ile Ile Phe Gln Asn Asn Glu Asn Ile Val Gln
420 425 430

Ser Trp His Ile Asp Gly Tyr Ser Phe Phe Val Val Gly Met Asp Gly
435 440 445

Gly Gln Trp Thr Gln Ser Ser Arg Asn Gln Tyr Asn Leu Arg Asp Ala
450 455 460

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

Tyr Val Ala Leu Asp Asn Val Gly Met Trp Asn Val Arg Ser Glu Phe
485 490 495

Trp Ala Arg Gln Tyr Leu Gly Gln Gln Phe Tyr Leu Arg Val Tyr Thr
500 505 510

Pro Ser Thr Ser Leu Arg Asp Glu Phe Pro Ile Pro Lys Asn Ala Leu
515 520 525

Leu Cys Gly Lys Ala Thr Leu Ser Pro Pro Arg Gly Ser
530 535 540

<210> 172
<211> 546
<212> PRT
<213> Euphorbia

<220>
<221> misc_feature
<222> (391)..(391)
<223> Xaa puede ser cualquier aminoácido de origen natural

<400> 172

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

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

Phe Phe Asn Trp Asn Val Thr Tyr Gly Asp Ile Tyr Pro Leu Gly Val
35 40 45

Arg Gln Arg Gly Ile Leu Ile Asn Gly Gln Phe Pro Gly Pro Asp Ile
50 55 60

His Ser Val Thr Asn Asp Asn Leu Ile Ile Asn Val Tyr Asn Ser Leu
65 70 75 80

Asp Glu Pro Phe Leu Leu Ser Trp Asn Gly Val Gln Gln Arg Arg Asn
85 90 95

Ser Tyr Val Asp Gly Val Tyr Gly Thr Thr Cys Pro Ile Pro Pro Gly
100 105 110

Gln Asn Tyr Thr Tyr Ile Met Gln Val Lys Asp Gln Ile Gly Ser Phe
115 120 125

Tyr Tyr Phe Pro Ser Leu Gly Phe His Lys Ala Ala Gly Gly Phe Gly
130 135 140

Gly Ile Arg Ile Leu Ser Arg Pro Arg Ile Pro Val Pro Phe Ala Asp
145 150 155 160

Pro Asp Gly Asp Tyr Thr Ile Leu Ile Gly Asp Trp Tyr Lys Ser Asn
165 170 175

His Thr Val Leu Arg Ala Gln Leu Asp Gly Gly Lys Lys Leu Pro Leu
180 185 190

Ala Asp Gly Ile Leu Ile Asn Gly Arg Gly Pro Asn Gly Tyr Ser Leu
195 200 205

Thr Val Glu Gln Gly Lys Thr Tyr Arg Leu Arg Ile Ser Asn Val Gly
210 215 220

Leu Gln Asn Ser Leu Asn Phe Arg Ile Gln Asn His Lys Met Lys Leu
225 230 235 240

Val Glu Val Glu Gly Thr His Thr Leu Gln Thr Thr Tyr Ser Ser Leu
245 250 255

Asp Val His Leu Gly Gln Ser Tyr Ser Val Leu Phe Thr Ala Asp Gln
260 265 270

Pro Gly Gln Asp Tyr Tyr Ile Val Val Ser Ser Arg Phe Thr Ser Pro
275 280 285

Val Ile Thr Thr Thr Gly Val Leu His Tyr Ser Asn Ser Ala Gly Pro
290 295 300

Val Ser Gly Pro Pro Pro Gly Gly Pro Thr Ile Gln Val Asp Trp Ser
305 310 315 320

Leu Asn Gln Ala Arg Ser Ile Arg Thr Asn Leu Thr Ala Ser Gly Pro
325 330 335

Arg Pro Asn Pro Gln Gly Ser Tyr His Tyr Gly Met Ile Asn Thr Thr
340 345 350

Arg Thr Ile Ile Phe Ser Ser Ser Ala Gly Gln Val Asn Gly Lys Gln
355 360 365

Arg Tyr Ala Val Asn Ser Val Ser Phe Ile Pro Gln Asp Thr Pro Leu
370 375 380

Lys Leu Ala Asp Tyr Phe Xaa Ile Gln Gly Val Phe Lys Glu Asn Ser
385 390 395 400

Ile Ala Ser Lys Pro Tyr Gly Gly Gly Ile Tyr Leu Val Thr Ser Val
405 410 415

Leu Thr Val Asp Tyr Arg Ser Tyr Val Glu Ile Val Phe Val Asn Asp
420 425 430

Glu Asp Ile Leu Gln Ser Tyr His Leu Asp Gly Tyr Ser Phe Phe Val
435 440 445

Val Gly Met Asp Gly Gly Gln Trp Thr Pro Ala Ser Arg Asn Gly Tyr
450 455 460

Asn Leu Arg Asp Gly Val Ala Arg Cys Thr Ile Gln Val Tyr Pro Lys
465 470 475 480

Ser Trp Ser Ala Ile Tyr Ile Pro Leu Asp Asn Val Gly Met Trp Asn
485 490 495

Leu Arg Ser Glu Tyr Trp Ala Arg Gln Tyr Leu Gly Gln Gln Leu Tyr
500 505 510

Leu Arg Val Tyr Thr Ser Ser Thr Ser Leu Arg Asp Glu Tyr Pro Ile
515 520 525

Pro Lys Asn Ala Leu Leu Cys Gly Lys Ala Ala Gly Arg His Thr Arg
530 535 540

Pro Leu
545

<210> 173
<211> 539
<212> PRT
<213> Aristolochia

<400> 173

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

Val Val Thr Ala Glu Asp Pro Tyr Arg Phe Phe Thr Trp Asn Val Thr
20 25 30

Tyr Gly Asp Ile Tyr Pro Leu Gly Val Arg Gln Gln Gly Ile Leu Ile
35 40 45

Asn Gly Gln Phe Pro Gly Pro Asp Ile His Ser Val Thr Asn Asp Asn
50 55 60

Leu Ile Ile Asn Val Phe Asn Ser Leu Pro Glu Pro Phe Leu Ile Ser
65 70 75 80

Trp Asn Gly Ile Gln Gln Arg Arg Asn Ser Trp Glu Asp Gly Val Tyr
85 90 95

Gly Thr Thr Cys Pro Ile Pro Pro Gly Arg Asn Phe Thr Tyr Ile Leu
100 105 110

Gln Val Lys Asp Gln Ile Gly Ser Leu Phe Tyr Phe Pro Ser Leu Ala
115 120 125

Phe His Lys Ala Ala Gly Gly Phe Gly Gly Ile Arg Ile Leu Ser Arg
130 135 140

Pro Arg Ile Pro Val Pro Phe Pro Asp Pro Ala Gly Asp Phe Thr Val
145 150 155 160

Leu Ile Gly Asp Trp Tyr Lys Ala Asn His Thr Asp Leu Arg Ala Lys
165 170 175

Leu Asp Arg Gly Lys Lys Leu Pro Leu Pro Asp Gly Ile Leu Ile Asn
180 185 190

Gly Arg Gly Pro Asn Gly Ala Tyr Phe Thr Val Glu Gln Gly Lys Thr
195 200 205

Tyr Arg Phe Arg Ile Ser Asn Val Gly Leu Gln Asn Ser Leu Asn Ile
210 215 220

Arg Phe Gln Asn His Lys Met Lys Leu Val Glu Val Glu Gly Thr His
225 230 235 240

Thr Val Gln Asn Thr Tyr Ser Ser Leu Asp Val His Val Gly Gln Ser
245 250 255

Tyr Ser Val Leu Val Thr Met Asp Gln Pro Gly Leu Asp Tyr Tyr Ile
260 265 270

Val Val Ser Thr Arg Phe Thr Asn Pro Val Leu Thr Thr Thr Gly Thr
275 280 285

Leu His Tyr Ser Asn Ser Val Gly Arg Val Ser Gly Pro Pro Pro Gly
290 295 300

Gly Pro Thr Ile Gln Ile Asp Trp Ser Leu Asn Gln Ala Arg Ser Val
305 310 315 320

Arg Thr Asn Leu Thr Ala Ser Gly Pro Arg Pro Asn Pro Gln Gly Ser
325 330 335

Tyr His Tyr Gly Leu Ile Asn Thr Thr Arg Thr Ile Val Leu Ala Asn
340 345 350

Ser Ala Gly Leu Val Asp Gly Lys Gln Arg Tyr Ala Val Asn Ser Val
355 360 365

Ser Phe Val Pro Ala Asp Thr Pro Leu Lys Leu Ala Asp Phe Phe Lys
370 375 380

Ile Ser Gly Val Phe Arg Val Gly Ser Ile Ser Asp Arg Pro Thr Gly
385 390 395 400

Gly Gly Ile Tyr Lys Asp Thr Ser Val Leu Gly Ala Asp Phe Arg Ala
405 410 415

Tyr Ile Glu Ile Val Phe Gln Asn Asp Glu Asp Ile Val Gln Ser Trp
420 425 430

His Leu Asp Gly Tyr Ser Phe Phe Val Val Gly Met Asp Gly Gly Thr
435 440 445

Trp Thr Thr Ala Ser Arg Asn Ser Tyr Asn Leu Arg Asp Ala Val Ser
450 455 460

Arg Cys Thr Thr Gln Val Tyr Pro Lys Ser Trp Thr Ala Ile Tyr Met
465 470 475 480

Ala Leu Asp Asn Val Gly Met Trp Asn Leu Arg Ser Glu Phe Trp Ala
485 490 495

Arg Gln Tyr Leu Gly Gln Gln Phe Tyr Leu Arg Val Tyr Ser Pro Val
500 505 510

Glu Ser Ile Arg Asp Glu Tyr Pro Ile Pro Arg Asn Ala Arg Leu Cys
515 520 525

Gly Arg Ala Ser Gly Arg His Thr Arg Pro Leu
530 535

<210> 174
<211> 545
<212> PRT
<213> Quercus

<400> 174

Met Pro Leu Asn Ile Ala Gly Ser Val Leu Ser Ala Val Leu Cys Ile
1 5 10 15

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

Phe Asn Trp Asn Val Thr Tyr Gly Asp Ile Tyr Pro Leu Gly Val Arg
35 40 45

Gln Gln Gly Ile Leu Ile Asn Gly Gln Phe Pro Gly Pro Asp Ile His
50 55 60

Ser Val Thr Asn Asp Asn Leu Ile Ile Asn Val Phe Asn Ser Leu Asn
65 70 75 80

Glu Pro Phe Leu Leu Ser Trp Asn Gly Ile Gln Asn Arg Arg Asn Ser
85 90 95

Phe Glu Asp Gly Val Asn Gly Thr Thr Cys Pro Ile Pro Pro Gly Gln
100 105 110

Asn Phe Thr Tyr Ile Leu Gln Val Lys Asp Gln Ile Gly Ser Phe Tyr
115 120 125

Tyr Phe Pro Ser Leu Ala Phe His Lys Ala Ala Gly Gly Phe Gly Gly
130 135 140

Ile Arg Ile Leu Ser Arg Pro Arg Ile Pro Val Pro Phe Pro Asp Pro
145 150 155 160

Ala Gly Asp Tyr Thr Val Leu Ile Gly Asp Trp Tyr Lys Ala Asn His
165 170 175

Thr Asp Leu Lys Ala Leu Leu Asp Arg Gly Lys Lys Leu His Phe Pro
180 185 190

Asp Gly Ile Leu Ile Asn Gly Arg Gly Pro Gly Gly Ala Ala Tyr Thr
195 200 205

Val Glu Gln Gly Lys Thr Tyr Arg Phe Arg Ile Ser Asn Val Gly Leu
210 215 220

Gln His Ser Leu Asn Phe Arg Ile Gln Gly His Arg Leu Thr Leu Ala
225 230 235 240

Glu Val Glu Gly Thr His Thr Leu Gln Thr Ser Tyr Ser Ser Leu Asp
245 250 255

Val His Val Gly Gln Ser Tyr Ser Val Leu Val Thr Met Asp Gln Pro
260 265 270

Gly Gln Asp Tyr Tyr Ile Val Val Ser Ser Arg Phe Thr Thr Pro Ile
275 280 285

Leu Thr Thr Thr Gly Val Leu His Tyr Ser Asn Ser Ala Gly Pro Val
290 295 300

Ser Gly Pro Pro Pro Gly Gly Pro Thr Ile Gln Val Asp Trp Ser Leu
305 310 315 320

Asn Gln Ala Arg Ser Ile Arg Thr Asn Leu Thr Ala Ser Gly Pro Arg
325 330 335

Pro Asn Pro Gln Gly Ser Tyr His Tyr Gly Leu Ile Asn Thr Thr Lys
340 345 350

Thr Ile Arg Leu Gln Asn Ser Ala Gly Leu Val Asp Gly Lys Gln Arg
355 360 365

Tyr Ala Val Asn Ser Val Ser Tyr Val Ala Ala Asp Thr Pro Leu Lys
370 375 380

Ile Ala Asp Tyr Phe Gln Ile Gln Gly Val Phe Arg Val Gly Ser Ile
385 390 395 400

Ser Ser Asn Pro Thr Gly Gly Gly Ile Tyr Leu Asp Thr Ala Val Met
405 410 415

Gly Ala Asp Tyr Arg Ala Phe Ile Glu Ile Val Phe Glu Asn Thr Glu
420 425 430

Asp Ile Ile Gln Ser Trp His Leu Asp Gly Tyr Ser Phe Trp Val Val
435 440 445

Gly Met Asp Gly Gly Leu Trp Thr Thr Ala Ser Arg Asn Gln Tyr Asn
450 455 460

Leu Arg Asp Ala Val Ser Arg Val Thr Thr Gln Val Tyr Pro Lys Ser
465 470 475 480

Trp Thr Ala Ile Tyr Leu Ala Leu Asp Asn Val Gly Met Trp Asn Leu
485 490 495

Arg Ser Glu Phe Trp Ala Arg Gln Tyr Leu Gly Gln Gln Phe Tyr Leu
500 505 510

Arg Val Tyr Thr Pro Ser Thr Ser Ile Arg Asp Glu Phe Pro Ile Pro
515 520 525

Lys Asn Ala Leu Leu Cys Gly Arg Ala Lys Gly Arg His Thr Arg Pro
530 535 540

Leu
545

<210> 175
<211> 540
<212> PRT
<213> Actinidia deliciosa

<400> 175

Met Pro Leu Asn Leu Ala Ala Val Phe Cys Leu Ala Val Ser Leu Phe
1 5 10 15

Ala Val Val Gly Ala Asp Asp Pro Tyr Arg Phe Phe Asn Trp Asn Val
20 25 30

Thr Tyr Gly Asp Ile Tyr Pro Leu Gly Val Arg Gln Gln Gly Ile Leu
35 40 45

Ile Asn Gly Gln Phe Pro Gly Pro Asp Ile Tyr Ser Val Thr Asn Asp

50 55 60

Asn Leu Ile Ile Asn Val Phe Asn Ser Leu Asp Glu Pro Phe Leu Leu
65 70 75 80

Ser Trp Asn Gly Ile Gln Gln Arg Arg Asn Ser Tyr Gln Asp Gly Val
85 90 95

Tyr Gly Thr Thr Cys Pro Ile Pro Pro Gly Lys Asn Phe Thr Tyr Ile
100 105 110

Leu Gln Val Lys Asp Gln Ile Gly Ser Phe Tyr Tyr Phe Pro Ser Leu
115 120 125

Ala Phe His Lys Ala Ala Gly Gly Phe Gly Gly Ile Arg Ile Leu Ser
130 135 140

Arg Pro Arg Ile Pro Val Pro Phe Pro Asp Pro Ala Gly Asp Tyr Thr
145 150 155 160

Val Leu Ile Gly Asp Trp Tyr Lys Ser Asn His Thr Asp Leu Lys Ala
165 170 175

Lys Leu Asp Arg Gly Lys Lys Leu Pro Leu Ala Asp Gly Ile Leu Ile
180 185 190

Asn Gly Arg Gly Pro Asn Gly Ala Ser Phe Thr Val Glu Gln Gly Lys

195 200 205

Thr Tyr Arg Leu Arg Ile Ser Asn Val Gly Leu Gln Asn Ser Leu Asn
210 215 220

Phe Arg Ile Gln Gly His Arg Met Thr Leu Val Glu Val Glu Gly Thr
225 230 235 240

His Ser Val Gln Thr Ser Tyr Ser Trp Leu Asp Val His Pro Gly Gln
245 250 255

Ser Tyr Ser Val Leu Val Lys Ala Asp Gln Pro Ala Gln Asp Tyr Phe
260 265 270

Val Ala Val Ser Thr Arg Phe Thr Thr Asp Val Leu Thr Thr Ser Ala
275 280 285

Ile Phe His Tyr Ser Asn Ser Ala Gly Pro Val Ser Gly Pro Pro Pro
290 295 300

Gly Gly Pro Thr Ile Gln Ile Asp Glu Ser Leu Asn Gln Ala Arg Ser
305 310 315 320

Ile Arg Thr Asn Leu Thr Ala Ser Gly Pro Arg Pro Asn Pro Gln Gly
325 330 335

Ser Tyr His Tyr Gly Leu Ile Asn Thr Thr Lys Thr Ile Arg Leu Ala

340 345 350

Asn Ser Ala Gly Leu Ile Asn Gly Lys Gln Arg Tyr Ala Val Asn Ser
355 360 365

Val Ser Phe Val Pro Ala Asp Thr Pro Leu Lys Leu Ala Asp Phe Phe
370 375 380

Thr Ile Gly Gly Val Phe Arg Val Gly Ser Ile Ser Asp Asn Pro Thr
385 390 395 400

Gly Gly Gly Leu Tyr Leu Asp Thr Ser Val Leu Gly Val Asp Tyr Arg
405 410 415

Ala Phe Ile Glu Ile Val Phe Glu Asn Lys Glu Asn Ile Val Gln Ser
420 425 430

Trp His Leu Asp Gly Tyr Ser Phe Phe Val Val Gly Met Asp Gly Gly
435 440 445

Leu Trp Ser Ser Ala Ser Arg Ser Gln Tyr Asn Leu Arg Asp Ala Ile
450 455 460

Ser Arg Ser Thr Val Gln Val Tyr Pro Lys Ser Trp Thr Ala Ile Tyr
465 470 475 480

Val Ala Leu Asp Asn Val Gly Met Trp Asn Leu Arg Ser Glu Phe Trp

485 490 495

Ala Arg Gln Tyr Leu Gly Gln Gln Leu Tyr Leu Arg Val Tyr Thr Ala
500 505 510

Ser Thr Ser Leu Arg Asp Glu Phe Pro Ile Pro Lys Asn Ala Leu Leu
515 520 525

Cys Gly Arg Ala Ser Gly Arg His Thr Arg Pro Leu
530 535 540

<210> 176
<211> 540
<212> PRT
<213> Eucalyptus

<400> 176

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

Ala Ile Val Gly Ala Glu Asn Pro Tyr Arg Phe Phe Asp Trp Asn Val
20 25 30

Thr Tyr Gly Asp Ile Tyr Pro Leu Gly Val Arg Gln Gln Gly Ile Leu
35 40 45

Ile Asn Gly Gln Phe Pro Gly Pro Asp Ile His Ser Val Thr Asn Asp
50 55 60

Asn Leu Ile Ile Asn Val Phe Asn Ser Leu Asp Val Pro Phe Leu Ile
65 70 75 80

Ser Trp Ser Gly Ile Gln Gln Arg Arg Asn Ser Tyr Glu Asp Gly Val
85 90 95

Tyr Gly Thr Thr Cys Pro Ile Pro Pro Gly Arg Asn Phe Thr Tyr Ile
100 105 110

Phe Gln Val Lys Asp Gln Ile Gly Ser Phe Phe Tyr Phe Pro Ser Leu
115 120 125

Lys Phe His Lys Ala Ala Gly Gly Phe Gly Gly Ile Arg Ile Leu Ser
130 135 140

Arg Pro Leu Ile Pro Val Pro Phe Ala Glu Pro Ala Gly Asp Tyr Thr
145 150 155 160

Val Leu Ile Gly Asp Trp Tyr Lys Ala Asn His Thr Thr Leu Ile Ala
165 170 175

Thr Leu Asp Arg Gly Lys Lys Leu Lys Tyr Pro Asp Gly Ile Leu Ile
180 185 190

Asn Gly Arg Gly Pro Asn Gly Ile Ser Phe Asp Val Gln Gln Gly Lys
195 200 205

Thr Tyr Arg Leu Arg Ile Ser Asn Val Gly Leu Met Asn Ser Leu Asn
210 215 220

Phe Arg Ile Gln Gly His Lys Met Leu Leu Val Glu Val Glu Gly Thr
225 230 235 240

His Val Met Gln Thr His Phe Ser Ser Leu Asp Val His Val Gly Gln
245 250 255

Ser Tyr Ser Val Leu Val Thr Ala Asp Gln Pro Ala Gln Asp Tyr Tyr
260 265 270

Ile Val Val Ser Thr Arg Phe Ser Ser Gln Ile Leu Thr Thr Thr Gly
275 280 285

Ile Leu Arg Tyr Ser Asn Ser Ala Gly Pro Val Ser Gly Pro Pro Pro
290 295 300

Gly Gly Pro Thr Ile Gln Ile Asp Trp Ser Leu Asn Gln Ala Arg Ala
305 310 315 320

Ile Arg Thr Asn Leu Thr Ala Ser Gly Pro Arg Pro Asn Pro Gln Gly
325 330 335

Ser Tyr His Tyr Gly Leu Ile Thr Pro Thr Arg Thr Ile Arg Leu Ser
340 345 350

Ser Ser Ala Gly Gln Val Asn Gly Lys Gln Arg Tyr Ala Val Asn Ser
355 360 365

Val Ser Phe Ile Pro Ala Asp Thr Pro Leu Lys Leu Ala Asp Tyr Phe
370 375 380

Asn Ile Gly Gly Val Phe Arg Val Asn Ser Ile Ser Asp Arg Pro Thr
385 390 395 400

Gly Gly Gly Ile Tyr Leu Asp Thr Ala Val Leu Gly Val Asp Tyr Arg
405 410 415

Ala Phe Val Glu Ile Val Phe Glu Asn Asn Glu Asn Ile Val Gln Ser
420 425 430

Trp His Leu Asp Gly Tyr Ser Phe Phe Val Val Gly Met Asp Gly Gly
435 440 445

Gln Trp Thr Thr Ala Ser Arg Asn Gln Tyr Asn Leu Arg Asp Ala Val
450 455 460

Phe Arg Ser Thr Thr Gln Val Tyr Pro Tyr Ser Trp Thr Ala Ile Tyr
465 470 475 480

Val Ala Leu Asp Asn Val Gly Met Trp Asn Leu Arg Thr Glu Phe Trp
485 490 495

Ala Arg His Tyr Leu Gly Gln Gln Leu Tyr Leu Arg Val Tyr Thr Thr
500 505 510

Ser Thr Ser Leu Arg Asp Glu Phe Pro Ile Pro Lys Asn Ala Leu Leu
515 520 525

Cys Gly Arg Ala Gln Gly Arg His Thr Arg Pro Phe
530 535 540

<210> 177
<211> 538
<212> PRT
<213> Amaranthus

<400> 177

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

Val Val Ala Asp Asp Pro Tyr Arg Phe Phe Asn Trp Asn Val Thr Tyr
20 25 30

Gly Asp Ile Tyr Pro Leu Gly Val Arg Gln Gln Gly Ile Leu Ile Asn
35 40 45

Gly Gln Phe Pro Gly Pro Asp Ile His Ser Val Thr Asn Asp Asn Leu
50 55 60

Ile Ile Asn Val Phe Asn Ser Leu Asp Val Pro Phe Leu Leu Ser Trp
65 70 75 80

Asn Gly Ile Gln Asn Arg Arg Asn Ser Phe Glu Asp Gly Val Tyr Gly
85 90 95

Thr Thr Cys Pro Ile Pro Pro Gly Lys Asn Phe Thr Tyr Ile Leu Gln
100 105 110

Val Lys Asp Gln Ile Gly Ser Phe Tyr Tyr Phe Pro Ser Leu Gly Phe
115 120 125

Gln Lys Ala Ala Gly Gly Phe Gly Gly Ile Arg Ile Leu Ser Arg Pro
130 135 140

Arg Ile Pro Val Pro Phe Pro Asp Pro Ala Gly Asp Tyr Thr Val Leu
145 150 155 160

Ile Gly Asp Trp Tyr Lys Ala Asn His Thr Asp Leu Gln Ala Thr Leu
165 170 175

Asp Ala Gly His Lys Leu Pro Pro Pro Asp Gly Ile Leu Ile Asn Gly
180 185 190

Arg Gly Ser Gly Ala Thr Ile Asn Val Glu Gln Gly Lys Thr Tyr Arg
195 200 205

Leu Arg Ile Ser Asn Val Gly Leu Gln Asn Ser Leu Asn Phe Arg Ile
210 215 220

Gln Gly His Lys Met Lys Val Val Glu Val Glu Gly Thr His Thr Leu
225 230 235 240

Gln Thr Thr Phe Ser Ser Leu Asp Val His Val Gly Gln Ser Tyr Ser
245 250 255

Val Leu Ile Thr Ala Asp Gln Pro Pro Arg Asp Tyr Tyr Val Val Ala
260 265 270

Ser Ser Arg Phe Thr Asn Pro Val Leu Thr Thr Thr Gly Phe Leu Arg
275 280 285

Tyr Ser Asn Ser Gly Gly Ser Val Gln Gly Pro Ile Pro Gly Gly Pro
290 295 300

Thr Ile Gln Ile Asp Trp Ser Leu Asn Gln Ala Arg Ala Ile Arg Thr
305 310 315 320

Asn Leu Thr Ala Ser Gly Pro Arg Pro Asn Pro Gln Gly Ser Tyr His
325 330 335

Tyr Gly Met Ile Asn Thr Thr Arg Thr Ile Arg Leu Gln Asn Ser Ala
340 345 350

Gly Gln Val Asn Gly Lys Gln Arg Tyr Ala Val Asn Ser Val Ser Phe
355 360 365

Ile Pro Ala Asp Thr Pro Leu Lys Leu Ala Asp Tyr Phe Lys Ile Gly
370 375 380

Gly Val Phe Ser Val Gly Ser Ile Pro Ser Asn Pro Thr Gly Ser Gly
385 390 395 400

Ile Tyr Leu Ala Thr Ser Val Met Gly Ala Asp Tyr Arg Ala Phe Ile
405 410 415

Glu Ile Val Phe Glu Asn Thr Glu Asp Ile Ile Gln Ser Trp His Leu
420 425 430

Asp Gly Tyr Ser Phe Phe Val Val Gly Met Asp Gly Gly Thr Trp Ser
435 440 445

Glu Ala Ser Arg Asn Gln Tyr Asn Leu Arg Asp Ala Val Phe Arg Cys
450 455 460

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

Asp Asn Val Gly Met Trp Asn Leu Arg Ser Glu Phe Trp Ala Arg Gln
485 490 495

Tyr Leu Gly Gln Gln Phe Tyr Leu Arg Val Tyr Thr Pro Ser Thr Ser
500 505 510

Leu Arg Asp Glu Tyr Pro Ile Pro Lys Asn Ala Leu Thr Cys Gly Arg
515 520 525

Ala Ala Gly Arg Arg Thr Arg Pro Ile Val
530 535

<210> 178
<211> 539
<212> PRT
<213> Cucumis sativus

<400> 178

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

Val Arg Ala Glu Asp Pro Tyr Arg Phe Phe Asp Trp Asn Val Thr Tyr
20 25 30

Gly Thr Ile Tyr Pro Leu Gly Leu Pro Gln Gln Gly Ile Leu Ile Asn
35 40 45

Gly Gln Phe Pro Gly Pro Asp Ile His Ser Val Thr Asn Asp Asn Ile
50 55 60

Ile Ile Asn Val Phe Asn Ser Leu Asp Glu Pro Phe Leu Leu Ser Trp
65 70 75 80

Asn Gly Ile Gln Gln Arg Arg Asn Ser Tyr Glu Asp Gly Val Tyr Gly
85 90 95

Thr Thr Cys Pro Ile Pro Pro Gly Lys Asn Phe Thr Tyr Ile Leu Gln
100 105 110

Met Lys Asp Gln Ile Gly Ser Phe Tyr Tyr Phe Pro Ser Leu Gly Phe
115 120 125

His Lys Ala Ala Gly Gly Phe Gly Gly Ile Arg Ile Leu Ser Arg Pro
130 135 140

Arg Ile Pro Val Pro Phe Pro Asp Pro Ala Gly Asp Tyr Thr Val Leu
145 150 155 160

Ile Gly Asp Trp Tyr Gln Ala Asn His Thr Thr Leu Arg Ala Gln Leu
165 170 175

Asp Asn Gly Ser Met Leu Pro Leu Pro Asp Gly Ile Leu Ile Asn Gly
180 185 190

Arg Gly Pro Asn Arg Thr Ala Ser Ile Asn Val Glu Gln Gly Lys Thr
195 200 205

Tyr Arg Leu Arg Ile Ser Asn Val Gly Leu Gln Ser Ser Leu Asn Phe
210 215 220

Arg Ile Gln Gly His Arg Met Lys Val Val Glu Val Glu Gly Thr His
225 230 235 240

Thr Leu Gln Thr Glu Phe Ser Ser Leu Asp Ile His Val Gly Gln Ser
245 250 255

Tyr Ser Val Leu Val Thr Ala Asp Gln Pro Ala Gln Asp Phe Tyr Ile
260 265 270

Val Val Ser Ser Arg Phe Thr Thr Pro Ile Leu Ser Thr Thr Ala Ile
275 280 285

Leu Arg Tyr Ala Asn Ser Ala Gly Ser Val Gln Gly Pro Pro Pro Gly
290 295 300

Gly Pro Thr Ile Gln Ile Asp Trp Ser Leu Asn Gln Ala Arg Ala Ile
305 310 315 320

Arg Thr Asn Leu Thr Ala Ser Gly Pro Arg Pro Asn Pro Gln Gly Ser
325 330 335

Tyr His Tyr Gly Met Ile Thr Thr Thr Arg Thr Ile Val Val Ala Asn
340 345 350

Ser Ala Gly Ile Val Asp Gly Lys Gln Arg Tyr Ala Val Asn Ser Val
355 360 365

Ser Phe Ile Pro Ala Asp Thr Pro Leu Lys Val Ala Asp Phe Phe Lys
370 375 380

Ile Gly Gly Val Phe Arg Val Gly Ser Ile Ser Asp Trp Pro Asn Gly
385 390 395 400

Gly Gly Ile Tyr Gln Asp Thr Ser Val Met Gly Ala Asp Tyr Arg Ala
405 410 415

Phe Val Glu Ile Val Phe Gln Asn Asn Glu Asp Leu Ile Gln Ser Trp
420 425 430

His Leu Asp Gly Tyr Ser Phe Phe Val Val Gly Met Asp Gly Gly Gln
435 440 445

Trp Thr Ser Asn Ser Arg Asn Gln Tyr Asn Leu Arg Asp Ala Ile Ala
450 455 460

Arg Cys Thr Val Gln Val Tyr Pro Lys Ser Trp Ser Ala Ile Tyr Val
465 470 475 480

Ala Leu Asp Asn Val Gly Met Trp Asn Ile Arg Thr Glu Phe Trp Ala
485 490 495

Arg Gln Tyr Leu Gly Gln Gln Phe Tyr Leu Arg Val Tyr Thr Pro Ser
500 505 510

Thr Ser Leu Arg Asp Glu Tyr Pro Ile Pro Lys Asn Ala Leu Leu Cys
515 520 525

Gly Arg Ala Thr Gly Arg Arg Thr Arg Pro Leu
530 535

<210> 179
<211> 541
<212> PRT
<213> Lactuca sativa

<400> 179

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

Ala Ile Ala Gly Ala Glu Asp Pro Tyr Arg Phe Phe Asn Trp Asn Val
20 25 30

Thr Tyr Gly Asp Ile Tyr Pro Leu Gly Val Arg Gln Gln Gly Ile Leu
35 40 45

Ile Asn Gly Gln Phe Pro Gly Pro Asp Ile His Ser Val Thr Asn Asp
50 55 60

Asn Leu Ile Ile Asn Val Phe Asn Ser Leu Thr Glu Pro Phe Leu Val

65 70 75 80

Ser Trp Asn Gly Val Gln Gln Arg Arg Asn Ser Tyr Glu Asp Gly Val
85 90 95

Phe Gly Thr Thr Cys Pro Ile Pro Pro Gly Lys Asn Phe Thr Tyr Ile
100 105 110

Leu Gln Val Lys Asp Gln Ile Gly Ser Phe Tyr Tyr Phe Pro Ser Leu
115 120 125

Ala Phe His Lys Ala Ala Gly Gly Phe Gly Gly Ile Arg Ile Leu Ser
130 135 140

Arg Pro Arg Ile Pro Val Pro Phe Asp Glu Pro Ala Gly Asp Tyr Thr
145 150 155 160

Val Leu Ile Gly Asp Trp Tyr Lys Ala Asn His Thr Thr Leu Lys Thr
165 170 175

Val Leu Asp Gly Gly His Lys Ile Pro Phe Pro Asp Gly Ile Leu Ile
180 185 190

Asn Gly Arg Gly Pro Gly Gly Ala Ser Phe Ala Val Glu Gln Gly Lys
195 200 205

Thr Tyr Arg Leu Arg Ile Ser Asn Val Gly Leu Gln Asn Ser Leu Asn

210 215 220

Phe Arg Ile Gln Asn His Lys Met Lys Leu Val Glu Val Glu Gly Thr
225 230 235 240

His Thr Val Gln Gln Thr Tyr Ser Ser Leu Asp Val His Cys Gly Gln
245 250 255

Ser Tyr Ser Val Leu Ile Thr Ala Asp Gln Pro Gly Gln Asp Tyr Tyr
260 265 270

Ile Val Val Ser Ser Arg Phe Thr Thr Pro Ile Leu Thr Thr Thr Gly
275 280 285

Val Leu His Tyr Ala Asn Ser Ala Gly Gln Pro Ser Gly Pro Ile Pro
290 295 300

Gly Gly Pro Thr Ile Gln Val Asp Trp Ser Leu Asn Gln Ala Arg Ser
305 310 315 320

Ile Arg Thr Asn Leu Thr Ala Ser Gly Pro Arg Pro Asn Pro Gln Gly
325 330 335

Ser Tyr His Tyr Gly Met Ile Asn Thr Ser Arg Thr Ile Val Leu Gln
340 345 350

Ser Ser Ala Gly Gln Val Gly Gly Lys Gln Arg Tyr Gly Ile Asn Ser

355 360 365

Val Ser Phe Lys Pro Ser Asp Asp Thr Pro Leu Lys Leu Ala Asp Tyr
370 375 380

Phe Asn Ile Gly Gly Val Phe Arg Val Gly Ser Ile Ser Asp Arg Pro
385 390 395 400

Thr Gly Gly Gly Leu Tyr Thr Asp Thr Ser Val Met Gly Ala Asp Tyr
405 410 415

Arg Ala Phe Val Glu Ile Val Phe Glu Asn Pro Ser Asp Ile Val Leu
420 425 430

Ser Tyr His Ile Asp Gly Tyr Gln Phe Phe Val Val Gly Met Asp Gly
435 440 445

Gly Glu Trp Thr Gln Ala Ser Arg Ala Gly Tyr Asn Leu Arg Asp Gly
450 455 460

Val Ala Arg Ser Thr Ile Gln Val Tyr Pro Lys Ser Trp Ser Ala Leu
465 470 475 480

Tyr Val Gly Leu Asp Asn Val Gly Met Trp Asn Val Arg Thr Glu Phe
485 490 495

Trp Ala Arg Gln Tyr Leu Gly Glu Gln Phe Tyr Leu Arg Val Tyr Thr

500 505 510

Asn Ser Gly Ser Ile Arg Asp Glu Phe Pro Ile Pro Lys Asn Ala Arg
515 520 525

Val Cys Gly Lys Ala Thr Gly Arg His Thr Arg Pro Leu
530 535 540

<210> 180
<211> 162
<212> PRT
<213> Brassica rapa

<400> 180

Val Phe Ser Ile Leu Phe Thr Val Thr Ala Glu Asp Pro Tyr Arg Phe
1 5 10 15

Phe Asn Trp Asn Val Thr Tyr Gly Asp Ile Tyr Pro Leu Gly Val Arg
20 25 30

Gln Gln Gly Ile Leu Ile Asp Gly Lys Phe Pro Gly Pro Asp Ile His
35 40 45

Ser Val Thr Asn Asp Asn Leu Val Ile Asn Ile Phe Asn Asn Leu Asp
50 55 60

Glu Pro Phe Leu Leu Ser Trp Asn Gly Val Gln Gln Arg Arg Asn Ser
65 70 75 80

Tyr Val Asp Gly Val Tyr Gly Thr Thr Cys Pro Ile Pro Pro Gly Lys
85 90 95

Asn Tyr Thr Tyr Met Leu Gln Val Lys Asp Gln Ile Gly Ser Phe Tyr
100 105 110

Tyr Phe Pro Ser Leu Ala Phe His Lys Ala Ala Gly Gly Phe Gly Gly
115 120 125

Ile Arg Ile Leu Ser Arg Pro Arg Ile Pro Val Pro Phe Leu Thr Pro
130 135 140

Pro Glu Ile Thr Leu Phe Ser Ser Glu Thr Gly Thr Asn Pro Ile Thr
145 150 155 160

Arg Ile

<210> 181
<211> 547
<212> PRT
<213> Populus

<400> 181

Met Pro Leu Asn Leu Ala Gly Lys Thr Ala Val Leu Cys Thr Phe Leu
1 5 10 15

Cys Val Ser Val Ser Ile Ile Ser Ser Val Lys Ala Glu Asp Pro Tyr
20 25 30

Arg Phe Phe Asp Trp Asn Val Thr Tyr Gly Phe Ile Tyr Pro Leu Gly
35 40 45

Val Arg Gln Gln Gly Ile Leu Ile Asn Gly Gln Phe Pro Gly Pro Asp
50 55 60

Ile His Ser Val Thr Asn Asp Asn Leu Ile Ile Asn Val Tyr Asn Ser
65 70 75 80

Leu Asp Glu Pro Phe Leu Leu Ser Trp Asn Gly Ile Gln Gln Arg Arg
85 90 95

Asn Ser Phe Glu Asp Gly Val Ile Gly Thr Thr Cys Pro Ile Pro Pro
100 105 110

Gly Lys Asn Phe Thr Tyr Ile Leu Gln Val Lys Asp Gln Ile Gly Ser
115 120 125

Phe Tyr Tyr Phe Pro Ser Leu Gly Phe His Lys Ala Ala Gly Gly Phe
130 135 140

Gly Gly Ile Arg Ile Leu Ser Arg Pro Arg Ile Pro Val Pro Phe Asp
145 150 155 160

Asp Pro Ala Gly Asp Tyr Thr Ile Leu Ile Gly Asp Trp Tyr Leu Ser
165 170 175

Asn His Thr Asp Leu Lys Ala Val Leu Asp Gly Gly Arg Lys Leu Pro
180 185 190

Phe Pro Asp Gly Ile Leu Ile Asn Gly Arg Gly Arg Asn Gly Tyr Tyr
195 200 205

Leu Thr Val Glu Gln Gly Lys Thr Tyr Arg Leu Arg Ile Ser Asn Val
210 215 220

Gly Leu Gln Asn Ser Leu Asn Phe Arg Ile Gln Asn His Lys Met Lys
225 230 235 240

Leu Val Glu Val Glu Gly Thr His Thr Leu Gln Thr Thr Tyr Ser Ser
245 250 255

Leu Asp Val His Val Gly Gln Ser Tyr Ser Val Leu Phe Thr Ala Asp
260 265 270

Gln Pro Gly Gln Asp Tyr Tyr Ile Val Val Thr Ser Arg Phe Thr Ser
275 280 285

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

Ala Val Ser Gly Pro Phe Pro Gly Gly Pro Thr Ile Glu Val Asp Trp
305 310 315 320

Ser Leu Asn Gln Ala Arg Ser Ile Arg Thr Asn Leu Thr Ala Ser Gly
325 330 335

Pro Arg Pro Asn Pro Gln Gly Ser Tyr His Tyr Gly Met Ile Asn Thr
340 345 350

Thr Arg Thr Ile Ile Val Ala Asn Ser Ala Gly Gln Val Asn Gly Asn
355 360 365

Gln Arg Tyr Gly Val Asn Ser Val Ser Phe Ile Ala Pro Asp Thr Pro
370 375 380

Met Lys Ile Ala Asp Tyr Phe Lys Ile Gln Gly Val Phe Lys Glu Asn
385 390 395 400

Gly Ile Thr Asp Arg Pro Tyr Gly Gly Gly Leu Tyr Leu Asp Thr Ala
405 410 415

Val Leu Thr Val Pro Tyr Arg Ala Tyr Val Glu Ile Val Phe Gln Asn
420 425 430

Asp Glu Asp Ile Leu Gln Ser Trp His Leu Asp Gly Tyr Ser Phe Phe
435 440 445

Val Val Gly Met Asp Gly Gly Gln Trp Thr Thr Ala Ser Arg Asp Gln
450 455 460

Tyr Asn Leu Arg Asp Ala Val Ala Arg Cys Thr Thr Gln Val Tyr Pro
465 470 475 480

Lys Ala Trp Thr Ala Ile Tyr Ile Pro Leu Asp Asn Val Gly Met Trp
485 490 495

Asn Leu Arg Thr Glu Phe Trp Ala Arg Gln Tyr Leu Gly Gln Gln Phe
500 505 510

Tyr Leu Arg Val Tyr Thr Asp Ser Thr Ser Leu Arg Asp Glu Phe Pro
515 520 525

Ile Pro Lys Asn Ala Leu Leu Cys Gly Arg Ala Ser Gly Arg Arg Thr
530 535 540

Arg Pro Leu
545

<210> 182
<211> 538
<212> PRT
<213> Glycine max

<400> 182

Met Pro Leu Lys Leu Ala Gly Val Ala Thr Val Gly Ser Leu Leu Leu
1 5 10 15

Cys Val Ala Ile Ser Leu Phe His Ile Ala Gly Ala Glu Asp Pro Tyr
20 25 30

Arg Phe Phe Asn Trp Asn Ile Thr Tyr Gly Asp Ile Tyr Pro Leu Gly
35 40 45

Val Arg Gln Thr Gly Ile Leu Ile Asn Gly Gln Phe Pro Gly Pro Asp
50 55 60

Ile His Ser Val Thr Asn Asp Asn Leu Ile Ile Asn Val Phe Asn Ser
65 70 75 80

Leu Asp Glu Pro Phe Leu Leu Ser Trp Asn Gly Ile Gln Gln Arg Arg
85 90 95

Asn Ser Phe Glu Asp Gly Val Phe Gly Thr Thr Cys Pro Ile Pro Ala
100 105 110

Gly Lys Asn Phe Thr Tyr Ile Leu Gln Val Lys Asp Gln Ile Gly Thr
115 120 125

Phe Tyr Tyr Phe Pro Ser Leu Ala Phe His Lys Ala Ala Gly Gly Phe
130 135 140

Gly Gly Ile Arg Ile Leu Ser Arg Pro Arg Ile Pro Val Pro Phe Pro
145 150 155 160

Asp Pro Ala Gly Asp Tyr Thr Val Leu Ile Gly Asp Trp Tyr Lys Ser
165 170 175

Asn His Thr Thr Leu Lys Ala Arg Leu Asp Arg Gly Lys Lys Leu Pro
180 185 190

Phe Pro Asp Gly Ile Leu Ile Asn Gly Arg Gly Pro Asn Gly Val Ser
195 200 205

Phe Asn Val Glu Gln Gly Lys Thr Tyr Arg Leu Arg Ile Ser Asn Val
210 215 220

Gly Leu Gln His Ser Leu Asn Phe Arg Ile Gln Asn His Lys Met Lys
225 230 235 240

Leu Val Glu Val Glu Gly Thr His Thr Leu Gln Thr Met Tyr Ser Ser
245 250 255

Leu Asp Val His Val Gly Gln Ser Tyr Ser Val Leu Val Thr Ala Asp
260 265 270

Gln Pro Ala Gln Asp Tyr Tyr Ile Val Val Ser Thr Arg Phe Ser Tyr
275 280 285

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

Pro Val Ser Gly Pro Pro Pro Gly Gly Pro Thr Ile Gln Ile Asp Trp
305 310 315 320

Ser Leu Asn Gln Ala Arg Ser Ile Arg Thr Asn Leu Thr Ala Ser Gly
325 330 335

Pro Arg Pro Asn Pro Gln Gly Ser Tyr His Tyr Gly Met Ile Asn Thr
340 345 350

Thr Lys Thr Ile Ile Leu Ala Ser Ser Ala Gly Gln Val Asn Gly Lys
355 360 365

Gln Arg Tyr Ala Ile Asn Ser Val Ser Tyr Val Val Pro Asp Thr Pro
370 375 380

Leu Lys Leu Ala Asp Tyr Phe Lys Ile Ser Gly Val Phe Arg Pro Gly
385 390 395 400

Ser Ile Ser Asp Arg Pro Thr Gly Gly Gly Ile Tyr Leu Asp Thr Ser
405 410 415

Val Leu Gln Ala Asp Tyr Arg Asn Phe Val Glu Ile Val Phe Gln Asn
420 425 430

Asn Glu Asn Ile Val Gln Ser Tyr His Leu Asp Gly Tyr Ser Phe Phe
435 440 445

Val Val Gly Met Asp Gly Gly Gln Trp Thr Thr Ala Ser Arg Asn Gln
450 455 460

Tyr Asn Leu Arg Asp Ala Val Ala Arg Cys Thr Thr Gln Val Tyr Pro
465 470 475 480

Phe Ser Trp Thr Ala Ile Tyr Ile Ala Leu Asp Asn Val Gly Met Trp
485 490 495

Asn Leu Arg Ser Glu Phe Trp Ala Arg Gln Tyr Leu Gly Gln Gln Leu
500 505 510

Tyr Leu Arg Val Tyr Thr Asn Asn Thr Asn Leu Asn Gln Arg Arg Val
515 520 525

Pro Cys Ser Lys Glu Cys Asn Ser Leu Trp
530 535

<210> 183
<211> 543
<212> PRT
<213> Eucalyptus

<400> 183

Met Arg Gln Gly Leu Glu Gly Ala Gly Ala Leu Phe Leu Cys Ala Cys

1 5 10 15

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

Asn Trp Asn Val Thr Tyr Gly Asp Ile Tyr Pro Leu Gly Val Arg Gln
35 40 45

Gln Gly Ile Leu Ile Asn Gly Gln Phe Pro Gly Pro Asp Ile Tyr Ser
50 55 60

Val Thr Asn Asp Asn Leu Ile Ile Asn Val Ile Asn Ser Leu Asn Glu
65 70 75 80

Pro Phe Leu Leu Ser Trp Asn Gly Ile Gln Gln Arg Arg Asn Ser Phe
85 90 95

Glu Asp Gly Val Tyr Gly Thr Thr Cys Pro Ile Pro Pro Gly Lys Asn
100 105 110

Phe Thr Tyr Ile Leu Gln Val Lys Asp Gln Ile Gly Ser Phe Tyr Tyr
115 120 125

Phe Pro Ser Leu Ala Phe His Lys Ala Ala Gly Gly Phe Gly Gly Ile
130 135 140

Arg Ile Leu Ser Arg Pro Leu Ile Pro Val Pro Phe Pro Pro Pro Ala

145 150 155 160

Gly Asp Tyr Thr Ile Leu Ile Gly Asp Trp Tyr Lys Ala Asn His Thr
165 170 175

Asp Leu Arg Ala Ile Leu Asp Asn Gly Lys Val Leu Pro Phe Pro Asp
180 185 190

Gly Ile Leu Ile Asn Gly Arg Gly Ser Gly Ala Ser Phe Thr Val Glu
195 200 205

Gln Gly Lys Thr Tyr Arg Leu Arg Ile Ser Asn Val Gly Leu Met Asn
210 215 220

Ser Leu Asn Phe Arg Ile Gln Gly His Lys Met Val Leu Ala Glu Val
225 230 235 240

Glu Gly Thr His Thr Val Gln Asn Thr Tyr Glu Ser Leu Asp Val His
245 250 255

Val Gly Gln Ser Leu Ser Val Leu Val Thr Ala Asp Gln Pro Gly Lys
260 265 270

Asp Tyr Tyr Ile Val Val Ser Ser Arg Phe Thr Thr Gln Val Leu Thr
275 280 285

Thr Thr Gly Val Leu His Tyr Ser Asn Ser Ala Gly Pro Val Ser Gly

290 295 300

Pro Val Pro Gly Gly Pro Thr Thr Gln Ile Asp Trp Ser Leu Asn Gln
305 310 315 320

Ala Arg Ser Ile Arg Thr Asn Leu Thr Ala Ser Gly Pro Arg Pro Asn
325 330 335

Pro Gln Gly Ser Tyr His Tyr Gly Met Ile Asn Thr Thr Arg Thr Ile
340 345 350

Arg Leu Ala Asn Ser Ala Gly Pro Val Asn Gly Lys Gln Arg Tyr Ala
355 360 365

Val Asn Ser Val Ser Phe Ile Pro Ala Asp Thr Pro Leu Lys Leu Ala
370 375 380

Asp Tyr Phe Lys Ile Asp Gly Val Phe Arg Val Gly Ser Ile Ser Asp
385 390 395 400

Asn Pro Thr Gly Ser Gly Ile Tyr Leu Asp Thr Ser Val Met Arg Val
405 410 415

Asp Tyr Arg Ala Tyr Ile Glu Ile Val Phe Glu Asn Ser Glu Asp Thr
420 425 430

Ile Gln Ser Trp His Leu Asn Gly Tyr Ala Phe Phe Val Val Gly Met

435 440 445

Asp Gly Gly Gln Trp Thr Pro Ala Ser Arg Asn Gln Tyr Asn Leu Arg
450 455 460

Asp Gly Val Ser Arg Cys Thr Ile Gln Val Tyr Pro Lys Ser Trp Ser
465 470 475 480

Ala Ile Tyr Ile Pro Leu Asp Asn Val Gly Met Trp Asn Leu Arg Ser
485 490 495

Glu Ser Trp Ala Arg Gln Tyr Leu Gly Gln Gln Phe Tyr Met Gln Val
500 505 510

Tyr Thr Thr Ser Thr Ser Leu Arg Asp Glu Tyr Pro Ile Pro Lys Asn
515 520 525

Ala Ile Leu Cys Gly Arg Ala Ser Gly Arg His Thr Arg Pro Leu
530 535 540

<210> 184
<211> 541
<212> PRT
<213> Arabidopsis

<400> 184

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

Leu Leu Phe Ala Val Thr Ala Glu Asp Pro Tyr Arg Phe Phe Glu Trp
20 25 30

Asn Ile Thr Tyr Gly Asp Ile Tyr Pro Leu Gly Val Arg Gln Gln Gly
35 40 45

Ile Leu Ile Asn Gly Ala Phe Pro Gly Pro Asp Ile His Ser Val Thr
50 55 60

Asn Asp Asn Leu Ile Ile Asn Val Tyr Asn Ser Leu Asp Glu Pro Phe
65 70 75 80

Leu Leu Ser Trp Asn Gly Ile Gln Gln Arg Arg Asn Ser Phe Val Asp
85 90 95

Gly Val Tyr Gly Thr Thr Cys Pro Ile Pro Pro Gly Lys Asn Tyr Thr
100 105 110

Tyr Ile Leu Gln Met Lys Asp Gln Ile Gly Ser Phe Tyr Tyr Phe Pro
115 120 125

Ser Leu Gly Phe His Lys Ala Ala Gly Gly Phe Gly Gly Ile Arg Ile
130 135 140

Leu Ser Arg Pro Arg Ile Pro Val Pro Phe Pro Asp Pro Ala Gly Asp
145 150 155 160

Thr Thr Val Leu Ile Gly Asp Trp Tyr Lys Ala Asn His Thr Asp Leu
165 170 175

Arg Ala Gln Leu Asp Asn Gly Lys Lys Leu Pro Leu Pro Asp Gly Ile
180 185 190

Leu Ile Asn Gly Arg Ser Ser Gly Ala Thr Leu Asn Val Glu Gln Gly
195 200 205

Lys Thr Tyr Arg Phe Arg Ile Ser Asn Val Gly Leu Gln Asp Ser Leu
210 215 220

Asn Phe Arg Ile Gln Asp His Lys Met Lys Val Val Glu Val Glu Gly
225 230 235 240

Thr His Thr Leu Gln Thr Thr Phe Ser Ser Leu Asp Val His Val Gly
245 250 255

Gln Ser Tyr Ser Val Leu Val Thr Ala Asp Gln Thr Pro Arg Asp Tyr
260 265 270

Tyr Val Val Val Ser Ser Arg Phe Thr Ser Asn Val Leu Thr Thr Thr
275 280 285

Gly Ile Phe Arg Tyr Ser Asn Ser Ala Gly Gly Val Ser Gly Pro Ile
290 295 300

Pro Gly Gly Pro Thr Ile Gln Ile Asp Trp Ser Leu Asn Gln Ala Arg
305 310 315 320

Ala Ile Arg Thr Asn Leu Ser Ala Ser Gly Pro Arg Pro Asn Pro Gln
325 330 335

Gly Ser Tyr His Tyr Gly Met Ile Asn Thr Thr Arg Thr Ile Arg Leu
340 345 350

Ala Ser Ser Ala Gly Gln Val Asp Gly Lys Gln Arg Tyr Ala Val Asn
355 360 365

Ser Val Ser Phe Lys Pro Ala Asp Thr Pro Leu Lys Ile Ala Asp Tyr
370 375 380

Phe Lys Ile Asp Gly Val Tyr Arg Ser Gly Ser Ile Gln Tyr Gln Pro
385 390 395 400

Thr Gly Gly Gly Ile Tyr Leu Asp Thr Ser Val Met Gln Val Asp Tyr
405 410 415

Arg Thr Phe Val Glu Ile Ile Phe Glu Asn Ser Glu Asp Ile Val Gln
420 425 430

Ser Trp His Leu Asp Gly Tyr Ser Phe Trp Val Val Gly Met Asp Gly
435 440 445

Gly Gln Trp Ser Pro Asp Ser Arg Asn Glu Tyr Asn Leu Arg Asp Ala
450 455 460

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

Leu Ile Ala Leu Asp Asn Val Gly Met Trp Asn Leu Arg Ser Glu Phe
485 490 495

Trp Ala Arg Gln Tyr Leu Gly Gln Gln Leu Tyr Leu Arg Val Tyr Thr
500 505 510

Pro Ser Thr Ser Leu Arg Asp Glu Tyr Pro Ile Pro Lys Asn Ala Leu
515 520 525

Leu Cys Gly Arg Ala Ser Gly Arg Ser Thr Arg Pro Leu
530 535 540

<210> 185
<211> 546
<212> PRT
<213> Castanea

<400> 185

Met Pro Leu Asn Leu Ala Gly Gly Val Leu Ser Gly Ala Val Leu Cys
1 5 10 15

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

Phe Phe Asn Trp Asn Val Thr Tyr Gly Asp Ile Tyr Pro Leu Gly Val
35 40 45

Arg Gln Gln Gly Ile Leu Ile Asn Gly Gln Phe Pro Gly Pro Asp Ile
50 55 60

His Ser Val Thr Asn Asp Asn Leu Ile Ile Asn Val Phe Asn Ser Leu
65 70 75 80

Asp Glu Pro Phe Leu Leu Ser Trp Asn Gly Ile Gln Asn Arg Arg Asn
85 90 95

Ser Phe Glu Asp Gly Val Asn Gly Thr Thr Cys Pro Ile Pro Pro Gly
100 105 110

Gln Asn Phe Thr Tyr Ile Leu Gln Val Lys Asp Gln Ile Gly Ser Phe
115 120 125

Tyr Tyr Tyr Pro Ser Leu Ala Phe His Lys Ala Ala Gly Gly Phe Gly
130 135 140

Gly Ile Arg Ile Leu Ser Arg Pro Arg Ile Pro Val Pro Phe Pro Asp
145 150 155 160

Pro Ala Gly Asp Tyr Thr Val Leu Ile Gly Asp Trp Tyr Lys Ala Asn
165 170 175

His Thr Asp Leu Lys Asp Ile Leu Asp Arg Gly Lys Lys Leu His Phe
180 185 190

Pro Asp Gly Ile Leu Ile Asn Gly Arg Gly Pro Gly Gly Ala Tyr Tyr
195 200 205

Thr Val Glu Gln Gly Lys Thr Tyr Arg Phe Arg Ile Ser Asn Val Gly
210 215 220

Leu Gln His Ser Leu Asn Phe Arg Ile Gln Gly His Arg Leu Thr Leu
225 230 235 240

Val Glu Val Glu Gly Thr His Thr Leu Gln Thr Ser Tyr Ser Ser Leu
245 250 255

Asp Val His Val Gly Gln Ser Tyr Ser Val Leu Val Thr Met Asp Gln
260 265 270

Pro Gly Gln Asp Tyr Tyr Ile Val Val Ser Ser Arg Phe Ser Thr Pro
275 280 285

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

Val Ser Gly Pro Pro Pro Gly Gly Pro Thr Ile Gln Val Asp Trp Ser
305 310 315 320

Leu Asn Gln Ala Arg Ser Ile Arg Thr Asn Leu Thr Ala Ser Gly Pro
325 330 335

Arg Pro Asn Pro Gln Gly Ser Tyr His Tyr Gly Leu Ile Asn Thr Thr
340 345 350

Lys Thr Ile Arg Leu Gln Asn Ser Ala Gly Leu Val Ser Gly Lys Gln
355 360 365

Arg Tyr Ala Val Asn Ser Val Ser Tyr Val Ala Ala Asp Thr Pro Leu
370 375 380

Lys Ile Ala Asp Tyr Phe Gln Ile Gln Gly Val Phe Arg Val Gly Ser
385 390 395 400

Ile Ser Ser Asn Pro Thr Gly Gly Gly Ile Tyr Leu Asp Thr Ala Val
405 410 415

Met Gly Ala Asp Tyr Arg Ala Phe Ile Glu Ile Val Phe Glu Asn Thr
420 425 430

Glu Asp Ile Ile Gln Ser Trp His Leu Asn Gly Tyr Ser Phe Trp Val
435 440 445

Val Gly Met Asp Gly Gly Leu Trp Thr Thr Ala Ser Arg Asn Gln Tyr
450 455 460

Asn Leu Arg Asp Ala Val Ser Arg Val Thr Thr Gln Val Tyr Pro Lys
465 470 475 480

Ser Trp Thr Ala Ile Tyr Leu Ala Leu Asp Asn Val Gly Met Trp Asn
485 490 495

Leu Arg Thr Glu Phe Trp Ala Arg Gln Tyr Leu Gly Gln Gln Phe Tyr
500 505 510

Leu Arg Val Tyr Thr Pro Thr Thr Ser Ile Arg Asp Glu Phe Pro Ile
515 520 525

Pro Lys Asn Ala Leu Leu Cys Gly Arg Ala Lys Gly Arg His Thr Arg
530 535 540

Pro Leu
545

<210> 186
<211> 540
<212> PRT
<213> Nicotiana tabacum

<400> 186

Met Val Pro Leu Lys Leu Ala Ile Ala Ala Phe Leu Val Val Gly Leu
1 5 10 15

Val Val Asn Thr Val Ala Glu Asp Pro Tyr Arg Phe Phe Glu Trp Asn
20 25 30

Val Thr Tyr Gly Thr Ile Tyr Pro Leu Gly Val Pro Gln Gln Gly Ile
35 40 45

Leu Ile Asn Gly Gln Phe Pro Gly Pro Asp Ile Tyr Ser Val Thr Asn
50 55 60

Asp Asn Leu Ile Ile Asn Val Phe Asn Ser Leu Asp Glu Pro Phe Leu
65 70 75 80

Leu Ser Trp Asn Gly Ile Gln Asn Arg Arg Asn Ser Phe Glu Asp Gly
85 90 95

Val Tyr Gly Thr Thr Cys Pro Ile Pro Pro Gly Lys Asn Phe Thr Tyr
100 105 110

Ile Leu Gln Met Lys Asp Gln Ile Gly Ser Tyr Tyr Tyr Phe Pro Ser
115 120 125

Leu Ala Phe His Lys Ala Ala Gly Gly Phe Gly Gly Ile Lys Ile Leu
130 135 140

Ser Arg Pro Arg Ile Pro Val Pro Phe Pro Asp Pro Ala Asp Asp Tyr
145 150 155 160

Thr Val Leu Ile Gly Asp Trp Tyr Lys Lys Asn His Thr Ala Leu Lys
165 170 175

Ala Ile Leu Asp Gly Gly Lys Lys Leu Pro Phe Pro Asp Gly Ile Leu
180 185 190

Ile Asn Gly Arg Gly Pro Asn Gly Val Ser Phe Thr Val Glu Gln Gly
195 200 205

Lys Thr Tyr Arg Leu Arg Ile Ser Asn Val Gly Leu Gln Asn Ser Leu
210 215 220

Asn Phe Arg Ile Glu Gly His Lys Met Lys Leu Val Glu Val Glu Gly
225 230 235 240

Thr His Thr Leu Gln Thr Thr Tyr Ser Ser Leu Asp Val His Val Gly
245 250 255

Gln Thr Tyr Ser Val Leu Ile Thr Ala Asp Gln Glu Ala Lys Asp His
260 265 270

Tyr Ile Val Val Ser Ser Arg Phe Thr Ser Pro Val Leu Thr Thr Thr
275 280 285

Gly Val Leu His Tyr Ser Asn Ser Asn Thr Pro Val Ser Gly Pro Pro
290 295 300

Pro Gly Gly Pro Thr Ile Gln Ile Asp Trp Ser Leu Asn Gln Ala Arg
305 310 315 320

Ser Ile Arg Thr Asn Leu Ser Ala Ser Gly Pro Arg Pro Asn Pro Gln
325 330 335

Gly Ser Tyr His Tyr Gly Met Ile Asn Thr Thr Arg Thr Ile Arg Leu
340 345 350

Ala Ser Ser Ala Gly Gln Val Asn Gly Lys Gln Arg Tyr Ala Val Asn
355 360 365

Ser Val Ser Phe Val Pro Leu Asp Thr Pro Leu Lys Leu Leu Asp Tyr
370 375 380

Phe Lys Val Gly Gly Phe Arg Val Gly Ser Ile Ser Asp Ala Pro Ser
385 390 395 400

Gly Gly Gly Ile Phe Leu Asp Thr Ser Val Leu Gly Ala Asp Tyr Arg
405 410 415

Gln Phe Ile Glu Ile Val Phe Glu Asn Asn Glu Asp Ile Val Gln Ser
420 425 430

Trp His Leu Asn Gly Tyr Ser Phe Trp Val Val Gly Met Asp Gly Gly
435 440 445

Gln Trp Thr Gln Ala Ser Arg Asn Gly Tyr Asn Leu Arg Asp Ala Val
450 455 460

Ala Arg Cys Thr Thr Gln Val Tyr Pro Lys Ser Trp Thr Ala Ile Tyr
465 470 475 480

Ile Ala Leu Asp Asn Val Gly Met Trp Asn Leu Arg Thr Glu Phe Trp
485 490 495

Ala Arg Gln Tyr Leu Gly Gln Gln Leu Tyr Met Arg Val Tyr Thr Thr
500 505 510

Ser Thr Ser Leu Arg Asp Glu Tyr Pro Ile Pro Arg Asn Ala Arg Leu
515 520 525

Cys Gly Lys Val Ala Gly Arg His Thr Arg Pro Leu
530 535 540

<210> 187
<211> 540
<212> PRT
<213> Helianthus annuus

<400> 187

Met Pro Arg Asn Val Ala Val Leu Ile Ala Val Gly Ala Val Leu Val

1 5 10 15

Ala Ile Ala Gly Ala Glu Asp Pro Tyr Arg Phe Phe Thr Trp Asn Val
20 25 30

Thr Tyr Gly Asp Ile Tyr Pro Leu Gly Val Arg Gln Gln Gly Ile Leu
35 40 45

Ile Asn Gly Gln Phe Pro Gly Pro Asp Ile His Ser Val Thr Asn Asp
50 55 60

Asn Leu Ile Ile Asn Val Phe Asn Ser Leu Pro Glu Pro Phe Leu Ile
65 70 75 80

Ser Trp Asn Gly Ile Gln Gln Arg Arg Asn Ser Phe Glu Asp Gly Val
85 90 95

Tyr Gly Thr Thr Cys Pro Ile Pro Pro Gly Lys Asn Phe Thr Tyr Ile
100 105 110

Leu Gln Val Lys Asp Gln Ile Gly Ser Phe Tyr Tyr Phe Pro Ser Leu
115 120 125

Ala Phe His Lys Ala Ala Gly Gly Phe Gly Gly Ile Arg Ile Leu Ser
130 135 140

Arg Pro Arg Ile Pro Val Pro Phe Asp Glu Pro Ala Gly Asp Phe Thr

145 150 155 160

Val Leu Ile Gly Asp Trp Tyr Lys Ala Asn His Thr Ile Leu Arg Arg
165 170 175

Val Leu Asp Ala Gly His Arg Ile Pro Phe Pro Ala Gly Ile Leu Ile
180 185 190

Asn Gly Arg Gly Pro Gly Gly Ala Ser Phe Thr Val Glu Gln Gly Lys
195 200 205

Thr Tyr Arg Leu Arg Ile Ser Asn Val Gly Leu Gln Asn Ser Leu Asn
210 215 220

Phe Arg Ile Gln Asn His Lys Met Lys Leu Val Glu Val Glu Gly Thr
225 230 235 240

His Thr Val Gln Gln Thr Tyr Ser Ser Leu Asp Val His Leu Gly Gln
245 250 255

Ser Tyr Ser Val Leu Phe Thr Ala Asp Gln Pro Gly Gln Asp Tyr Tyr
260 265 270

Ile Val Val Ser Ser Arg Phe Thr Thr Pro Ile Leu Thr Thr Thr Gly
275 280 285

Val Leu His Tyr Ser Asn Ser Ala Gly Gln Val Ser Gly Pro Ile Pro

290 295 300

Gly Gly Pro Thr Ile Gln Val Asp Trp Ser Leu Asn Gln Ala Arg Ser
305 310 315 320

Ile Arg Thr Asn Leu Thr Ala Ser Gly Pro Arg Pro Asn Pro Gln Gly
325 330 335

Ser Tyr His Tyr Gly Met Ile Asn Thr Ser Arg Thr Ile Ile Leu Gln
340 345 350

Ser Ser Ser Gly Gln Val Asn Gly Met Gln Arg Tyr Gly Ile Asn Ser
355 360 365

Val Ser Phe Lys Pro Ala Asp Thr Pro Leu Lys Leu Ala Asp Tyr Phe
370 375 380

Asn Ile Gly Gly Val Phe Arg Val Gly Ser Ile Ser Asp Arg Pro Thr
385 390 395 400

Gly Gly Gly Leu Tyr Glu Asp Thr Ser Val Met Gly Ala Asp Phe Arg
405 410 415

Ala Tyr Val Glu Ile Val Phe Glu Asn Pro Ser Asn Ile Val Leu Ser
420 425 430

Tyr His Ile Asp Gly Tyr Gln Phe Phe Val Val Gly Met Asp Gly Gly

435 440 445

Gln Trp Thr Gln Ala Ser Arg Asn Gly Tyr Asn Leu Arg Asp Gly Val
450 455 460

Ala Arg Ser Thr Ile Gln Val Tyr Pro Lys Ser Trp Ser Ala Ile Tyr
465 470 475 480

Val Ala Leu Asp Asn Val Gly Met Trp Asn Val Arg Thr Glu Tyr Trp
485 490 495

Ala Arg Gln Tyr Leu Gly Glu Gln Phe Tyr Leu Arg Val Tyr Thr Asn
500 505 510

Ser Gly Ser Ile Arg Asp Glu Phe Pro Ile Pro Lys Asn Ala Arg Leu
515 520 525

Cys Gly Arg Ala Ala Gly Arg His Thr Arg Pro Leu
530 535 540

<210> 188
<211> 542
<212> PRT
<213> Arabidopsis lyrata

<400> 188

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

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

Trp Asn Val Thr Tyr Gly Asp Ile Tyr Pro Leu Gly Val Arg Gln Gln
35 40 45

Gly Ile Leu Ile Asn Gly Lys Phe Pro Gly Pro Asp Ile His Ser Val
50 55 60

Thr Asn Asp Asn Leu Ile Ile Asn Val His Asn Ser Leu Asp Glu Pro
65 70 75 80

Phe Leu Ile Ser Trp Asn Gly Ile Gln Asn Arg Arg Asn Ser Tyr Val
85 90 95

Asp Gly Met Tyr Gly Thr Thr Cys Pro Ile Pro Pro Arg Ser Asn Tyr
100 105 110

Thr Tyr Ile Leu Gln Val Lys Asp Gln Ile Gly Ser Phe Tyr Tyr Phe
115 120 125

Pro Ser Leu Ala Phe His Lys Ala Ala Gly Gly Phe Gly Gly Ile Arg
130 135 140

Ile Leu Ser Arg Pro Gly Ile Pro Val Pro Phe Ala Asp Pro Ala Gly
145 150 155 160

Asp Tyr Thr Val Leu Ile Gly Asp Trp Tyr Lys Ser Asn His Thr Asp
165 170 175

Leu Lys Ser Arg Leu Asp Arg Gly Arg Lys Leu Pro Pro Pro Asp Gly
180 185 190

Ile Leu Ile Asn Gly Arg Ser Asn Gly Ala Thr Leu Asn Val Glu Gln
195 200 205

Gly Lys Thr Tyr Arg Leu Arg Ile Ser Asn Val Gly Leu Gln Asp Ser
210 215 220

Leu Asn Phe Arg Ile Gln Asn His Arg Met Lys Leu Val Glu Val Glu
225 230 235 240

Gly Thr His Thr Leu Gln Thr Met Phe Ser Ser Leu Asp Val His Val
245 250 255

Gly Gln Ser Tyr Ser Val Leu Ile Thr Ala Asp Gln Ser Pro Arg Ala
260 265 270

Tyr Tyr Val Val Val Ser Ser Arg Phe Thr Asp Lys Ile Ile Thr Ser
275 280 285

Thr Gly Val Leu Arg Tyr Ser Gly Ser Ser Thr Pro Ala Ser Gly Pro
290 295 300

Ile Pro Gly Gly Pro Thr Ile Gln Val Asp Trp Ser Leu Asn Gln Ala
305 310 315 320

Arg Ala Ile Arg Thr Asn Leu Thr Ala Ser Gly Pro Arg Pro Asn Pro
325 330 335

Gln Gly Ser Tyr His Tyr Gly Leu Ile Pro Leu Ile Arg Thr Ile Val
340 345 350

Phe Gly Ser Ser Ala Gly Gln Ile Asn Gly Lys Gln Arg Tyr Gly Val
355 360 365

Asn Ser Val Ser Phe Val Pro Ala Asp Thr Pro Leu Lys Leu Ala Asp
370 375 380

Phe Phe Lys Ile Ser Gly Val Tyr Lys Ile Asn Ser Ile Ser Asp Lys
385 390 395 400

Pro Thr Tyr Gly Gly Leu Tyr Leu Asp Thr Ser Val Leu Gln Val Asp
405 410 415

Tyr Arg Thr Phe Ile Glu Ile Val Phe Glu Asn Gln Glu Asp Ile Val
420 425 430

Gln Ser Tyr His Leu Asn Gly Tyr Ser Phe Trp Val Val Gly Met Asp
435 440 445

Gly Gly Gln Trp Lys Thr Gly Ser Arg Asn Gly Tyr Asn Leu Arg Asp
450 455 460

Ala Val Ser Arg Ser Thr Val Gln Val Tyr Pro Lys Ser Trp Thr Ala
465 470 475 480

Ile Tyr Ile Ala Leu Asp Asn Val Gly Met Trp Asn Leu Arg Ser Glu
485 490 495

Phe Trp Ala Arg Gln Tyr Leu Gly Gln Gln Leu Tyr Leu Arg Val Phe
500 505 510

Thr Ser Ser Thr Ser Leu Arg Asp Glu Tyr Pro Ile Pro Lys Asn Ser
515 520 525

Arg Leu Cys Gly Arg Ala Arg Gly Arg His Thr Arg Pro Leu
530 535 540

<210> 189
<211> 541
<212> PRT
<213> Arabidopsis

<400> 189

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

Phe Phe Ala Ala Val Thr Ala Glu Ser Pro Tyr Arg Phe Phe Asp Trp
20 25 30

Asn Val Thr Tyr Gly Asp Ile Tyr Pro Leu Gly Val Arg Gln Gln Gly
35 40 45

Ile Leu Ile Asn Gly Gln Phe Pro Gly Pro Asp Ile His Ser Val Thr
50 55 60

Asn Asp Asn Leu Ile Ile Asn Val His Asn Ser Leu Asp Glu Pro Phe
65 70 75 80

Leu Ile Ser Trp Asn Gly Val Gln Asn Arg Arg Asn Ser Tyr Val Asp
85 90 95

Gly Met Tyr Gly Thr Thr Cys Pro Ile Pro Pro Arg Ser Asn Tyr Thr
100 105 110

Tyr Ile Leu Gln Val Lys Asp Gln Ile Gly Ser Phe Tyr Tyr Phe Pro
115 120 125

Ser Leu Ala Phe His Lys Ala Ala Gly Gly Phe Gly Gly Ile Arg Ile
130 135 140

Leu Ser Arg Pro Gly Ile Pro Val Pro Phe Ala Asp Pro Ala Gly Asp
145 150 155 160

Tyr Thr Val Leu Ile Gly Asp Trp Tyr Lys Phe Asn His Thr Asp Leu
165 170 175

Lys Ser Arg Leu Asp Arg Gly Arg Lys Leu Pro Ser Pro Asp Gly Ile
180 185 190

Leu Ile Asn Gly Arg Ser Asn Gly Ala Thr Leu Asn Val Glu Gln Gly
195 200 205

Lys Thr Tyr Arg Leu Arg Ile Ser Asn Val Gly Leu Gln Asp Ser Leu
210 215 220

Asn Phe Arg Ile Gln Asn His Arg Met Lys Leu Val Glu Val Glu Gly
225 230 235 240

Thr His Thr Leu Gln Thr Met Phe Ser Ser Leu Asp Val His Val Gly
245 250 255

Gln Ser Tyr Ser Val Leu Ile Thr Ala Asp Gln Ser Pro Arg Asp Tyr
260 265 270

Tyr Val Val Val Ser Ser Arg Phe Thr Asp Lys Ile Ile Thr Thr Thr
275 280 285

Gly Val Leu Arg Tyr Ser Gly Ser Ser Thr Pro Ala Ser Gly Pro Ile
290 295 300

Pro Gly Gly Pro Thr Ile Gln Val Asp Trp Ser Leu Asn Gln Ala Arg
305 310 315 320

Ala Ile Arg Thr Asn Leu Thr Ala Ser Gly Pro Arg Pro Asn Pro Gln
325 330 335

Gly Ser Tyr His Tyr Gly Leu Ile Pro Leu Ile Arg Thr Ile Val Phe
340 345 350

Gly Ser Ser Ala Gly Gln Ile Asn Gly Lys Gln Arg Tyr Gly Val Asn
355 360 365

Ser Val Ser Phe Val Pro Ala Asp Thr Pro Leu Lys Leu Ala Asp Phe
370 375 380

Phe Lys Ile Ser Gly Val Tyr Lys Ile Asn Ser Ile Ser Asp Lys Pro
385 390 395 400

Thr Tyr Gly Gly Leu Tyr Leu Asp Thr Ser Val Leu Gln Val Asp Tyr
405 410 415

Arg Thr Phe Ile Glu Ile Val Phe Glu Asn Gln Glu Asp Ile Val Gln
420 425 430

Ser Tyr His Leu Asn Gly Tyr Ser Phe Trp Val Val Gly Met Asp Gly
435 440 445

Gly Gln Trp Lys Thr Gly Ser Arg Asn Gly Tyr Asn Leu Arg Asp Ala
450 455 460

Val Ser Arg Ser Thr Val Gln Val Tyr Pro Lys Ser Trp Thr Ala Ile
465 470 475 480

Tyr Ile Ala Leu Asp Asn Val Gly Met Trp Asn Leu Arg Ser Glu Phe
485 490 495

Trp Ala Arg Gln Tyr Leu Gly Gln Gln Leu Tyr Leu Arg Val Phe Thr
500 505 510

Ser Ser Thr Ser Leu Arg Asp Glu Tyr Pro Ile Pro Lys Asn Ser Arg
515 520 525

Leu Cys Gly Arg Ala Arg Gly Arg His Thr Arg Pro Leu
530 535 540

<210> 190
<211> 224
<212> PRT
<213> Arabidopsis lyrata

<400> 190

Met Ala Glu Lys Glu Glu Asp Val Lys Leu Leu Gly Phe Trp Ala Ser
1 5 10 15

Pro Phe Ser Arg Arg Val Glu Met Ala Leu Lys Leu Lys Gly Val Pro
20 25 30

Tyr Glu Tyr Leu Glu Gln Asp Ile Val Asn Lys Ser Pro Leu Leu Leu
35 40 45

Gln Leu Asn Pro Val Tyr Lys Lys Val Pro Val Leu Val His Lys Gly
50 55 60

Lys Val Leu Ser Glu Ser His Val Val Leu Glu Tyr Ile Asp Gln Ile
65 70 75 80

Trp Lys Asn Asn Pro Ile Leu Pro Gln Asp Pro Tyr Glu Lys Ala Met
85 90 95

Ala Leu Phe Trp Ala Lys Phe Val Asp Glu Gln Val Gly Pro Val Ala
100 105 110

Phe Arg Tyr Val Ala Lys Ala Glu Lys Gly Ile Glu Val Ala Ile Lys
115 120 125

Glu Ala Gln Glu Leu Phe Met Phe Leu Glu Lys Glu Val Thr Gly Lys
130 135 140

Asp Phe Phe Gly Gly Glu Thr Ile Gly Phe Leu Asp Leu Val Ala Gly
145 150 155 160

Ser Met Ile Pro Phe Cys Leu Ala Arg Gly Trp Glu Gly Met Gly Ile
165 170 175

Asp Met Ile Pro Glu Glu Lys Phe Pro Glu Leu Asn Arg Trp Ile Lys
180 185 190

Asn Leu Lys Glu Ile Glu Ile Val Arg Glu Cys Ile Pro Pro Arg Glu
195 200 205

Lys Gln Ile Glu His Met Lys Lys Val Val Glu Arg Ile Lys Pro Ala
210 215 220

<210> 191
<211> 223
<212> PRT
<213> Raphanus sativus

<400> 191

Met Ala Glu Arg Glu Glu Asp Val Lys Leu Leu Gly Phe Trp Ala Ser
1 5 10 15

Pro Phe Ser Arg Arg Val Glu Met Ala Leu Lys Leu Lys Gly Val Pro
20 25 30

Tyr Glu Tyr Leu Glu Gln Asp Leu Met Asn Lys Ser Pro Leu Leu Leu
35 40 45

Glu Leu Asn Pro Val Tyr Lys Lys Val Pro Val Leu Val His Lys Gly

50 55 60

Lys Ile Leu Leu Glu Ser Gln Leu Ile Leu Glu Tyr Ile Asp Gln Thr
65 70 75 80

Trp Thr Asn Asn Pro Ile Leu Pro Arg Asp Pro Tyr Glu Lys Ala Met
85 90 95

Ala Leu Phe Trp Ala Lys Val Val Asp Glu Gln Val Lys Ile Arg Phe
100 105 110

Ser Thr Leu Val Lys Ala Glu Lys Gly Val Glu Val Ala Ile Glu Glu
115 120 125

Ala Arg Glu Leu Leu Thr Phe Leu Glu Lys Glu Val Thr Gly Lys Tyr
130 135 140

Leu Phe Gly Gly Lys Thr Ile Gly Phe Leu Asp Met Val Ala Gly Ser
145 150 155 160

Met Ile Pro Phe Cys Leu Ala Arg Gly Trp Glu Gly Met Gly Ile Asp
165 170 175

Met Ile Pro Glu Glu Lys Phe Pro Glu Leu Asn Arg Trp Ile Lys Asn
180 185 190

Leu Gln Glu Ile Glu Ile Val Thr Glu Cys Ile Pro His Arg Glu Lys

195 200 205

Gln Ile Glu His Met Lys Lys Val Ala Val Arg Ile Lys Ser Ala
210 215 220

<210> 192
<211> 224
<212> PRT
<213> Raphanus sativus

<400> 192

Met Ala Asn Lys Glu Lys Asp Val Lys Leu Leu Gly Phe Trp Ala Ser
1 5 10 15

Pro Phe Ser Arg Arg Val Glu Met Ala Leu Lys Leu Lys Gly Val Ser
20 25 30

Tyr Glu Tyr Leu Glu Gln Asp Ile Val Asp Lys Ser Ala Leu Leu Leu
35 40 45

Glu Leu Asn Pro Val Phe Lys Lys Val Pro Val Leu Val His Asn Gly
50 55 60

Lys Ile Leu Ala Glu Ser His Leu Ile Leu Glu Tyr Ile Asp Gln Thr
65 70 75 80

Trp Lys Ser Asn Pro Ile Leu Pro Gln Asp Pro Tyr Glu Lys Ala Met
85 90 95

Ala Arg Phe Trp Ala Lys Phe Val Asp Glu Gln Val Gly Pro Val Cys
100 105 110

Phe Lys Ser Val Val Lys Ala Glu Lys Gly Ile Glu Ile Ala Ile Glu
115 120 125

Glu Ala Gln Glu Leu Ile Thr Phe Leu Glu Lys Glu Leu Thr Gly Lys
130 135 140

Asp Phe Phe Gly Gly Lys Thr Ile Gly Phe Leu Asp Leu Val Ala Gly
145 150 155 160

Ser Met Ile Pro Phe Cys Leu Ala Arg Ser Trp Glu Gly Met Glu Ile
165 170 175

Asp Met Ile Pro Glu Glu Lys Phe Pro Glu Leu Asn Arg Trp Ile Arg
180 185 190

Asn Leu Asn Asp Ile Glu Val Val Ser Glu Cys Ile Pro His Arg Glu
195 200 205

Lys Gln Ile Glu His Met Met Lys Val Val Glu Arg Ile Lys Leu Ala
210 215 220

<210> 193
<211> 224

<212> PRT
<213> Canola

<400> 193

Met Ala Thr Lys Glu Glu Asp Val Lys Leu Leu Gly Phe Trp Ala Ser
1 5 10 15

Pro Phe Ser Arg Arg Val Glu Ile Ala Leu Lys Leu Lys Gly Val Thr
20 25 30

Tyr Glu Tyr Leu Glu Gln Asp Ile Phe Asn Lys Ser Ala Leu Leu Leu
35 40 45

Glu Leu Asn Pro Val Phe Lys Lys Val Pro Val Leu Val His Lys Gly
50 55 60

Lys Ile Leu Ala Glu Ser His Leu Ile Leu Glu Tyr Ile Asp Gln Thr
65 70 75 80

Trp Lys Asn Asn Pro Ile Leu Pro Gln Asp Pro Tyr Glu Lys Ala Met
85 90 95

Ala Arg Phe Trp Ala Lys Phe Val Asp Glu Gln Val Gly Pro Val Cys
100 105 110

Phe Lys Ser Val Val Lys Ala Asp Lys Gly Ile Asp Val Ala Ile Glu
115 120 125

Glu Ala Gln Glu Leu Ile Thr Phe Leu Glu Lys Glu Leu Ile Gly Lys
130 135 140

Asp Phe Phe Gly Gly Lys Thr Ile Gly Phe Leu Asp Met Val Ala Gly
145 150 155 160

Ser Met Ile Pro Phe Cys Val Ala Arg Ala Trp Glu Gly Met Glu Ile
165 170 175

Asp Met Ile Pro Glu Glu Lys Phe Pro Glu Leu Asn Arg Trp Ile Lys
180 185 190

Asn Leu Asn Gly Ile Glu Ile Val Arg Glu Cys Ile Pro Asn Arg Glu
195 200 205

Lys Gln Ile Asp His Met Met Lys Val Ala Glu Arg Ile Lys Leu Ala
210 215 220

<210> 194
<211> 224
<212> PRT
<213> Brassica rapa, Canola

<400> 194

Met Ala Thr Lys Glu Glu Asp Val Lys Leu Leu Gly Phe Trp Ala Ser
1 5 10 15

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

Tyr Glu Tyr Leu Glu Gln Asp Ile Phe Asn Lys Ser Ala Leu Leu Leu
35 40 45

Glu Leu Asn Pro Val Phe Lys Met Val Pro Val Leu Val His Lys Gly
50 55 60

Lys Ile Leu Ala Glu Ser Leu Leu Ile Leu Glu Tyr Ile Asp Gln Thr
65 70 75 80

Trp Lys Asn Asn Pro Ile Leu Pro Gln Asp Pro Tyr Glu Lys Ala Met
85 90 95

Ala Arg Leu Trp Ala Lys Phe Val Asp Glu Gln Val Gly Pro Val Cys
100 105 110

Phe Lys Ser Val Val Lys Ala Asp Lys Gly Ile Asp Val Ala Ile Glu
115 120 125

Glu Ala Gln Glu Leu Ile Thr Phe Leu Glu Lys Glu Leu Ser Gly Lys
130 135 140

Asp Phe Phe Gly Gly Lys Thr Ile Gly Phe Leu Asp Met Val Ala Gly
145 150 155 160

Ser Met Ile Pro Phe Cys Val Ala Arg Ala Trp Glu Gly Met Gly Ile
165 170 175

Asp Met Ile Pro Glu Glu Lys Phe Pro Glu Leu Asn Arg Trp Ile Lys
180 185 190

Asn Leu Asn Asp Ile Glu Ile Val Arg Glu Cys Ile Pro Gln Arg Glu
195 200 205

Lys Gln Ile Glu His Met Met Lys Val Ala Glu Arg Ile Lys Leu Ala
210 215 220

<210> 195
<211> 86
<212> PRT
<213> Arabidopsis lyrata

<400> 195

Met Ala Asn Val Ser Ala Leu Leu Thr Ile Ala Leu Leu Leu Cys Ser
1 5 10 15

Thr Leu Met Cys Thr Ala Arg Pro Glu Pro Ala Ile Ser Val Ser Ile
20 25 30

Thr Thr Ala Ala Asp Pro Cys Asn Met Glu Lys Lys Ile Glu Gly Lys
35 40 45

Leu Asp Asp Met Val Glu Glu Asn Cys Gly Ser Asp Asp Glu Asp Cys

50 55 60

Leu Met Arg Arg Thr Leu Val Ala His Thr Asp Tyr Ile Tyr Thr Gln
65 70 75 80

Lys Lys Lys Lys Asn Leu
85

<210> 196
<211> 1115
<212> PRT
<213> Medicago

<400> 196

Met Glu Ala Ser Ser Ser Ser Ser Cys Arg Ser Ser Ser Thr Thr Ser
1 5 10 15

Leu Cys Ser Tyr His Val Phe Leu Ser Phe Arg Gly Glu Asp Thr Arg
20 25 30

Lys Gly Phe Thr Asp His Leu Cys Ala Ala Leu Glu Arg Lys Gly Ile
35 40 45

Thr Thr Phe Arg Asp Asp Lys Asp Leu Glu Arg Gly Gln Val Ile Ser
50 55 60

Glu Lys Leu Ile Asn Ala Ile Lys Asp Ser Met Phe Ala Ile Thr Val
65 70 75 80

Leu Ser Pro Asp Tyr Ala Ser Ser Thr Trp Cys Leu Asp Glu Leu Gln
85 90 95

Met Ile Met Glu Cys Ser Asn Lys Gly Leu Glu Val Leu Pro Val Phe
100 105 110

Tyr Gly Val Asp Pro Ser Asp Val Arg His Gln Arg Gly Cys Phe Glu
115 120 125

Glu Ser Phe Arg Lys His Leu Glu Lys Phe Gly Gln His Ser Asp Arg
130 135 140

Val Asp Arg Trp Arg Asp Ala Phe Thr Gln Val Ala Ser Tyr Ser Gly
145 150 155 160

Trp Asp Ser Lys Gly Gln His Glu Ala Leu Leu Val Glu Ser Ile Ala
165 170 175

Gln His Ile His Arg Lys Leu Val Pro Lys Leu Ser Ser Cys Thr Glu
180 185 190

Asn Leu Val Gly Ile Glu Ser Lys Val Glu Glu Val Asn Lys Leu Ile
195 200 205

Gly Met Gly Leu Asn Asp Val Arg Phe Ile Gly Ile Trp Gly Met Gly
210 215 220

Gly Ile Gly Lys Ser Thr Ile Ala Arg Ala Val Tyr Glu Ala Ile Arg
225 230 235 240

Cys Glu Phe Gln Leu Thr Cys Phe Leu Glu Asn Val Arg Glu Ile Ser
245 250 255

Glu Thr Asn Gly Leu Val His Leu Gln Arg Gln Leu Leu Ser His Met
260 265 270

Ser Ile Ser Arg Asn Asp Phe His Asn Leu Tyr Asp Gly Lys Lys Thr
275 280 285

Ile Gln Asn Ser Phe Arg Arg Lys Lys Val Leu Leu Val Leu Asp Asp
290 295 300

Val Asn Glu Leu Asn Gln Leu Glu Asn Met Ala Gly Lys Gln Asp Trp
305 310 315 320

Phe Gly Pro Gly Ser Arg Val Ile Ile Thr Thr Arg Asp Lys His Leu
325 330 335

Leu Met Thr His Gly Val His Lys Thr Tyr Glu Val Trp Met Leu Phe
340 345 350

Gln Asn Glu Ala Leu Asn Leu Phe Cys Leu Lys Ala Phe Lys Gly Asp
355 360 365

Lys Pro Gln Glu Gly Tyr Leu Asp Leu Ser Lys Glu Val Val Asp Tyr
370 375 380

Thr Gly Gly Leu Pro Leu Ala Leu Glu Val Phe Gly Ser Tyr Leu Tyr
385 390 395 400

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

Val Pro Leu Arg Lys Ile Gln Asp Lys Leu Glu Ile Ser Tyr Glu Ser
420 425 430

Leu Asp Pro Met Glu Lys Asp Val Phe Leu Asp Ile Ala Cys Phe Phe
435 440 445

Lys Gly Met Lys Ile Asp Lys Val Ile Asp Ile Leu Glu Asn Cys Gly
450 455 460

Tyr Phe Pro Lys Ile Ile Ile Gln Val Leu Ile Asp Arg Ser Leu Ile
465 470 475 480

Thr Leu Asp Arg Val Asn Asn Lys Leu Gly Met His Asp Leu Leu Gln
485 490 495

Glu Met Gly Arg Asn Ile Val Phe Gln Glu Ser Pro Asn Asp Pro Gly
500 505 510

Arg Cys Ser Arg Leu Trp Ser Lys Glu Asp Ile Asp Ser Val Leu Thr
515 520 525

Lys Asn Lys Gly Thr Glu Lys Ile Ser Ser Val Val Leu Asn Leu Leu
530 535 540

Gln Pro Tyr Glu Ala Arg Trp Ser Thr Glu Ala Phe Ser Lys Thr Ser
545 550 555 560

Gln Leu Lys Leu Leu Asn Leu Asn Glu Val Gln Leu Pro Leu Gly Leu
565 570 575

Ser Cys Leu Pro Cys Ser Leu Lys Val Leu Arg Trp Arg Gly Cys Pro
580 585 590

Leu Lys Thr Leu Ala Gln Thr Asn Gln Leu Asp Glu Val Val Asp Ile
595 600 605

Lys Leu Ser His Ser Lys Ile Glu Lys Leu Trp His Gly Val Tyr Phe
610 615 620

Met Glu Lys Leu Lys Tyr Leu Asn Leu Lys Phe Ser Lys Asn Leu Lys
625 630 635 640

Arg Leu Pro Asp Phe Ser Gly Val Pro Asn Leu Glu Lys Leu Ile Leu
645 650 655

Lys Gly Cys Ser Ile Leu Thr Glu Val His Leu Ser Leu Val His His
660 665 670

Lys Lys Val Val Val Val Ser Leu Lys Asn Cys Lys Ser Leu Lys Ser
675 680 685

Leu Pro Gly Lys Leu Glu Met Ser Ser Leu Lys Lys Leu Ile Leu Ser
690 695 700

Gly Cys Ser Glu Phe Lys Phe Leu Pro Glu Phe Gly Glu Lys Met Glu
705 710 715 720

Asn Leu Ser Ile Leu Ala Leu Lys Gly Thr Asp Ile Arg Lys Leu Pro
725 730 735

Leu Ser Leu Gly Ser Leu Val Gly Leu Thr Asn Leu Asn Leu Lys Asp
740 745 750

Cys Lys Ser Leu Val Cys Leu Pro Asp Thr Ile His Gly Leu Asn Ser
755 760 765

Leu Ile Ile Leu Asn Ile Ser Gly Cys Ser Arg Leu Cys Arg Leu Pro
770 775 780

Asp Gly Leu Lys Glu Ile Gln Cys Leu Lys Glu Leu His Ala Asn Asp
785 790 795 800

Thr Ala Ile Asp Glu Leu Pro Ser Phe Ile Phe Tyr Leu Asp Asn Leu
805 810 815

Lys Val Leu Ser Phe Ala Gly Cys Gln Gly Pro Pro Ala Met Ser Thr
820 825 830

Asn Trp Phe Pro Phe Asn Trp Met Phe Gly Gly Gln Ser Ala Ser Thr
835 840 845

Gly Phe Arg Leu Pro Thr Ser Phe Leu Ser Leu His Ser Leu Lys Tyr
850 855 860

Leu Asn Leu Ser Tyr Cys Asn Leu Ser Glu Glu Ser Ile Pro Asn Tyr
865 870 875 880

Phe His His Leu Ser Ser Leu Lys Ser Leu Asp Leu Thr Gly Asn Asn
885 890 895

Phe Val Ile Ile Pro Ser Ser Ile Ser Lys Leu Ser Arg Leu Arg Phe
900 905 910

Leu Cys Leu Asn Trp Cys Glu Gln Leu Gln Leu Leu Pro Glu Leu Pro
915 920 925

Ser Arg Ile Met Gln Leu Asp Ala Ser Asn Cys Asp Ser Leu Glu Thr
930 935 940

Arg Lys Phe Asp Pro Ile Glu Ser Phe Met Lys Gly Arg Cys Leu Pro
945 950 955 960

Ala Thr Arg Phe Asp Met Leu Ile Pro Phe Pro Gly Asp Glu Ile Pro
965 970 975

Ser Trp Cys Val Ser Gln Gly Ser Val Ser Trp Ala Lys Val His Ile
980 985 990

Pro Asn Asn Leu Pro Gln Asp Glu Trp Val Gly Phe Ala Leu Cys Phe
995 1000 1005

Gln Leu Val Ser Tyr Thr Phe Pro Pro Glu Leu Cys Asn His Glu
1010 1015 1020

Ile Asp Cys Tyr Leu Phe Ser Pro Asn Gly Lys Gln Leu Ile Leu
1025 1030 1035

Ile Ser Thr Arg Arg Leu Pro Pro Met Asp Pro Cys Tyr Pro His
1040 1045 1050

Leu Tyr Ile Leu Tyr Leu Ser Ile Glu Gln Phe Arg Asp Lys Ile
1055 1060 1065

Leu Gln Asp Asp Tyr Trp Asp Gly Val Glu Phe Ser Leu Lys Cys
1070 1075 1080

Tyr Cys Cys His Ser Leu Arg Ile Phe Ser Ser Gly Cys Arg Leu
1085 1090 1095

Val Cys Lys Gln Val Val Glu Val Phe Gln Asp Gln Thr Val Val
1100 1105 1110

Ser Pro
1115

<210> 197
<211> 300
<212> PRT
<213> Arabidopsis lyrata

<400> 197

Met Ala Gln Lys Val Glu Ala Ala Gly Gly Thr Gly Gly Ala Ser Trp
1 5 10 15

Asp Asp Gly Val His Asp Gly Val Arg Lys Val His Val Gly Gln Gly
20 25 30

Gln Asp Gly Val Ser Ser Ile Lys Val Val Tyr Ala Lys Asp Ser Gln
35 40 45

Asp Val Glu Gly Gly Glu Tyr Gly Lys Lys Thr Leu Leu Gly Phe Glu
50 55 60

Thr Phe Glu Val Asp Ala Asp Asp Tyr Ile Val Ala Val Lys Val Thr
65 70 75 80

Tyr Asp Asn Val Phe Gly Gln Asp Ser Asp Ile Ile Thr Ser Ile Thr
85 90 95

Phe Thr Thr Phe Lys Gly Lys Thr Ser Pro Pro Tyr Gly Leu Glu Thr
100 105 110

Glu Lys Lys Phe Val Leu Lys Asp Lys Asn Gly Gly Lys Pro Val Gly
115 120 125

Phe His Gly Arg Ala Gly Glu Ala Leu His Ala Leu Gly Ala Tyr Phe
130 135 140

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

Gly Gly Asp Glu Gly Thr Ala Trp Asp Asp Gly Ala Tyr Asp Gly Val
165 170 175

Lys Lys Val Tyr Val Gly Gln Gly Gln Asp Gly Ile Ser Ala Val Lys
180 185 190

Phe Glu Tyr Asn Lys Gly Ala Glu Asp Ile Leu Gly Gly Glu His Gly
195 200 205

Lys Arg Thr Leu Leu Gly Phe Glu Glu Phe Glu Leu Asp Tyr Pro Ser
210 215 220

Glu Tyr Ile Thr Ala Val Glu Gly Thr Tyr Asp Arg Ile Phe Gly Ser
225 230 235 240

Asp Gly Val Val Ile Thr Met Leu Arg Phe Lys Thr Asn Lys Gln Met
245 250 255

Ser Ala Pro Phe Gly Leu Glu Ala Gly Thr Ala Phe Glu Leu Lys Glu
260 265 270

Glu Gly His Lys Ile Ile Gly Phe His Gly Lys Ala Ser Glu Leu Leu
275 280 285

His Gln Phe Gly Val His Val Met Pro Ile Thr Asn
290 295 300

<210> 198
<211> 300
<212> PRT
<213> Arabidopsis

<400> 198

Met Ala Gln Lys Val Glu Ala Gln Gly Gly Ile Gly Gly Asp Val Trp
1 5 10 15

Asp Asp Gly Ala His Asp Gly Val Arg Lys Val His Val Gly Gln Gly
20 25 30

Leu Asp Gly Val Ser Phe Ile Asn Val Val Tyr Glu Asn Gly Ser Gln
35 40 45

Glu Val Val Gly Gly Glu His Gly Lys Lys Ser Leu Ile Gly Ile Glu
50 55 60

Thr Phe Glu Val Asp Ala Asp Asp Tyr Ile Val Ala Val Gln Val Thr
65 70 75 80

Tyr Asp Lys Ile Phe Gly Tyr Asp Ser Asp Ile Ile Thr Ser Ile Thr
85 90 95

Phe Ser Thr Phe Lys Gly Lys Thr Ser Pro Pro Tyr Gly Leu Asp Thr
100 105 110

Glu Asn Lys Phe Val Leu Lys Glu Lys Asn Gly Gly Lys Leu Val Gly
115 120 125

Phe His Gly Arg Ala Gly Glu Ile Leu Tyr Ala Leu Gly Ala Tyr Phe
130 135 140

Thr Thr Thr Thr Thr Pro Leu Thr Pro Ala Lys Lys Leu Pro Ala Val
145 150 155 160

Gly Gly Asp Glu Gly Thr Ala Trp Asp Asp Gly Ala Phe Asp Gly Val
165 170 175

Lys Lys Val Tyr Ile Gly Gln Ala Gln Asp Gly Ile Ser Ala Val Lys
180 185 190

Phe Val Tyr Asp Lys Gly Ala Glu Asp Ile Val Gly Asp Glu His Gly
195 200 205

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

Glu Tyr Ile Thr Ala Val Glu Gly Thr Tyr Asp Lys Ile Phe Gly Phe
225 230 235 240

Glu Thr Glu Val Ile Asn Met Leu Arg Phe Lys Thr Asn Lys Lys Thr
245 250 255

Ser Pro Pro Phe Gly Ile Glu Ala Gly Thr Ala Phe Glu Leu Lys Glu
260 265 270

Glu Gly Cys Lys Ile Val Gly Phe His Gly Lys Val Ser Ala Val Leu
275 280 285

His Gln Phe Gly Val His Ile Leu Pro Val Thr Asn
290 295 300

<210> 199
<211> 300
<212> PRT
<213> Arabidopsis lyrata

<400> 199

Met Val Gln Lys Val Glu Ala Gln Gly Gly Met Gly Gly Asn Val Trp
1 5 10 15

Asp Asp Gly Val His Asp Gly Val Arg Lys Val His Val Gly Gln Gly
20 25 30

Gln Asp Gly Val Ser Phe Ile Asn Val Val Tyr Glu Asn Gly Ser Glu
35 40 45

Glu Val Val Gly Gly Glu His Gly Lys Lys Ser Leu Ile Gly Ile Glu
50 55 60

Thr Phe Glu Val Asp Ala Asp Asp Tyr Ile Val Ala Val Gln Val Thr
65 70 75 80

Tyr Asp Lys Ile Phe Gly Phe Asp Ser Glu Val Ile Thr Ser Ile Thr
85 90 95

Phe Ser Thr Phe Lys Gly Lys Thr Ser Pro Pro Phe Gly Leu Asp Thr
100 105 110

Glu Asn Lys Phe Val Leu Lys Glu Lys Asn Gly Gly Lys Leu Val Gly

115 120 125

Phe His Gly Arg Ala Gly Glu Ile Leu Tyr Ala Leu Gly Ala Tyr Phe
130 135 140

Thr Thr Thr Thr Thr Pro Leu Asn Pro Ala Lys Lys Leu Pro Ala Val
145 150 155 160

Gly Gly Asp Glu Gly Thr Ala Trp Asp Asp Gly Ala Tyr Asp Gly Val
165 170 175

Lys Lys Val Tyr Ile Gly Gln Ala Gln Asp Gly Ile Ser Ala Val Lys
180 185 190

Phe Val Tyr Asp Lys Gly Ala Ala Asp Ile Val Gly Asp Glu His Gly
195 200 205

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

Glu Tyr Ile Thr Ala Val Glu Gly Thr Tyr Asp Lys Ile Phe Gly Ser
225 230 235 240

Glu Thr Glu Val Ile Asn Met Leu Arg Phe Lys Thr Asn Lys Gln Thr
245 250 255

Ser Pro Pro Phe Gly Ile Glu Ala Gly Thr Ala Phe Glu Leu Lys Glu

260 265 270

Glu Gly Ser Lys Ile Val Gly Phe His Gly Lys Val Ser Ser Leu Leu
275 280 285

His Gln Phe Gly Val His Val Leu Pro Val Thr Asn
290 295 300

<210> 200
<211> 300
<212> PRT
<213> Raphanus sativus

<400> 200

Met Ala Gln Lys Val Glu Ala Gln Gly Gly Val Gly Gly Asp Val Trp
1 5 10 15

Asp Asp Gly Val Tyr Asp Gly Val Arg Lys Val His Val Gly Gln Gly
20 25 30

Gln Asp Gly Val Ser Phe Ile Asn Ala Val Tyr Glu Lys Gly Ser Gln
35 40 45

Glu Val Glu Gly Gly Glu His Gly Asn Lys Thr Leu Leu Gly Phe Glu
50 55 60

Thr Phe Glu Val Asp Ala Asp Asp Tyr Ile Ile Ala Val Gln Val Thr
65 70 75 80

Tyr Asp Lys Ile Phe Gly His Glu Ser Asp Val Ile Thr Ser Ile Thr
85 90 95

Phe Tyr Thr Ser Lys Gly Lys Ala Ser Pro Pro Tyr Gly Leu Glu Thr
100 105 110

Asp Lys Lys Phe Val Leu Lys Glu Lys Asn Gly Gly Lys Leu Leu Gly
115 120 125

Phe His Gly Arg Ala Gly Glu Val Leu His Ala Leu Gly Ala Tyr Phe
130 135 140

Val Thr Thr Thr Thr Pro Leu Thr Pro Ala Lys Lys Leu Pro Ala Val
145 150 155 160

Gly Gly Asp Gly Gly Thr Ala Trp Asp Asp Gly Ala Tyr Asp Gly Val
165 170 175

Arg Lys Leu Phe Val Gly Gln Ala Gln Asp Gly Ile Ser Val Val Lys
180 185 190

Phe Val Tyr Asp Lys Gly Ala Glu Glu Ile Ile Gly Asp Glu His Gly
195 200 205

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

Glu Tyr Ile Thr Ser Val Glu Gly Thr Tyr Asp Lys Ile Phe Gly Ser
225 230 235 240

Asp Ser Glu Val Val Thr Met Leu Arg Phe Lys Thr Asn Lys Gln Thr
245 250 255

Ser Ala Pro Phe Gly Ile Glu Ala Gly Thr Pro Phe Glu Leu Lys Glu
260 265 270

Glu Gly Ser Lys Ile Val Gly Phe His Gly Lys Val Ser Glu Leu Leu
275 280 285

His Gln Phe Gly Val His Val Leu Pro Ile Thr Tyr
290 295 300

<210> 201
<211> 578
<212> PRT
<213> Arabidopsis lyrata

<400> 201

Met Ala Val Thr Glu Val Glu Asn Pro Leu Leu Gly Glu Ile Thr Cys
1 5 10 15

Gly Thr Leu Leu Gln Lys Leu Gln Glu Ile Trp Asp Glu Val Gly Glu
20 25 30

Ser Asp Glu Glu Arg Asp Lys Leu Leu Leu Gln Ile Glu Glu Glu Cys
35 40 45

Leu Asn Val Tyr Lys Lys Lys Val Glu Leu Ala Ala Lys Ser Arg Ala
50 55 60

Glu Leu Leu Gln Thr Leu Ser Asp Ala Thr Val Glu Leu Ser Asn Leu
65 70 75 80

Thr Thr Ala Leu Gly Glu Lys Ser Tyr Ile Asp Ile Pro Asp Lys Thr
85 90 95

Ser Gly Thr Ile Lys Glu Gln Leu Ser Ala Ile Ala Pro Ala Leu Glu
100 105 110

Gln Leu Trp Gln Gln Lys Glu Glu Arg Val Arg Ala Phe Ser Asp Val
115 120 125

Gln Ser Gln Ile Gln Lys Ile Cys Glu Glu Ile Ala Gly Gly Leu Asn
130 135 140

Asn Gly Pro His Val Val Asp Glu Ser Asp Leu Ser Leu Lys Arg Leu
145 150 155 160

Asp Asp Phe Gln Arg Lys Leu Gln Glu Leu Gln Lys Glu Lys Ser Asp
165 170 175

Arg Leu Gln Lys Val Leu Glu Phe Val Ser Thr Val His Asp Leu Cys
180 185 190

Ala Val Leu Gly Leu Asp Phe Leu Ser Thr Val Thr Glu Val His Pro
195 200 205

Ser Leu Asp Glu Ala Asn Gly Val Gln Thr Lys Ser Ile Ser Asn Glu
210 215 220

Thr Leu Ala Arg Leu Ala Lys Thr Val Leu Thr Leu Lys Glu Asp Lys
225 230 235 240

Met Gln Arg Leu Lys Lys Leu Gln Glu Leu Ala Thr Gln Leu Thr Asp
245 250 255

Leu Trp Asn Leu Met Asp Thr Pro Asp Glu Glu Arg Glu Leu Phe Asp
260 265 270

His Val Thr Cys Asn Ile Ser Ala Ser Val His Glu Val Thr Ala Ser
275 280 285

Gly Ala Leu Ala Leu Asp Leu Ile Glu Gln Ala Glu Val Lys Val Asp
290 295 300

Arg Leu Asp Gln Leu Lys Ser Ser Arg Met Lys Glu Ile Ala Phe Lys
305 310 315 320

Lys Gln Ser Glu Leu Glu Glu Ile Tyr Ala Arg Ala His Ile Glu Ile
325 330 335

Lys Pro Glu Val Val Arg Glu Arg Ile Met Ser Leu Ile Asp Ala Gly
340 345 350

Asn Thr Glu Pro Thr Glu Leu Leu Ala Asp Met Asp Ser Gln Ile Ala
355 360 365

Lys Ala Lys Glu Glu Ala Phe Ser Arg Lys Glu Ile Leu Asp Arg Val
370 375 380

Glu Lys Trp Met Ser Ala Cys Glu Glu Glu Ser Trp Leu Glu Asp Tyr
385 390 395 400

Asn Arg Asp Gln Asn Arg Tyr Ser Ala Ser Arg Gly Ala His Leu Asn
405 410 415

Leu Lys Arg Ala Glu Lys Ala Arg Ile Leu Val Ser Lys Ile Thr Ala
420 425 430

Met Val Asp Thr Leu Val Ala Lys Thr Arg Ala Trp Glu Glu Asp Asn
435 440 445

Ser Met Ser Phe Glu Tyr Asp Gly Val Pro Leu Leu Ala Met Leu Asp
450 455 460

Glu Tyr Thr Met Leu Arg Gln Glu Arg Glu Asp Glu Lys Arg Arg Leu
465 470 475 480

Lys Glu Gln Lys Lys Gln Gln Glu Gln Pro His Thr Asp Gln Asp Ser
485 490 495

Ala Phe Gly Ser Lys Pro Ser Pro Ala Arg Pro Val Ser Ala Lys Lys
500 505 510

Thr Val Gly Thr Arg Ala Asn Gly Gly Gly Leu Asn Glu Thr Pro Ile
515 520 525

Arg Arg Leu Ser Met Asn Ser Ser Gln Asn Gly Ser Lys Ser Lys Arg
530 535 540

Asp Ser Leu Asn Lys Ile Ala Ser Pro Ser Asn Leu Val Ala Asn Thr
545 550 555 560

Lys Glu Asp Gly Ala Ser Pro Val Cys Arg Val Asp Pro Val Met Ala
565 570 575

Ser Pro

<210> 202
<211> 587
<212> PRT

<213> Arabidopsis lyrata

<400> 202

Met Ala Val Thr Asp Ala Glu Ser Pro His Leu Gly Glu Ile Thr Cys
1 5 10 15

Gly Thr Leu Leu Gln Lys Leu Gln Glu Ile Trp Asp Glu Val Gly Glu
20 25 30

Ser Asp Glu Gln Arg Asp Lys Leu Leu Leu Gln Ile Glu Gln Glu Cys
35 40 45

Leu Asp Val Tyr Lys Arg Lys Val Glu Gln Ala Ala Lys Ser Arg Ala
50 55 60

Glu Leu Leu Gln Thr Leu Ser Asp Ala Asn Ala Glu Leu Ser Ser Leu
65 70 75 80

Thr Thr Ser Leu Gly Glu Lys Ser Leu Val Gly Ile Pro Asp Lys Ser
85 90 95

Ser Gly Thr Ile Lys Glu Gln Leu Ala Ala Ile Ala Pro Ala Leu Glu
100 105 110

Gln Leu Trp Gln Gln Lys Glu Glu Arg Val Arg Glu Phe Ser Asp Val
115 120 125

Gln Ser Gln Ile Gln Lys Ile Cys Gly Glu Ile Ala Gly Gly Leu Ser
130 135 140

Asn Glu Val Pro Ile Val Asp Glu Ser Asp Leu Ser Leu Lys Lys Leu
145 150 155 160

Asp Asp Phe Gln Ser Gln Leu Gln Glu Leu Gln Lys Glu Lys Ser Asp
165 170 175

Arg Leu His Lys Val Leu Asp Phe Val Ser Thr Val His Asp Leu Cys
180 185 190

Ala Val Leu Gly Leu Asp Phe Leu Ser Thr Val Thr Glu Val His Pro
195 200 205

Ser Leu Asp Glu Glu Thr Gly Val Gln Ser Lys Ser Ile Ser Asn Glu
210 215 220

Thr Leu Ser Arg Leu Ala Lys Thr Val Leu Thr Leu Lys Asp Asp Lys
225 230 235 240

Lys Gln Arg Leu Gln Lys Leu Gln Glu Leu Ala Thr Gln Leu Ile Asp
245 250 255

Leu Trp Asn Leu Met Asp Thr Pro Asp Glu Glu Arg Glu Leu Phe Asp
260 265 270

His Val Thr Cys Asn Ile Ser Ser Ser Val Asp Glu Val Thr Val Pro
275 280 285

Gly Ala Leu Ala Arg Asp Leu Ile Glu Gln Ala Glu Val Glu Val His
290 295 300

Arg Leu Asp Gln Leu Lys Ala Ser Arg Met Lys Glu Ile Ala Phe Lys
305 310 315 320

Lys Gln Ser Glu Leu Glu Glu Ile Tyr Ala Arg Ala His Val Glu Ile
325 330 335

Asn Pro Glu Ser Ala Arg Glu Arg Ile Met Ser Leu Ile Asp Thr Gly
340 345 350

Asn Val Glu Pro Thr Glu Leu Leu Ala Asp Met Asp Ser Gln Ile Ala
355 360 365

Lys Ala Lys Glu Glu Ala Phe Ser Arg Lys Asp Ile Leu Asp Arg Val
370 375 380

Glu Lys Trp Met Ser Ala Cys Glu Glu Glu Ser Trp Leu Glu Asp Tyr
385 390 395 400

Asn Arg Asp Gln Asn Arg Tyr Ser Ala Ser Arg Gly Ala His Leu Asn
405 410 415

Leu Lys Arg Ala Glu Lys Ala Arg Ile Leu Val Ser Lys Ile Pro Ala
420 425 430

Met Val Asp Thr Leu Val Ala Lys Thr Arg Ala Trp Glu Glu Glu His
435 440 445

Ser Met Ser Phe Ala Tyr Asp Gly Val Pro Leu Leu Ala Met Leu Asp
450 455 460

Glu Tyr Gly Met Leu Arg Gln Glu Arg Glu Glu Glu Lys Arg Arg Leu
465 470 475 480

Arg Glu Gln Lys Lys Val Gln Glu Gln Pro His Ile Glu Gln Asp Ser
485 490 495

Ala Phe Ser Thr Arg Pro Ser Pro Ala Arg Pro Val Ser Ala Lys Lys
500 505 510

Thr Val Gly Pro Arg Ala Asn Asn Gly Gly Ala Asn Gly Thr Pro Asn
515 520 525

Arg Arg Leu Ser Leu Asn Ala Asn Gln Asn Gly Ser Arg Ser Thr Ala
530 535 540

Lys Glu Ala Gly Arg Arg Glu Thr Leu Asn Arg Pro Ala Ala Pro Thr
545 550 555 560

Asn Tyr Val Ala Ile Ser Lys Glu Glu Ala Ala Ser Ser Pro Val Ser
565 570 575

Gly Ala Val Asp His Lys Val Pro Ala Ser Pro
580 585

<210> 203
<211> 587
<212> PRT
<213> Arabidopsis

<400> 203

Met Ala Val Thr Asp Thr Glu Ser Pro His Leu Gly Glu Ile Thr Cys
1 5 10 15

Gly Thr Leu Leu Glu Lys Leu Gln Glu Ile Trp Asp Glu Val Gly Glu
20 25 30

Ser Asp Asp Glu Arg Asp Lys Leu Leu Leu Gln Ile Glu Gln Glu Cys
35 40 45

Leu Asp Val Tyr Lys Arg Lys Val Glu Gln Ala Ala Lys Ser Arg Ala
50 55 60

Glu Leu Leu Gln Thr Leu Ser Asp Ala Asn Ala Glu Leu Ser Ser Leu
65 70 75 80

Thr Met Ser Leu Gly Asp Lys Ser Leu Val Gly Ile Pro Asp Lys Ser

85 90 95

Ser Gly Thr Ile Lys Glu Gln Leu Ala Ala Ile Ala Pro Ala Leu Glu
100 105 110

Gln Leu Trp Gln Gln Lys Glu Glu Arg Val Arg Glu Phe Ser Asp Val
115 120 125

Gln Ser Gln Ile Gln Lys Ile Cys Gly Asp Ile Ala Gly Gly Leu Ser
130 135 140

Asn Glu Val Pro Ile Val Asp Glu Ser Asp Leu Ser Leu Lys Lys Leu
145 150 155 160

Asp Asp Phe Gln Ser Gln Leu Gln Glu Leu Gln Lys Glu Lys Ser Asp
165 170 175

Arg Leu Arg Lys Val Leu Glu Phe Val Ser Thr Val His Asp Leu Cys
180 185 190

Ala Val Leu Gly Leu Asp Phe Leu Ser Thr Val Thr Glu Val His Pro
195 200 205

Ser Leu Asp Glu Asp Thr Ser Val Gln Ser Lys Ser Ile Ser Asn Glu
210 215 220

Thr Leu Ser Arg Leu Ala Lys Thr Val Leu Thr Leu Lys Asp Asp Lys

225 230 235 240

Lys Gln Arg Leu Gln Lys Leu Gln Glu Leu Ala Thr Gln Leu Ile Asp
245 250 255

Leu Trp Asn Leu Met Asp Thr Pro Asp Glu Glu Arg Glu Leu Phe Asp
260 265 270

His Val Thr Cys Asn Ile Ser Ser Ser Val Asp Glu Val Thr Val Pro
275 280 285

Gly Ala Leu Ala Arg Asp Leu Ile Glu Gln Ala Glu Val Glu Val Asp
290 295 300

Arg Leu Asp Gln Leu Lys Ala Ser Arg Met Lys Glu Ile Ala Phe Lys
305 310 315 320

Lys Gln Ser Glu Leu Glu Glu Ile Tyr Ala Arg Ala His Val Glu Val
325 330 335

Asn Pro Glu Ser Ala Arg Glu Arg Ile Met Ser Leu Ile Asp Ser Gly
340 345 350

Asn Val Glu Pro Thr Glu Leu Leu Ala Asp Met Asp Ser Gln Ile Ser
355 360 365

Lys Ala Lys Glu Glu Ala Phe Ser Arg Lys Asp Ile Leu Asp Arg Val

370 375 380

Glu Lys Trp Met Ser Ala Cys Glu Glu Glu Ser Trp Leu Glu Asp Tyr
385 390 395 400

Asn Arg Asp Gln Asn Arg Tyr Ser Ala Ser Arg Gly Ala His Leu Asn
405 410 415

Leu Lys Arg Ala Glu Lys Ala Arg Ile Leu Val Ser Lys Ile Pro Ala
420 425 430

Met Val Asp Thr Leu Val Ala Lys Thr Arg Ala Trp Glu Glu Glu His
435 440 445

Ser Met Ser Phe Ala Tyr Asp Gly Val Pro Leu Leu Ala Met Leu Asp
450 455 460

Glu Tyr Gly Met Leu Arg Gln Glu Arg Glu Glu Glu Lys Arg Arg Leu
465 470 475 480

Arg Glu Gln Lys Lys Val Gln Glu Gln Pro His Val Glu Gln Glu Ser
485 490 495

Ala Phe Ser Thr Arg Pro Ser Pro Ala Arg Pro Val Ser Ala Lys Lys
500 505 510

Thr Val Gly Pro Arg Ala Asn Asn Gly Gly Ala Asn Gly Thr His Asn

515 520 525

Arg Arg Leu Ser Leu Asn Ala Asn Gln Asn Gly Ser Arg Ser Thr Ala
530 535 540

Lys Glu Ala Gly Arg Arg Glu Thr Leu Asn Arg Pro Ala Ala Pro Thr
545 550 555 560

Asn Tyr Val Ala Ile Ser Lys Glu Glu Ala Ala Ser Ser Pro Val Ser
565 570 575

Gly Ala Ala Asp His Gln Val Pro Ala Ser Pro
580 585

<210> 204
<211> 197
<212> PRT
<213> Arabidopsis lyrata

<400> 204

Met Ile Lys Ser Val Thr Leu Arg Ser Phe His Leu Pro Ile Glu Phe
1 5 10 15

Asn Asp Thr Lys Phe Ala Ala Pro Ser Phe Pro Pro Ala Arg Ser Phe
20 25 30

Pro Val Val Arg Cys Ser Ser Thr Arg Asp Val Pro Lys Leu Glu Leu
35 40 45

Phe Ser Arg Gly Lys Phe Asp Arg Ile Leu Gln Asp Pro Pro Leu Ile
50 55 60

Glu Lys Ala Glu Thr Glu Leu Ser Asp Tyr Cys Ser Thr Leu Glu Gly
65 70 75 80

Asp Asp Ser Tyr Ser Cys Trp Arg Ala Tyr Phe Glu Leu Lys Asp Leu
85 90 95

Glu Arg Glu Lys Pro Lys Val Glu Val Glu Asn Leu Ile Leu Gln Thr
100 105 110

Gly Gly Val Lys Ser Leu Ile Gly Cys Leu His Gly Val Ala Ser Met
115 120 125

Glu Lys Asp Asn Lys Thr Lys Asn Gly Leu Asn Arg Glu Lys Gly Met
130 135 140

Lys Leu His Ile His Ile Pro Asp Gly Leu Pro Lys Ser Glu Gln Glu
145 150 155 160

Leu Glu Glu Glu Glu Lys Ser Lys Met Pro Asp Ser Ala Phe Thr Arg
165 170 175

Leu Leu Arg Thr Lys Gly Thr Ile Pro Ala Trp Phe Ser His Ala Pro
180 185 190

Asp His Glu Thr Asp
195

<210> 205
<211> 207
<212> PRT
<213> Thellungiella

<400> 205

Met Ile Lys Ser Val Thr Leu Arg Ser Phe Pro Leu Pro Ile Glu Phe
1 5 10 15

Asn Gly Lys Ser Lys Phe Leu Glu Pro Ser Thr Ser Tyr Phe Pro Ala
20 25 30

Arg Ser Phe Thr Val Val Arg Cys Ser Ser Thr Arg Asp Val Pro Lys
35 40 45

Leu Glu Leu Phe Ser Arg Gly Lys Phe Asp Arg Ile Leu Gln Asp Pro
50 55 60

Pro Leu Ile Glu Lys Ala Glu Ser Glu Leu Ser Asp Tyr Cys Ser Thr
65 70 75 80

Leu Glu Gly Asp Asp Ser Tyr Ser Cys Trp Lys Ala Tyr Phe Glu Leu
85 90 95

Lys Asp Leu Glu Lys Glu Lys Pro Lys Val Glu Val Glu Asn Leu Ile
100 105 110

Leu Gln Thr Gly Gly Leu Lys Ser Leu Ile Gly Cys Leu His Gly Val
115 120 125

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

Glu Glu Ser Asn Ser Lys Lys Gly Ser Met Lys Leu His Ile His Ile
145 150 155 160

Pro Asp Gly Leu Pro Lys Ser Gln Glu Glu Leu Glu Glu Glu Glu Lys
165 170 175

Ser Leu Met Pro Asp Ser Ala Phe Thr Arg Leu Leu Arg Thr Met Gly
180 185 190

Thr Ile Pro Ala Trp Phe Ser His Val Pro Asp His Glu Thr Asp
195 200 205

<210> 206
<211> 200
<212> PRT
<213> Brassica oleracea, Canola

<400> 206

Met Ile Lys Ser Val Thr Leu Arg Pro Phe Pro Leu Pro Ile Glu Phe
1 5 10 15

His Gly Lys Pro Gln Phe Val Glu Pro Ser Lys Ser Cys Phe Ala Val
20 25 30

Val Arg Cys Ser Ser Thr Arg Asp Val Pro Lys Leu Glu Leu Phe Ser
35 40 45

Arg Gly Lys Phe Asp Arg Val Leu Gln Asp Pro Pro Leu Ile Glu Lys
50 55 60

Thr Glu Asn Glu Leu Ser Asp Tyr Cys Ser Thr Leu Glu Gly Asp Ala
65 70 75 80

Ser Tyr Ser Cys Trp Arg Ala Tyr Phe Glu Leu Lys Asp Leu Glu Lys
85 90 95

Glu Lys Pro Lys Val Glu Val Glu Asn Leu Ile Leu Gln Thr Gly Gly
100 105 110

Val Lys Ser Leu Ile Gly Cys Leu His Gly Leu Ala Ser Met Glu Lys
115 120 125

Glu Ser Lys Thr Lys Asn Gly Ser Glu Val Thr Glu Glu Ser Asp Ser
130 135 140

Asp Lys Met Lys Leu His Val His Val Pro Asp Gly Leu Pro Lys Ser
145 150 155 160

Gln Glu Glu Leu Glu Glu Glu Glu Lys Ser Arg Met Pro Asp Ser Ala
165 170 175

Phe Thr Arg Leu Leu Arg Ala Lys Gly Thr Ile Pro Ala Trp Phe Ser
180 185 190

His Ala Pro Asp His Glu Thr Asp
195 200

<210> 207
<211> 200
<212> PRT
<213> Canola

<400> 207

Met Ile Lys Ser Val Thr Leu Arg Pro Phe Pro Leu Pro Ile Glu Phe
1 5 10 15

His Gly Lys Pro Gln Phe Val Glu Pro Ser Lys Ser Cys Phe Ala Val
20 25 30

Val Arg Cys Ser Ser Thr Arg Asp Val Pro Lys Leu Glu Leu Phe Ser
35 40 45

Arg Gly Lys Phe Asp Arg Val Leu Gln Asp Pro Pro Leu Ile Glu Lys

50 55 60

Ala Glu Thr Glu Leu Ser Asp Tyr Cys Ser Thr Leu Glu Gly Asp Ala
65 70 75 80

Ser Tyr Ser Cys Trp Arg Ala Tyr Phe Glu Leu Lys Asp Leu Glu Lys
85 90 95

Glu Lys Pro Lys Val Glu Val Glu Asn Leu Ile Leu Gln Thr Gly Gly
100 105 110

Leu Lys Ser Leu Ile Gly Cys Leu His Gly Leu Ala Ser Met Lys Lys
115 120 125

Glu Ser Lys Thr Lys Asn Gly Leu Glu Val Thr Glu Glu Thr Asp Ser
130 135 140

Asp Lys Met Lys Pro His Val His Val Pro Asp Gly Leu Pro Lys Ser
145 150 155 160

Gln Glu Glu Leu Glu Glu Glu Glu Lys Ser Arg Met Pro Asp Ser Ala
165 170 175

Phe Thr Arg Leu Leu Arg Ala Lys Gly Thr Ile Pro Ala Trp Phe Ser
180 185 190

His Ala Pro Asp His Glu Thr Asp

195 200

<210> 208
<211> 200
<212> PRT
<213> Brassica rapa

<400> 208

Met Ile Lys Ser Val Thr Leu Arg Pro Phe Pro Leu Pro Ile Glu Phe
1 5 10 15

His Gly Lys Pro Gln Phe Val Glu Pro Ser Lys Ser Cys Phe Ala Val
20 25 30

Val Arg Cys Ser Ser Thr Arg Asp Val Pro Lys Leu Glu Leu Phe Ser
35 40 45

Arg Gly Lys Phe Asp Arg Val Leu Gln Asp Pro Pro Leu Ile Glu Lys
50 55 60

Ala Glu Thr Glu Leu Ser Asp Tyr Cys Ser Thr Leu Glu Gly Asp Ala
65 70 75 80

Ser Tyr Ser Cys Trp Arg Ala Tyr Phe Glu Leu Lys Asp Leu Glu Lys
85 90 95

Glu Lys Pro Lys Val Glu Val Glu Asn Leu Ile Leu Gln Thr Gly Gly
100 105 110

Leu Lys Leu Leu Ile Gly Cys Leu His Gly Leu Ala Ser Met Lys Lys
115 120 125

Glu Ser Lys Thr Lys Asn Gly Leu Glu Val Thr Glu Glu Thr Asp Ser
130 135 140

Asp Lys Met Lys Pro His Val His Val Pro Asp Gly Leu Pro Lys Ser
145 150 155 160

Gln Glu Glu Leu Glu Glu Glu Glu Lys Ser Arg Met Pro Asp Ser Ala
165 170 175

Phe Thr Arg Leu Leu Arg Ala Lys Gly Thr Ile Pro Ala Trp Phe Ser
180 185 190

His Ala Pro Asp His Glu Thr Asp
195 200

<210> 209
<211> 200
<212> PRT
<213> Raphanus sativus

<400> 209

Met Ile Lys Ser Val Thr Leu Arg Pro Phe Pro Leu Pro Ile Glu Phe
1 5 10 15

His Gly Lys Pro Lys Phe Val Gln Thr Ser Lys Ser Cys Phe Pro Val
20 25 30

Val Arg Cys Ser Ser Thr Arg Asp Val Pro Lys Leu Glu Leu Phe Ser
35 40 45

Arg Gly Gln Phe Asp Arg Val Leu Gln Asp Pro Pro Leu Ile Glu Lys
50 55 60

Thr Glu Thr Glu Leu Ser Asp Tyr Cys Cys Lys Leu Glu Gly Asp Asp
65 70 75 80

Ser Tyr Ser Cys Trp Arg Ala Tyr Phe Glu Leu Lys Asp Leu Glu Lys
85 90 95

Glu Lys Pro Lys Val Glu Val Glu Asn Leu Ile Leu Gln Thr Asp Gly
100 105 110

Val Lys Ser Leu Ile Gly Cys Leu His Gly Ile Ala Ser Met Glu Lys
115 120 125

Glu Ser Lys Thr Lys Asn Gly Leu Glu Val Arg Glu Glu Ser Asp Ser
130 135 140

Asp Lys Met Lys Leu His Val His Val Pro Asp Gly Leu Pro Lys Ser
145 150 155 160

Gln Gln Glu Leu Glu Glu Glu Glu Lys Ser Arg Met Pro Asp Ser Ala
165 170 175

Phe Thr Arg Leu Leu Arg Ala Lys Gly Thr Ile Pro Ala Trp Phe Ser
180 185 190

His Pro Pro Asp His Lys Thr Asp
195 200

<210> 210
<211> 1152
<212> ADN
<213> Glycine max

<400> 210
cattttttctc tctttattac attttcatta tggtgaccaa gatatgatct gttatcaata 60

tatattcaat gacattcaca gtcccgagtc ctaacctgag ttgtgtctca acttgctctt 120

cttcttcttc tctttcaccc tccaaatttt ctcactctct ctttatcttc acctttttcag 180

tttaaagctt cagatcacaa ccgatccacc attcaccact ttctcttcac aagctcaagt 240

tactgacagg caaatctaac aagaaaagta gtctctgaag ccgatccagt gccttgtgaa 300

tttggaattg gtggtgaatt tagatctaaa agccatagca atgtctttta tcggtaccca 360

gcaaaagtgc aaggcttgtg agaaaacggt ttatcccgtt gatcagcttt ctgctgatgg 420

tactgcttat cacaaagctt gcttcagatg ctctcactgc aaaggaacat taaagctgag 480

taactattcc tcaatggaag gtgttcttta ctgtaagcct cactatgagc agctcttcaa 540

ggagagtggc tccttcagca agaacttcca gtcacctgca aagctagctg ataagacaac 600

tcctgagctg acaaggtctc ctagtaaagc tgcgagcatg ttttctggca cacaagaaaa 660

gtgtgccaca tgtggcaaaa ctgcttatcc attagagaag gtaacagtgg aagggcaggc 720

ctatcacaaa tcatgtttca agtgttcaca tggtggatgt cccataacgc catcgaatta 780

tgcagccctt gagggcattt tgtattgcaa gcaccacttc tcccagcttt ttaaggagaa 840

agggagctat aatcatctta ctaagtctgc atcagtcaaa cgggcagccg cagccacagc 900

agcagcaaca acagctgcct ctgttccaga atcttgaatg ttggttcctt caattgcctt 960

ttctttttca aatacatttt ggtttgtgaa gcaggtgttt gtatgtgtgg ccttttttggt 1020

ttttgattgt tctctcgtga ctttgatcat ttctgatatt tttacttaca catgcgtggc 1080

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agcgtgattt gc 1152

<210> 211
<211> 1172
<212> ADN
<213> Glycine max

<400> 211
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tatatgttag aactcttgca tattgaagag agtgaagtgc caaaaatgtg tttggatttg 180

tatagggaat acgggacaac tatggcagga ttaaaggtcc ttggttatga gtttgacaat 240

gacgagtttc atgcttacgt gcatggaagg ttaccatacg agaaactgaa gcctgatcca 300

gtattaagga accttctgct ttccatgcct cagcgtaaaa taatattcac caatgcagat 360

catgcacatg cagttaaagt tctcaacaga ttgggtttgg aagattgttt tgagggcatc 420

atatgctttg aaacgcttaa tcctcccaaa caaatcaatt gcatggatgt accaaatgat 480

aatcatgtgc tcacagattt aacagaaaat ggatgtttca attcccaccc acaaatcctc 540

tgtaaaccat ctgtggaagc ctttgaagct gctattcgga ttgctaatgt ggatccaaag 600

aaaacaattt tctttgatga cagtgttaga aatgttgaaa gtgcaaaaat aactggactt 660

aacactgttt tagtgggcca ttcagatttg gtccctggag ctgatcatgc cctgaacagc 720

attcataata tcaaagaagc gttacctgaa atttgggaga ttgaagatgg caaccaacag 780

caaaagattc aacccccaac agttgaaacc atggtcctag cttaa 825

<210> 239
<211> 276
<212> ADN
<213> Glycine max

<400> 239
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ttactactca tgtcctctat tatgctggca actgcagcca aaccactcgg gcgaaaatta 120

ctacaacaag gttatggcgg gccagttccc gactatggcc atcgagatcc agttcccgtc 180

cgcccaacag gtcgttatcg ccggccagat ccatttcccg cctatggcca tcgagatcca 240

gttcccgtcc gcccaataca ttatggacca ccatga 276

<210> 240
<211> 1620
<212> ADN
<213> Glycine max

<400> 240
atggaggcat cacccagtac tctggattgg agaggcagac catccaaccc tgccaaacac 60

ggtggaatga ttccggctgc ttttgttctt gggttgcaag catttgagat aatggcaata 120

gcggcagtgg gaaacaatct gataacttat gtggccaatg acatgcactt ccctttgtcc 180

aaggctgcca acctagtcac taactttgtt gggaccatct ttctcctctc tctcctcggc 240

ggctatctat cagactctta ccttggcagc ttctggacca tgctcctctt tggtttcgtc 300

gaactttctg gtttcatact gctatcagtc caagctcatg ttcctcaatt gaagccacct 360

ccatgcaatg tgaacgatgg agaacagtgc gtagaagcaa agggcatgaa ggccatgata 420

ttctttgtag cactctactt ggtggcatta gggagtgggt gtgtgaagcc aaacatgctt 480

gcttatggag gagaccagtt cgagcaaaac gacccaaagc agttaaagaa gctctcaacc 540

tacttcaatg ccgcatattt tgcattctct gtgggacaac ttgtgagcct aaccattctt 600

gtttgggtgc aaactcattc aggaatggac gttggcttcg gggtatccgc agctgtaatg 660

gcaatgggat tgataagctt gatatgtggc actctatatt acagaaacaa gcccccacaa 720

ggaagtattt taactcccgt ggctcaggtt cttgtcgctg cattttccaa aagaaacctt 780

ccatcttccc catcatccat gatcagagtg gaacaagttg agcaagtgaa gatattgcta 840

tctgttattc cgatattctc gtgcaccatc gttttcaaca ccatcttagc acaacttcag 900

acattctcag tccaacaagg gagagcaatg gacacccatc tcaccaaatc ctttaatatc 960

cctcccgcct cccttcagtc cattccttac attttgctca tctttttagt tcctctctat 1020

gacaccttct ttgtcccatt tgccagaaaa ttcaccggcc atgagtctgg aatctcacct 1080

ttgcgccgaa taggctttgg tctttttctg gctacctttt ctatggttgc agctgctctg 1140

ttggagaaaa agagaaggga cgcagctgtg aaccatcaca aagttttgtc catcttttgg 1200

ataaccccac aatacttgat atttggcttg tcagagatgt tcacagccat tggcctcctt 1260

gagttctttt ataaacagtc cttgaaaggg atgcaagcat tctttacagc catcacatat 1320

tgctcttact catttggctt ttacttgagc acacttttgg tttctttggt caataagatc 1380

acttcaactt cttcttcttc agctgctggc tggcttcaca acaacgacct taaccaggac 1440

aggcttgatc ttttctattg gttactggct gtcttaagct tcctcaactt cctcaactat 1500

ctcttttggt ccagacgcta ttctcatgct ccttccgcac taccccaacc taataatgcc 1560

aaggaaatca acccctactc acaactacat gatcaccatc acaataatat tattccatag 1620

<210> 241
<211> 999
<212> ADN
<213> Glycine max

<400> 241
atgagaggga gctgctggtg gaaccgtcgg acagagcagc gcttccgcct actcgcgatc 60

tccaccgtta aatcactcaa gatcaagctt ctcctctgtt gctgcgtcgc cttcacgctt 120

ctcgcgtttt ccacaagcgc ttcttccttc gtcctatgga tcaacaacca aacgccgcct 180

ccacctcctc gcttccccga ttccaggaaa gggtattcta tagtaatgaa cacatggaag 240

agatatgatc ttctaaagca gtccatcaag cattattcat cgtgtcctcg acttgaatca 300

gtacatatcg tgtggagtga acctgatcct ccgtcagata atcttttaaa atttctgcac 360

cacgttgtaa agtccaagtc taaagatgga agatatgtga aattgaggtt tgatatcaac 420

aaggaagaca gtttgaacaa tagatttaaa gaaattaagg atttggagac agatgctgtc 480

ttttctattg atgatgatgt catatttcct tgctctacgg tggaatttgc atttgatgtt 540

tggcaaagtg cacctgatac aatggttgga tttgtacctc gtgtccattg ggtggattca 600

atggaaggta atgacaacaa atttatatat ggcggatggt ggtctgtgtg gtggacaggt 660

acatatagca tggtgctttc caaggcagca ttctttcaca aaaagtattt caatatctac 720

acaaatgaaa tgccatcatc aattagagaa tatgtaacca agaacaggaa ttgtgaagat 780

attgcaatgt ctttccttgt tgcaaatgct actggtgcac cccccatatg ggttaaaggt 840

aaaatattcg agattggatc gactggaatc agtagtttgg gaggtcacag tgaaagaaga 900

acagaatgcg tcaacagatt tgctgccgtg tatgggcgga tgcccttggt atctacttca 960

gttaaggctg ttgatagccg caatatctgg ttttggtga 999

<210> 242
<211> 1005
<212> ADN

<213> Glycine max

<400> 242

atgagaggga gctgctggtg ctggaaccgt cggacagagc agcggttccg cctcctcgcg 60

atctccaccg ttaaatcact caagatcaag cttctcctct tttgctgcgt cgccttcacg 120

cttctcgcct tttccaccag cgcttcttcc ttcgtcctat ggatcaacaa ccaaacgccg 180

ccgcctccgc cacctcgctt ccccgattcc gggaaagggt attctatagt aatgaacaca 240

tggaagagat atgatcttct aaagcagtcc atcaagcatt attcatcatg tcctcgactt 300

gaatcagtac atattgtgtg gagtgaacct gatcctccat cggatattct tttaaaattt 360

ctgcaccacg ttgtaaagtc caagtctaaa gatggaagat atgtgaaatt gaggtttgat 420

atcaacaagg aagacagttt gaacaataga tttaaagaaa ttaaggattt ggagacagat 480

gctgtctttt ctattgatga tgatgttata tttccttgct ctacggtgga atttgcattt 540

gatgtttggc aaagtgcacc tgatacaatg gttggatttg tacctcgtgt ccattgggtg 600

gattcattgg aaggtaatga cagcaaattt atatatggcg gatggtggtc tgtgtggtgg 660

acgggtacat atagcatggt gctttccaag gcagcattct ttcacaaaaa gtatttcaat 720

atctacacaa atgagatgcc atcatcaatt agagaatatg taaccaagaa caggaattgt 780

gaagatattg caatgtcttt ccttgttgca aatgctaccg gtgcaccccc catatgggtt 840

aaaggtaaaa tattagagat tggatcgact ggaatcagta gtttgggagg tcacagtgaa 900

agaagaacag aatgcgtcaa cagatttgtt gccgcgtatg ggcggatgcc cttggtatct 960

acttcagtta aggctgttga tagccgcaat atctggtttt ggtga 1005

<210> 243
<211> 198
<212> PRT
<213> Glycine max

<400> 243

Met Ser Phe Ile Gly Thr Gln Gln Lys Cys Lys Ala Cys Glu Lys Thr
1 5 10 15

Val Tyr Pro Val Asp Gln Leu Ser Ala Asp Gly Thr Ala Tyr His Lys
20 25 30

Ala Cys Phe Arg Cys Ser His Cys Lys Gly Thr Leu Lys Leu Ser Asn
35 40 45

Tyr Ser Ser Met Glu Gly Val Leu Tyr Cys Lys Pro His Tyr Glu Gln
50 55 60

Leu Phe Lys Glu Ser Gly Ser Phe Ser Lys Asn Phe Gln Ser Pro Ala
65 70 75 80

Lys Leu Ala Asp Lys Thr Thr Pro Glu Leu Thr Arg Ser Pro Ser Lys
85 90 95

Ala Ala Ser Met Phe Ser Gly Thr Gln Glu Lys Cys Ala Thr Cys Gly
100 105 110

Lys Thr Ala Tyr Pro Leu Glu Lys Val Thr Val Glu Gly Gln Ala Tyr
115 120 125

His Lys Ser Cys Phe Lys Cys Ser His Gly Gly Cys Pro Ile Thr Pro
130 135 140

Ser Asn Tyr Ala Ala Leu Glu Gly Ile Leu Tyr Cys Lys His His Phe
145 150 155 160

Ser Gln Leu Phe Lys Glu Lys Gly Ser Tyr Asn His Leu Thr Lys Ser
165 170 175

Ala Ser Val Lys Arg Ala Ala Ala Ala Thr Ala Ala Ala Thr Thr Ala
180 185 190

Ala Ser Val Pro Glu Ser
195

<210> 244
<211> 247
<212> PRT
<213> Glycine max

<400> 244

Met Ala Thr Met Leu Thr Lys Glu His Gly Leu Asn Leu Lys Glu Thr
1 5 10 15

Glu Leu Cys Leu Gly Leu Pro Gly Gly Gly Gly Gly Gly Gly Gly Gly
20 25 30

Gly Gly Gly Gly Gly Gly Glu Val Glu Thr Pro Arg Ala Thr Gly Lys
35 40 45

Arg Gly Phe Ser Glu Thr Val Asp Leu Lys Leu Asn Leu His Ser Lys
50 55 60

Glu Asp Leu Asn Glu Asn Leu Lys Asn Val Ser Lys Glu Lys Thr Leu
65 70 75 80

Leu Lys Asp Pro Ala Lys Pro Pro Ala Lys Ala Gln Val Val Gly Trp
85 90 95

Pro Pro Val Arg Ser Tyr Arg Lys Asn Met Met Ala Val Gln Lys Val
100 105 110

Ser Thr Glu Asp Val Ala Glu Lys Thr Thr Ser Ser Thr Ala Asn Pro
115 120 125

Gly Ala Phe Val Lys Val Ser Met Asp Gly Ala Pro Tyr Leu Arg Lys
130 135 140

Val Asp Leu Thr Met Tyr Lys Ser Tyr Lys Glu Leu Ser Asp Ala Leu
145 150 155 160

Ala Lys Met Phe Ser Ser Phe Thr Met Gly Asn Tyr Gly Ala Gln Gly
165 170 175

Met Ile Asp Phe Met Asn Glu Ser Lys Leu Met Asp Leu Leu Asn Ser
180 185 190

Ser Glu Tyr Val Pro Ser Tyr Glu Asp Lys Asp Gly Asp Trp Met Leu
195 200 205

Val Gly Asp Val Pro Trp Glu Met Phe Val Glu Ser Cys Lys Arg Leu
210 215 220

Arg Ile Met Lys Gly Ser Glu Ala Ile Gly Leu Ala Pro Arg Ala Met
225 230 235 240

Glu Lys Cys Lys Ser Arg Ser
245

<210> 245
<211> 242
<212> PRT
<213> Glycine max

<400> 245

Met Ala Thr Met Leu Thr Lys Glu His Gly Leu Asn Leu Lys Glu Thr
1 5 10 15

Glu Leu Cys Leu Gly Leu Pro Gly Gly Gly Gly Gly Gly Gly Gly Gly

20 25 30

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

Thr Val Asp Leu Lys Leu Asn Leu His Ser Lys Glu Asp Leu Asn Glu
50 55 60

Asn Leu Lys Asn Val Ser Lys Glu Lys Thr Leu Leu Lys Asp Pro Ala
65 70 75 80

Lys Pro Pro Ala Lys Ala Gln Val Val Gly Trp Pro Pro Val Arg Ser
85 90 95

Tyr Arg Lys Asn Met Met Ala Val Gln Lys Val Ser Thr Glu Asp Val
100 105 110

Ala Glu Lys Thr Thr Ser Ser Thr Ala Asn Ser Gly Ala Phe Val Lys
115 120 125

Val Ser Met Asp Gly Ala Pro Tyr Leu Arg Lys Val Asp Leu Thr Met
130 135 140

Tyr Lys Ser Tyr Lys Glu Leu Ser Asp Ala Leu Ala Lys Met Phe Ser
145 150 155 160

Ser Phe Thr Met Gly Asn Tyr Gly Ala Gln Gly Met Ile Asp Phe Met

165 170 175

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

Ser Tyr Glu Asp Lys Asp Gly Asp Trp Met Leu Val Gly Asp Val Pro
195 200 205

Trp Glu Met Phe Val Glu Ser Cys Lys Arg Leu Arg Ile Met Lys Gly
210 215 220

Ser Glu Ala Ile Gly Leu Ala Pro Arg Ala Met Glu Lys Cys Lys Ser
225 230 235 240

Arg Ser

<210> 246
<211> 584
<212> PRT
<213> Glycine max

<400> 246

Met Lys Arg Asp His Arg Asp Ser Cys Gly Gly Gly Gly Gly Gly Ser
1 5 10 15

Val Lys Gly Glu Cys Ser Ser Met Pro Ser Asn Gly Lys Ala Asn Met
20 25 30

Trp Glu Glu Gln Gln Gln Gln Gln Gln Gly Met Asp Glu Leu Leu Ala
35 40 45

Ala Leu Gly Tyr Lys Val Arg Ala Ser Asp Met Ala Asp Val Ala Gln
50 55 60

Lys Leu Glu Gln Leu Glu Met Val Met Gly Cys Ala Gln Glu Glu Gly
65 70 75 80

Ile Ser His Leu Ala Ser Asp Thr Val His Tyr Asp Pro Thr Asp Leu
85 90 95

Tyr Ser Trp Val Gln Thr Met Leu Thr Glu Leu Asn Pro Glu Pro Asn
100 105 110

Asn Asn Asn Asn Ser Leu Leu Gly Pro Ser Ser Leu Leu Ile Asp Asn
115 120 125

Asn Thr Ala Pro Val Phe Asn Asp Asp Ser Glu Tyr Asp Leu Arg Ala
130 135 140

Ile Pro Gly Ile Ala Ala Tyr Pro Pro Pro Pro Pro Gln Asp Asn Asn
145 150 155 160

Asn Asn Asn Asn Asn Leu Asp Glu Ile Glu Thr Ala Asn Asn Ile Asn
165 170 175

Lys Arg Leu Lys Pro Ser Pro Val Glu Ser Ala Asp Ser Ala Ser Glu
180 185 190

Pro Thr Arg Thr Val Leu Leu Val Asp His Gln Glu Ala Gly Val Arg
195 200 205

Leu Val His Thr Leu Leu Ala Cys Ala Glu Ala Val Gln Gln Glu Asn
210 215 220

Leu Lys Leu Ala Asp Ala Leu Val Lys His Val Gly Ile Leu Ala Ala
225 230 235 240

Ser Gln Ala Gly Ala Met Arg Lys Val Ala Ser Tyr Phe Ala Gln Ala
245 250 255

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

Ser Phe Ser Asp Val Leu His Met His Phe Tyr Glu Ser Cys Pro Tyr
275 280 285

Leu Lys Phe Ala His Phe Thr Ala Asn Gln Ala Ile Leu Glu Ala Phe
290 295 300

Ala Thr Ala Gly Arg Val His Val Ile Asp Phe Gly Leu Arg Gln Gly
305 310 315 320

Met Gln Trp Pro Ala Leu Met Gln Ala Leu Ala Leu Arg Pro Gly Gly
325 330 335

Pro Pro Thr Phe Arg Leu Thr Gly Ile Gly Pro Pro Gln Pro Asp Asn
340 345 350

Thr Asp Ala Leu Gln Gln Val Gly Trp Lys Leu Ala Gln Leu Ala Gln
355 360 365

Asn Ile Gly Val Gln Phe Glu Phe Arg Gly Phe Val Cys Asn Ser Leu
370 375 380

Ala Asp Leu Asp Pro Lys Met Leu Glu Ile Arg Pro Gly Glu Ala Val
385 390 395 400

Ala Val Asn Ser Val Phe Glu Leu His Arg Met Leu Ala Arg Pro Gly
405 410 415

Ser Val Asp Lys Val Leu Asp Thr Val Lys Lys Ile Lys Pro Lys Ile
420 425 430

Val Thr Ile Val Glu Gln Glu Ala Asn His Asn Gly Pro Gly Phe Leu
435 440 445

Asp Arg Phe Thr Glu Ala Leu His Tyr Tyr Ser Ser Leu Phe Asp Ser
450 455 460

Leu Glu Gly Ser Ser Ser Ser Thr Gly Leu Gly Ser Pro Asn Gln Asp
465 470 475 480

Leu Leu Met Ser Glu Leu Tyr Leu Gly Arg Gln Ile Cys Asn Val Val
485 490 495

Ala Asn Glu Gly Ala Asp Arg Val Glu Arg His Glu Thr Leu Ser Gln
500 505 510

Trp Arg Gly Arg Leu Asp Ser Ala Gly Phe Asp Pro Val His Leu Gly
515 520 525

Ser Asn Ala Phe Lys Gln Ala Ser Met Leu Leu Ala Leu Phe Ala Gly
530 535 540

Gly Asp Gly Tyr Arg Val Glu Glu Asn Asn Gly Cys Leu Met Leu Gly
545 550 555 560

Trp His Thr Arg Pro Leu Ile Ala Thr Ser Ala Trp Lys Leu Pro Ser
565 570 575

Pro Asn Asp Leu His Cys Lys Leu
580

<210> 247
<211> 1062

<212> PRT
<213> Glycine max

<400> 247

Met Lys Pro Phe Ser Leu Leu Val Leu Ser Leu Tyr Phe Phe Ser Val
1 5 10 15

Val Gly Gln Leu Pro Ser Gln Asp Ile Leu Ala Leu Leu Glu Phe Lys
20 25 30

Lys Gly Ile Lys His Asp Pro Thr Gly Tyr Val Leu Asn Ser Trp Asn
35 40 45

Glu Glu Ser Ile Asp Phe Asp Gly Cys Pro Ser Ser Trp Asn Gly Val
50 55 60

Leu Cys Asn Ala Gly Asn Val Ala Gly Val Val Leu Asp Asn Leu Gly
65 70 75 80

Leu Ser Ala Asp Pro Asp Leu Ser Val Phe Ser Asn Leu Thr Lys Leu
85 90 95

Val Lys Leu Ser Met Ser Asn Asn Ser Ile Ser Gly Thr Leu Pro Asp
100 105 110

Asn Ile Ala Asp Phe Lys Ser Leu Glu Phe Leu Asp Ile Ser Asn Asn
115 120 125

Leu Phe Ser Ser Ser Leu Pro Leu Gly Ile Gly Glu Leu Arg Ser Leu
130 135 140

Gln Asn Leu Ser Leu Ala Gly Asn Asn Phe Ser Gly Pro Ile Pro Asp
145 150 155 160

Ser Ile Ser Glu Met Ala Ser Ile Lys Ser Leu Asp Leu Ser Arg Asn
165 170 175

Ser Phe Ser Gly Met Leu Pro Val Thr Leu Thr Lys Thr Thr Ser Leu
180 185 190

Val Ser Leu Asn Leu Ser His Asn Gly Phe Thr Gly Lys Val Pro Lys
195 200 205

Gly Phe Glu Leu Ile Pro Ala Leu Glu Lys Leu Asp Leu His Gly Asn
210 215 220

Met Leu Glu Gly Asn Leu Asp Val Val Phe Met Leu Leu Ser Ser Ala
225 230 235 240

Ser Tyr Val Asp Leu Ser Glu Asn Met Leu Ser Ser Ser Asp Ser Lys
245 250 255

Lys Lys Phe Leu Pro Arg Ile Ser Glu Ser Ile Lys His Leu Asn Leu
260 265 270

Ser His Asn Lys Leu Thr Gly Ser Leu Ala Ser Gly Ala Ala Glu Pro
275 280 285

Val Phe Glu Asn Leu Lys Val Leu Asp Leu Ser Tyr Asn Gln Leu Asp
290 295 300

Gly Glu Leu Pro Gly Phe Asp Phe Val Tyr Asp Leu Glu Val Leu Arg
305 310 315 320

Leu Ser Asn Asn Arg Phe Ser Gly Phe Ile Pro Asn Gly Leu Leu Lys
325 330 335

Gly Asp Ser Leu Val Leu Thr Glu Leu Asp Leu Ser Ala Asn Asn Leu
340 345 350

Ser Gly Pro Leu Ser Ile Ile Thr Ser Thr Thr Leu His Ser Leu Asn
355 360 365

Leu Ser Ser Asn Glu Phe Thr Gly Asp Leu Pro Leu Leu Thr Gly Ser
370 375 380

Cys Ala Val Leu Asp Leu Ser Asn Asn Lys Leu Glu Gly Asn Leu Thr
385 390 395 400

Arg Met Leu Lys Trp Gly Asn Ile Glu Phe Leu Asp Leu Ser Gly Asn
405 410 415

His Leu Thr Gly Thr Ile Pro Glu Glu Thr Pro Gln Phe Leu Arg Leu
420 425 430

Ser Tyr Leu Asn Leu Ser His Asn Ser Leu Ser Ser Ser Leu Pro Lys
435 440 445

Val Leu Thr Gln Tyr Pro Lys Leu Arg Val Leu Asp Ile Ser Phe Asn
450 455 460

Gln Leu Asp Gly Leu Leu Leu Ala Asn Leu Leu Thr Leu Ser Thr Leu
465 470 475 480

Gln Glu Leu His Leu Glu Asn Asn Met Ile Ser Gly Gly Ile Lys Phe
485 490 495

Ser Ser Ser Ala Asp Gln Ser Asp Leu Gln Ile Leu Asp Leu Ser His
500 505 510

Asn Gln Leu Asn Gly Tyr Phe Pro Asp Glu Phe Gly Ser Leu Thr Gly
515 520 525

Leu Lys Val Leu Asn Ile Ala Gly Asn Asn Phe Ser Gly Ser Leu Pro
530 535 540

Thr Thr Ile Ala Asp Met Ser Ser Leu Asp Ser Leu Asp Ile Ser Glu
545 550 555 560

Asn His Phe Ala Gly Pro Leu Pro Ser Asn Ile Pro Lys Gly Leu Gln
565 570 575

Asn Phe Asn Ala Ser Gln Asn Asp Leu Ser Gly Leu Val Pro Glu Val
580 585 590

Leu Arg Lys Phe Pro Ser Ser Ser Phe Phe Pro Gly Asn Thr Lys Leu
595 600 605

His Phe Pro Asn Gly Pro Pro Gly Ser Val Ser Ser Pro Ala Lys Ser
610 615 620

Ser Lys Arg Lys His Met Asn Thr Ile Val Lys Val Ile Ile Ile Val
625 630 635 640

Ser Cys Val Val Ala Leu Phe Ile Leu Ile Leu Leu Ala Val Phe Ile
645 650 655

His Tyr Ile Arg Ile Ser Arg Ser Pro Gln Glu Tyr Asp Ala Ser Lys
660 665 670

Asp Ile His Arg His Pro Gln Pro Ile Ile Ser Ala Pro Val Arg Thr
675 680 685

Thr Asp Arg Gly Gly Ala Leu Val Val Ser Ala Glu Asp Leu Val Thr
690 695 700

Ser Arg Lys Glu Ser Pro Ser Glu Ile Ile Ser Ser Asp Glu Lys Met
705 710 715 720

Ala Ala Val Thr Gly Phe Ser Pro Ser Lys Gln Ser His Phe Ser Trp
725 730 735

Ser Pro Glu Ser Gly Asp Ser Leu Thr Gly Glu Asn Leu Ala Arg Leu
740 745 750

Asp Thr Arg Ser Pro Asp Arg Leu Ile Gly Glu Leu His Phe Leu Asp
755 760 765

Asp Thr Ile Thr Leu Thr Pro Glu Glu Leu Ser Arg Ala Pro Ala Glu
770 775 780

Val Leu Gly Arg Ser Ser His Gly Thr Ser Tyr Lys Ala Thr Leu Glu
785 790 795 800

Asn Gly Leu Leu Leu Arg Val Lys Trp Leu Arg Glu Gly Val Ala Lys
805 810 815

Gln Arg Lys Glu Phe Val Lys Glu Met Lys Lys Phe Ala Asn Ile Arg
820 825 830

His Pro Asn Val Val Gly Leu Arg Gly Tyr Tyr Trp Gly Pro Thr Gln
835 840 845

His Glu Lys Leu Ile Leu Ser Asp Tyr Ile Ser Pro Gly Ser Leu Ala
850 855 860

Ser Phe Leu Tyr Asp Arg Pro Gly Arg Lys Gly Pro Pro Leu Thr Trp
865 870 875 880

Ala Gln Arg Leu Lys Ile Ala Val Asp Val Ala Arg Gly Leu Asn Tyr
885 890 895

Leu His Phe Asp Arg Ala Val Pro His Gly Asn Leu Lys Ala Thr Asn
900 905 910

Val Leu Leu Asp Thr Thr Asp Met Asn Ala Arg Val Ala Asp Tyr Cys
915 920 925

Leu His Arg Leu Met Thr Arg Ala Gly Asn Ile Glu Gln Ile Leu Asp
930 935 940

Ala Gly Val Leu Gly Tyr Arg Ala Pro Glu Leu Ala Ala Ser Lys Lys
945 950 955 960

Pro Met Pro Ser Phe Lys Ser Asp Val Tyr Ala Phe Gly Val Ile Leu
965 970 975

Leu Glu Leu Leu Thr Gly Arg Cys Ala Gly Asp Val Ile Ser Ser Glu
980 985 990

Glu Gly Gly Val Asp Leu Thr Asp Trp Val Arg Leu Arg Val Ala Glu
995 1000 1005

Gly Arg Gly Ser Glu Cys Phe Asp Ala Thr Leu Met Pro Glu Met
1010 1015 1020

Ser Asn Pro Ile Ala Glu Lys Gly Met Lys Glu Val Leu Gly Ile
1025 1030 1035

Val Met Arg Cys Ile Arg Ser Val Ser Glu Arg Pro Gly Ile Lys
1040 1045 1050

Thr Ile Tyr Glu Asp Leu Ser Ser Ile
1055 1060

<210> 248
<211> 510
<212> PRT
<213> Glycine max

<400> 248

Met Phe Ile Glu Ser Phe Lys Val Glu Ser Pro Asn Val Lys Tyr Thr
1 5 10 15

Glu Thr Glu Ile Gln Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
20 25 30

His Glu Asn Asn Asn Gly Thr Tyr Gln Trp Val Val Lys Pro Lys Thr
35 40 45

Val Lys Tyr Glu Phe Lys Thr Asn Thr His Val Pro Lys Leu Gly Val
50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
65 70 75 80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Ile
85 90 95

Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
100 105 110

Val Gly Ser Phe Gln Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
115 120 125

Leu Pro Met Val Asn Pro Asp Asp Val Val Phe Gly Gly Trp Asp Ile
130 135 140

Ser Asn Leu Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
165 170 175

Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Asp
180 185 190

Arg Ala Thr Asn Val Ile Arg Gly Thr Lys Lys Glu Gln Val Gln Gln
195 200 205

Ile Ile Lys Asp Ile Lys Glu Phe Lys Glu Ser Thr Lys Val Asp Lys
210 215 220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Val
225 230 235 240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Phe Ala Ser Leu Asp Arg
245 250 255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
260 265 270

Met Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
275 280 285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Arg Asn Ser Leu Ile Gly Gly
290 295 300

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

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

His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
340 345 350

Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Asn
355 360 365

Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
370 375 380

Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
385 390 395 400

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

His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
420 425 430

Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Glu Phe Lys Ala Glu
435 440 445

Asn Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Ser Thr Pro Val Val Asn
465 470 475 480

Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Leu Arg Ala Cys
485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510

<210> 249
<211> 535
<212> PRT
<213> Glycine max

<400> 249

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

Thr Ile Thr Arg Leu Ile Phe Thr Val Gly Lys Thr Glu Gln Trp Lys
20 25 30

Ala Pro Ile Leu Pro Glu Leu Asp Ile Asp Asn Ile Ser His Lys Leu
35 40 45

His Asp Asp Pro Glu Thr Ile Gln Met Ala Ser Arg Asp Tyr Gly His
50 55 60

Leu Thr His Glu Phe Pro Leu Ala Val Phe Arg Pro Ser Ser Ile Asp

65 70 75 80

Asp Ile Val Thr Leu Ile Lys Ser Ser Tyr Asn Ser Phe Ala Pro Phe
85 90 95

Asp Ile Ala Ala Arg Gly Gln Gly His Ser Thr His Gly Gln Ala Met
100 105 110

Ala Arg Asp Gly Ile Val Val Asp Met Ala Ser Leu Arg Lys Gln Arg
115 120 125

Asn Gly Val Ala Ile Ser Val Ser Lys Asp Pro Leu Met Gly His Tyr
130 135 140

Ala Asp Val Gly Gly Glu Gln Leu Trp Ile Asp Val Leu His Ala Thr
145 150 155 160

Leu Glu Tyr Gly Leu Ala Pro Val Ser Trp Thr Asp Tyr Leu Tyr Leu
165 170 175

Thr Val Gly Gly Thr Leu Ser Asn Ala Gly Ile Ser Gly Gln Ser Phe
180 185 190

Arg Tyr Gly Pro Gln Ile Ser Asn Val His Glu Met Asp Val Ile Thr
195 200 205

Gly Lys Gly Glu Phe Val Thr Cys Ser Ser Gln Lys Asn Leu Glu Leu

210 215 220

Phe His Ala Val Leu Gly Gly Leu Gly Gln Phe Gly Val Ile Ala Arg
225 230 235 240

Ala Arg Ile Ala Leu Glu Pro Ala Pro Lys Arg Val Lys Trp Val Arg
245 250 255

Leu Leu Tyr Ser Asp Phe Ser Ala Phe Thr Lys Asp Gln Glu Arg Leu
260 265 270

Ile Ser Ile Asn Gly Arg Lys Gln Lys Asn Ala Leu Asp Phe Leu Glu
275 280 285

Gly Met Leu Leu Met Asn Gln Gly Pro Ile Asn Asn Trp Arg Ser Ser
290 295 300

Phe Phe Pro Leu Ser Asp His Pro Arg Ile Ala Ser Leu Ile Thr Glu
305 310 315 320

His Ser Ile Leu Tyr Cys Leu Glu Val Ala Lys Tyr Tyr Asp Glu Gln
325 330 335

Thr Glu Leu Asn Val Asp Lys Glu Ile Glu Val Leu Leu Gln Gly Leu
340 345 350

Ala Tyr Ile Pro Gly Phe Asn Tyr Glu Lys Asn Val Ser Tyr Val Glu

355 360 365

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

Leu Trp Glu Val Pro His Pro Trp Leu Asn Leu Phe Ile Pro Lys Ser
385 390 395 400

Gln Ile Leu Asp Phe Asn Ser Gly Val Phe Lys Asp Ile Val Leu Lys
405 410 415

Arg Asn Ile Ser Ser Gly Pro Val Leu Val Tyr Pro Met Asn Arg Asn
420 425 430

Lys Trp Asp Asp Arg Met Ser Ala Ser Ile Pro Asp Glu Asp Val Phe
435 440 445

Tyr Thr Val Gly Phe Leu His Ser Ser Gly Phe Asp Thr Trp Lys Ala
450 455 460

Tyr Asp Ala Gln Asn Arg Glu Ile Leu Glu Phe Cys Arg Asp Ala Gly
465 470 475 480

Ile Met Val Lys Gln Tyr Leu Pro Asn His Ser Thr Gln Glu Asp Trp
485 490 495

Thr Asn His Phe Gly Ala Lys Trp Met Lys Phe Leu Glu Arg Lys His

500 505 510

Gln Phe Asp Pro Arg Met Ile Leu Ser Pro Gly Gln Lys Ile Phe His
515 520 525

Lys Lys Leu Gln Pro Val Phe
530 535

<210> 250
<211> 419
<212> PRT
<213> Glycine max

<400> 250

Met Gly Ile Pro Trp Asp Asp Val Val Val Ile Gln Gln Gly Lys Asp
1 5 10 15

His Asn Glu Pro Cys Ile Val Thr Val Asn Cys Pro Asp Lys Ala Gly
20 25 30

Leu Gly Cys Asp Leu Cys Arg Ile Ile Leu Glu Phe Gly Leu Arg Ile
35 40 45

Thr Arg Ala Asp Ile Ser Thr Asp Gly Arg Trp Cys Tyr Ile Val Tyr
50 55 60

Trp Val Leu Ala His Pro Ala Ser Leu Asn Val Asp Trp Glu Ser Leu
65 70 75 80

Lys Thr Arg Leu Leu Ser Ala Cys Pro Ser Cys Leu Leu Ser Tyr His
85 90 95

Phe Asn Gln His Ser Thr Ser Pro Ser Pro Pro Pro Ile Tyr Leu Leu
100 105 110

Lys Val Trp Cys Val Asp Gln Lys Gly Leu Leu His Asp Ile Asn Glu
115 120 125

Ile Leu Cys Asn Leu Glu Leu Ile Ile Gln Arg Val Lys Ala Met Pro
130 135 140

Thr Pro Asp Gly Arg Val Leu Asp Met Phe Phe Ile Thr Asp Gly Met
145 150 155 160

Glu Leu Leu His Thr Lys Lys Arg Gln Asp Tyr Val Cys Glu Tyr Leu
165 170 175

Met Asp Ala Leu Gly Glu Arg Cys Ile Ser Ser Glu Leu Gln Leu Ala
180 185 190

Gly Pro Glu Tyr Gly His Leu Gln Gly Phe Ser Ser Leu Pro Pro Ala
195 200 205

Phe Ala Glu Glu Leu Phe Ser Ser Glu Leu Leu Asp Lys Leu Ser Leu
210 215 220

His Pro Leu Ser Gln Asp Met Thr Thr Leu Lys Thr Pro Thr Val Thr
225 230 235 240

Val Asp Asn Ser Leu Ser Pro Val His Thr Leu Leu Gln Ile Gln Cys
245 250 255

Val Asp Gln Lys Gly Leu Cys Tyr Asp Ile Met Arg Ile Ser Lys Asp
260 265 270

Ser Asp Ile Lys Val Ala Phe Gly Arg Phe Ser Ser Ser Val Lys Gly
275 280 285

Phe Arg Asn Ile Asp Leu Phe Val Gln His Asn Asp Gly Lys Lys Ile
290 295 300

Ile Asp Pro Glu Ser Gln Lys Thr Leu Cys Ser Cys Leu Lys Glu Glu
305 310 315 320

Met Leu His Pro Leu Arg Val Thr Ile Val Asn Arg Gly Pro Asp Thr
325 330 335

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

Arg Val Phe Tyr Asp Val Thr Leu Thr Leu Lys Ala Leu Gly Val Gly
355 360 365

Ile Phe Ser Ala Glu Val Val Arg His Ser Thr Gln Glu Arg Gln Trp
370 375 380

Glu Val Tyr Arg Phe Leu Leu Glu Glu Ser Arg Asp Phe Pro Leu Thr
385 390 395 400

Arg Ser Gln Ala Arg Thr Gln Ile Val Asp Lys Val Arg Arg Thr Leu
405 410 415

Met Gly Trp

<210> 251
<211> 113
<212> PRT
<213> Glycine max

<400> 251

Met Ser Pro Lys Tyr Met Ser Leu Phe Leu Leu Val Ile Leu Gly Met
1 5 10 15

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

Glu Asp Gly His Asp His His His His His Pro Pro Lys Lys His Trp
35 40 45

Pro Pro Thr Thr Gln Asn Glu Pro Ser Asn Val Glu Asn Lys Glu Asn
50 55 60

Thr Glu Val Glu Asp Gly His Asp His His His His Tyr Pro Pro Lys
65 70 75 80

Lys His Trp Pro Pro Thr Thr Gln Asn Glu Pro Ser Lys Val Glu Asn
85 90 95

Lys Asp Gly His Tyr Lys Pro Pro His Lys Lys His Pro Pro Ser Gly
100 105 110

Asn

<210> 252
<211> 355
<212> PRT
<213> Glycine max

<400> 252

Met Ala Thr Gln Ser Glu Glu Asn Ala Thr Lys Phe Leu Gln Ala Tyr
1 5 10 15

Thr Gln Ile Asp Asp His Ser Leu Arg Phe Ile His Ser Met Ser Leu
20 25 30

Lys Cys Ala Ile Asp Leu Ser Ile Pro Asp Ile Ile His Lys Tyr Gly
35 40 45

Gln Pro Met Pro Leu Ser Gln Leu Ile Ala Ser Leu Pro Ile His Pro
50 55 60

Ser Lys Thr Cys Tyr Ile His Arg Leu Met Arg Leu Phe Thr His Ser
65 70 75 80

Gly Phe Phe Ser Arg His Asp Leu Val Glu Asn Glu Gln Glu Val Ile
85 90 95

Thr Tyr Glu Leu Thr Asp Ala Ser Arg Leu Leu Leu Lys Asp His Pro
100 105 110

Phe Ser Leu Arg Pro Leu Leu Leu Val Thr Leu Asp Pro Ser Val Ile
115 120 125

Lys Ser Trp Cys Gln Phe Ser Thr Trp Leu Thr Ser Glu Asp Arg Thr
130 135 140

Pro Phe Gln Thr Glu Asn Gly Val Thr Tyr Phe Asp Tyr Ala Lys Arg
145 150 155 160

Asp Pro Lys Phe Gly His Phe Tyr Asn Asp Ala Met Ala Lys Asp Thr
165 170 175

Arg Phe Ala Ser Ser Val Val Ile Glu Asn Tyr Lys Glu Val Phe Glu
180 185 190

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

Lys Ala Ile Ala Lys Ala Phe Pro Gln Val Lys Cys Thr Val Phe Asp
210 215 220

Leu Pro His Val Val Asp Gly Leu Gln Gly Thr Glu Asn Ile Glu Tyr
225 230 235 240

Val Gly Gly Asp Met Phe Glu Val Ile Pro Ala Ala Asp Cys Ile Met
245 250 255

Leu Lys Trp Val Leu His Cys Trp Asn Asp Glu Glu Cys Met Lys Ile
260 265 270

Leu Lys Lys Cys Lys Glu Ala Ile Pro Ser Asp Gly Lys Val Ile Ile
275 280 285

Met Glu Leu Val Met Glu His Asn Lys Glu Asp Asn Lys Leu Ile Glu
290 295 300

Met Gln Leu Cys Cys Asp Met Leu Met Met Ser Leu Phe Ala Gly Lys
305 310 315 320

Asp Arg Thr Glu Lys Glu Trp Ala His Leu Ile Ala Ser Ala Gly Phe
325 330 335

Ser Asn Tyr Lys Ile Thr His Ile Phe Asp Leu Tyr His Ile Ile Val
340 345 350

Val Tyr Pro
355

<210> 253
<211> 355
<212> PRT
<213> Glycine max

<400> 253

Met Ala Thr Gln Ser Glu Glu Asn Ala Thr Lys Phe Leu Gln Ala Tyr
1 5 10 15

Thr Gln Ile Asp Asp His Ser Leu Gly Phe Ile His Ser Met Ser Leu
20 25 30

Lys Cys Ala Ile Asp Leu Ser Ile Pro Asp Ile Ile His Lys Tyr Gly
35 40 45

Gln Pro Met Pro Leu Ser Gln Leu Ile Ala Ser Leu Pro Ile His Pro
50 55 60

Ser Lys Thr Cys Tyr Ile His Arg Leu Met Arg Leu Leu Thr His Ser

65 70 75 80

Gly Phe Phe Ser Arg His Asp Leu Val Glu Asn Glu Gln Glu Val Ile
85 90 95

Thr Tyr Glu Leu Thr Asp Ala Ser Arg Leu Leu Leu Lys Asp His Pro
100 105 110

Phe Ser Leu Arg Pro Leu Leu Leu Val Thr Leu Asp Pro Ser Val Ile
115 120 125

Lys Ser Trp Cys Gln Phe Ser Thr Trp Leu Thr Ser Glu Asp Arg Thr
130 135 140

Pro Phe Gln Thr Glu Asn Gly Val Thr Tyr Phe Asp Tyr Ala Lys Arg
145 150 155 160

Asp Pro Lys Phe Gly His Phe Tyr Asn Asp Ala Met Ala Lys Asp Thr
165 170 175

Arg Phe Ala Ser Ser Val Val Ile Glu Asn Tyr Lys Glu Val Phe Glu
180 185 190

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

Lys Ala Ile Ala Lys Ala Phe Pro Gln Val Lys Cys Thr Val Phe Asp

210 215 220

Leu Pro His Val Val Asp Gly Leu Gln Gly Thr Glu Asn Ile Glu Tyr
225 230 235 240

Val Gly Gly Asp Met Phe Glu Val Ile Pro Ala Ala Asp Cys Ile Met
245 250 255

Leu Lys Trp Val Leu His Cys Trp Asn Asp Glu Glu Cys Met Lys Ile
260 265 270

Leu Lys Lys Cys Lys Glu Ala Ile Pro Ser Asp Gly Lys Val Ile Ile
275 280 285

Met Glu Leu Val Met Glu His Asn Lys Glu Asp Asn Lys Leu Ile Glu
290 295 300

Met Gln Leu Cys Cys Asp Met Leu Met Met Ser Leu Phe Ala Gly Lys
305 310 315 320

Asp Arg Thr Glu Lys Glu Trp Ala His Leu Ile Ala Ser Ala Gly Phe
325 330 335

Ser Asn Tyr Lys Ile Thr His Ile Phe Asp Leu Tyr His Ile Ile Val
340 345 350

Val Tyr Pro

355

<210> 254
<211> 560
<212> PRT
<213> Glycine max

<400> 254

Met Asp Ser Trp Val Arg Met Leu Phe Leu Ile Ala Cys Ile Val Pro
1 5 10 15

Ala Leu Val Glu Cys Lys Val Arg His Tyr Lys Phe Asn Val Val Leu
20 25 30

Lys Asn Thr Thr Arg Leu Cys Ser Ser Lys Pro Ile Val Thr Val Asn
35 40 45

Gly Lys Phe Pro Gly Pro Thr Leu Tyr Ala Arg Glu Asp Asp Thr Val
50 55 60

Leu Val Lys Val Asn Asn Leu Val Asn His Asn Val Thr Ile His Trp
65 70 75 80

His Gly Val Arg Gln Leu Arg Thr Gly Trp Ala Asp Gly Pro Ala Tyr
85 90 95

Ile Thr Gln Cys Pro Ile Leu Ser Gly Gln Ser Tyr Leu Tyr Asn Phe
100 105 110

Thr Leu Thr Gly Gln Arg Gly Thr Leu Leu Trp His Ala His Val Asn
115 120 125

Trp Leu Arg Ser Thr Leu His Gly Ala Ile Val Ile Leu Pro Lys Arg
130 135 140

Gly Val Pro Tyr Pro Phe Pro Lys Pro Asp Lys Glu Leu Val Val Ile
145 150 155 160

Leu Gly Glu Trp Trp Lys Ser Asp Thr Glu Asp Val Ile Asn Glu Ala
165 170 175

Leu Lys Ser Gly Leu Ala Pro Asn Val Ser Asp Ala His Thr Ile Asn
180 185 190

Gly Leu Pro Gly Ile Val Ser Val Ala Asn Cys Ser Thr Gln Asp Val
195 200 205

Tyr Lys Leu Pro Val Glu Ser Gly Lys Thr Tyr Leu Leu Arg Ile Ile
210 215 220

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

Phe Thr Val Val Glu Val Asp Ala Ser Tyr Val Lys Pro Phe Lys Thr
245 250 255

Asp Thr Leu Ser Ile Ala Pro Gly Gln Thr Thr Asn Ala Leu Leu Thr
260 265 270

Ala Asp Gln Asn Ser Gly Lys Tyr Thr Ile Val Ala Ser Thr Phe Met
275 280 285

Asp Ser Pro Val Val Ala Val Asp Asn Leu Thr Ala Thr Ala Thr Leu
290 295 300

His Tyr Thr Gly Thr Leu Ala Thr Thr Pro Thr Leu Leu Thr Thr Pro
305 310 315 320

Pro Pro Arg Asn Ala Thr Gln Val Ala Asn Asn Phe Thr Asn Ser Leu
325 330 335

Lys Ser Leu Asn Ser Lys Lys Tyr Pro Ala Lys Val Pro Gln Lys Val
340 345 350

Asp His Ser Leu Leu Leu Thr Val Gly Leu Gly Ile Asn Pro Cys Pro
355 360 365

Ser Cys Thr Ala Gly Asn Gly Ser Arg Val Val Ala Ala Val Asn Asn
370 375 380

Val Thr Phe Val Met Pro Thr Thr Ala Leu Leu Gln Ala His Tyr Phe
385 390 395 400

Asn Ile Lys Gly Val Phe Thr Thr Asp Phe Pro Gly Asn Pro Ser His
405 410 415

Val Tyr Asn Tyr Thr Ala Thr Pro Pro Ala Ala Ala Trp Gln Thr Thr
420 425 430

Asn Gly Thr Lys Ala Tyr Arg Leu Ala Phe Asn Ser Thr Val Gln Val
435 440 445

Val Leu Gln Asp Thr Gly Val Ile Ala Pro Glu Ser His Pro Val His
450 455 460

Leu His Gly Phe Asn Phe Phe Val Val Gly Ser Asp Val Gly Asn Tyr
465 470 475 480

Asp Pro Lys Thr Asp Gln Asn Asn Phe Asn Leu Ala Asp Pro Val Glu
485 490 495

Arg Asn Thr Ile Gly Val Pro Thr Gly Gly Trp Val Ala Phe Arg Phe
500 505 510

Arg Ala Asp Asn Pro Gly Val Trp Phe Leu His Cys His Phe Glu Val
515 520 525

His Thr Thr Trp Gly Leu Lys Met Ala Phe Leu Val Asp Asn Gly Lys
530 535 540

Gly Pro Asn Glu Ser Leu Leu Pro Pro Pro Lys Asp Leu Pro Lys Cys
545 550 555 560

<210> 255
<211> 560
<212> PRT
<213> Glycine max

<400> 255

Met Asp Ser Trp Val Arg Met Leu Phe Leu Ile Ala Cys Ile Val Pro
1 5 10 15

Ala Leu Val Glu Cys Lys Val Arg His Tyr Lys Phe Asn Val Val Leu
20 25 30

Lys Asn Thr Thr Arg Leu Cys Ser Ser Lys Pro Ile Val Thr Val Asn
35 40 45

Gly Lys Phe Pro Gly Pro Thr Leu Tyr Ala Arg Glu Asp Asp Thr Val
50 55 60

Leu Val Lys Val Asn Asn Leu Val Asn His Asn Val Thr Ile His Trp
65 70 75 80

His Gly Val Arg Gln Leu Arg Thr Gly Trp Ala Asp Gly Pro Ala Tyr
85 90 95

Ile Thr Gln Cys Pro Ile Leu Ser Gly Gln Ser Tyr Leu Tyr Asn Phe
100 105 110

Thr Leu Thr Gly Gln Arg Gly Thr Leu Leu Trp His Ala His Val Asn
115 120 125

Trp Leu Arg Ser Thr Leu His Gly Ala Ile Val Ile Leu Pro Lys Arg
130 135 140

Gly Val Pro Tyr Pro Phe Pro Lys Pro Asp Lys Glu Leu Val Val Ile
145 150 155 160

Leu Gly Glu Trp Trp Lys Ser Asp Thr Glu Asp Val Ile Asn Glu Ala
165 170 175

Leu Lys Ser Gly Leu Ala Pro Asn Val Ser Asp Ala His Thr Ile Asn
180 185 190

Gly Leu Pro Gly Ile Val Ser Val Ala Asn Cys Ser Thr Gln Asp Val
195 200 205

Tyr Lys Leu Pro Val Glu Ser Gly Lys Thr Tyr Leu Leu Arg Ile Ile
210 215 220

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

Phe Thr Val Val Glu Val Asp Ala Ser Tyr Val Lys Pro Phe Lys Thr
245 250 255

Asp Thr Leu Ser Ile Ala Pro Gly Gln Thr Thr Asn Ala Leu Leu Thr
260 265 270

Ala Asp Gln Asn Ser Gly Lys Tyr Thr Ile Val Ala Ser Thr Phe Met
275 280 285

Asp Ser Pro Val Val Ala Val Asp Asn Leu Thr Ala Thr Ala Thr Leu
290 295 300

His Tyr Thr Gly Thr Leu Ala Thr Thr Pro Thr Leu Leu Thr Thr Pro
305 310 315 320

Pro Pro Arg Asn Ala Thr Gln Val Ala Asn Asn Phe Thr Asn Ser Leu
325 330 335

Lys Ser Leu Asn Ser Lys Lys Tyr Pro Ala Lys Val Pro Gln Lys Val
340 345 350

Asp His Ser Leu Leu Leu Thr Val Gly Leu Gly Ile Asn Pro Cys Pro
355 360 365

Ser Cys Thr Ala Gly Asn Gly Ser Arg Val Val Ala Ala Val Asn Asn
370 375 380

Val Thr Phe Val Met Pro Thr Thr Ala Leu Leu Gln Ala His Tyr Phe
385 390 395 400

Asn Ile Lys Gly Val Phe Thr Thr Asp Phe Pro Gly Asn Pro Ser His
405 410 415

Val Tyr Asn Tyr Thr Ala Thr Pro Pro Ala Ala Ala Trp Gln Thr Thr
420 425 430

Asn Gly Thr Lys Ala Tyr Arg Leu Ala Phe Asn Ser Thr Val Gln Val
435 440 445

Val Leu Gln Asp Thr Gly Val Ile Ala Pro Glu Ser His Pro Val His
450 455 460

Leu His Gly Phe Asn Phe Phe Val Val Gly Ser Gly Val Gly Asn Tyr
465 470 475 480

Asp Pro Lys Thr Asp Gln Asn Asn Phe Asn Leu Ala Asp Pro Val Glu
485 490 495

Arg Asn Thr Ile Gly Val Pro Thr Gly Gly Trp Val Ala Phe Arg Phe
500 505 510

Arg Ala Asp Asn Pro Gly Val Trp Phe Leu His Cys His Phe Glu Val
515 520 525

His Thr Thr Trp Gly Leu Lys Met Ala Phe Leu Val Asp Asn Gly Lys
530 535 540

Gly Pro Asn Glu Ser Leu Leu Pro Pro Pro Lys Asp Leu Pro Lys Cys
545 550 555 560

<210> 256
<211> 274
<212> PRT
<213> Glycine max

<400> 256

Met Asp Thr Ser Tyr Arg Thr Gly Gly Val Lys Tyr Glu Cys Leu Leu
1 5 10 15

Phe Asp Met Asp Asp Thr Leu Tyr Pro Leu Ser Leu Gly Leu Asn Leu
20 25 30

Phe Cys Arg Lys Asn Ile Gln Glu Tyr Met Leu Glu Leu Leu His Ile
35 40 45

Glu Glu Ser Glu Val Pro Lys Met Cys Leu Asp Leu Tyr Arg Glu Tyr
50 55 60

Gly Thr Thr Met Ala Gly Leu Lys Val Leu Gly Tyr Glu Phe Asp Asn
65 70 75 80

Asp Glu Phe His Ala Tyr Val His Gly Arg Leu Pro Tyr Glu Lys Leu
85 90 95

Lys Pro Asp Pro Val Leu Arg Asn Leu Leu Leu Ser Met Pro Gln Arg
100 105 110

Lys Ile Ile Phe Thr Asn Ala Asp His Ala His Ala Val Lys Val Leu
115 120 125

Asn Arg Leu Gly Leu Glu Asp Cys Phe Glu Gly Ile Ile Cys Phe Glu
130 135 140

Thr Leu Asn Pro Pro Lys Gln Ile Asn Cys Met Asp Val Pro Asn Asp
145 150 155 160

Asn His Val Leu Thr Asp Leu Thr Glu Asn Gly Cys Phe Asn Ser His
165 170 175

Pro Gln Ile Leu Cys Lys Pro Ser Val Glu Ala Phe Glu Ala Ala Ile
180 185 190

Arg Ile Ala Asn Val Asp Pro Lys Lys Thr Ile Phe Phe Asp Asp Ser
195 200 205

Val Arg Asn Val Glu Ser Ala Lys Ile Thr Gly Leu Asn Thr Val Leu
210 215 220

Val Gly His Ser Asp Leu Val Pro Gly Ala Asp His Ala Leu Asn Ser
225 230 235 240

Ile His Asn Ile Lys Glu Ala Leu Pro Glu Ile Trp Glu Ile Glu Asp
245 250 255

Gly Asn Gln Gln Gln Lys Ile Gln Pro Pro Thr Val Glu Thr Met Val
260 265 270

Leu Ala

<210> 257
<211> 91
<212> PRT
<213> Glycine max

<400> 257

Met Ala Phe Val Gly Ala Ser Lys Met Met Ser Ser Phe Gly Ala Leu
1 5 10 15

Leu Ala Ile Leu Leu Leu Leu Met Ser Ser Ile Met Leu Ala Thr Ala
20 25 30

Ala Lys Pro Leu Gly Arg Lys Leu Leu Gln Gln Gly Tyr Gly Gly Pro
35 40 45

Val Pro Asp Tyr Gly His Arg Asp Pro Val Pro Val Arg Pro Thr Gly

50 55 60

Arg Tyr Arg Arg Pro Asp Pro Phe Pro Ala Tyr Gly His Arg Asp Pro
65 70 75 80

Val Pro Val Arg Pro Ile His Tyr Gly Pro Pro
85 90

<210> 258
<211> 539
<212> PRT
<213> Glycine max

<400> 258

Met Glu Ala Ser Pro Ser Thr Leu Asp Trp Arg Gly Arg Pro Ser Asn
1 5 10 15

Pro Ala Lys His Gly Gly Met Ile Pro Ala Ala Phe Val Leu Gly Leu
20 25 30

Gln Ala Phe Glu Ile Met Ala Ile Ala Ala Val Gly Asn Asn Leu Ile
35 40 45

Thr Tyr Val Ala Asn Asp Met His Phe Pro Leu Ser Lys Ala Ala Asn
50 55 60

Leu Val Thr Asn Phe Val Gly Thr Ile Phe Leu Leu Ser Leu Leu Gly
65 70 75 80

Gly Tyr Leu Ser Asp Ser Tyr Leu Gly Ser Phe Trp Thr Met Leu Leu
85 90 95

Phe Gly Phe Val Glu Leu Ser Gly Phe Ile Leu Leu Ser Val Gln Ala
100 105 110

His Val Pro Gln Leu Lys Pro Pro Pro Cys Asn Val Asn Asp Gly Glu
115 120 125

Gln Cys Val Glu Ala Lys Gly Met Lys Ala Met Ile Phe Phe Val Ala
130 135 140

Leu Tyr Leu Val Ala Leu Gly Ser Gly Cys Val Lys Pro Asn Met Leu
145 150 155 160

Ala Tyr Gly Gly Asp Gln Phe Glu Gln Asn Asp Pro Lys Gln Leu Lys
165 170 175

Lys Leu Ser Thr Tyr Phe Asn Ala Ala Tyr Phe Ala Phe Ser Val Gly
180 185 190

Gln Leu Val Ser Leu Thr Ile Leu Val Trp Val Gln Thr His Ser Gly
195 200 205

Met Asp Val Gly Phe Gly Val Ser Ala Ala Val Met Ala Met Gly Leu
210 215 220

Ile Ser Leu Ile Cys Gly Thr Leu Tyr Tyr Arg Asn Lys Pro Pro Gln
225 230 235 240

Gly Ser Ile Leu Thr Pro Val Ala Gln Val Leu Val Ala Ala Phe Ser
245 250 255

Lys Arg Asn Leu Pro Ser Ser Pro Ser Ser Met Ile Arg Val Glu Gln
260 265 270

Val Glu Gln Val Lys Ile Leu Leu Ser Val Ile Pro Ile Phe Ser Cys
275 280 285

Thr Ile Val Phe Asn Thr Ile Leu Ala Gln Leu Gln Thr Phe Ser Val
290 295 300

Gln Gln Gly Arg Ala Met Asp Thr His Leu Thr Lys Ser Phe Asn Ile
305 310 315 320

Pro Pro Ala Ser Leu Gln Ser Ile Pro Tyr Ile Leu Leu Ile Phe Leu
325 330 335

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

Gly His Glu Ser Gly Ile Ser Pro Leu Arg Arg Ile Gly Phe Gly Leu
355 360 365

Phe Leu Ala Thr Phe Ser Met Val Ala Ala Ala Leu Leu Glu Lys Lys
370 375 380

Arg Arg Asp Ala Ala Val Asn His His Lys Val Leu Ser Ile Phe Trp
385 390 395 400

Ile Thr Pro Gln Tyr Leu Ile Phe Gly Leu Ser Glu Met Phe Thr Ala
405 410 415

Ile Gly Leu Leu Glu Phe Phe Tyr Lys Gln Ser Leu Lys Gly Met Gln
420 425 430

Ala Phe Phe Thr Ala Ile Thr Tyr Cys Ser Tyr Ser Phe Gly Phe Tyr
435 440 445

Leu Ser Thr Leu Leu Val Ser Leu Val Asn Lys Ile Thr Ser Thr Ser
450 455 460

Ser Ser Ser Ala Ala Gly Trp Leu His Asn Asn Asp Leu Asn Gln Asp
465 470 475 480

Arg Leu Asp Leu Phe Tyr Trp Leu Leu Ala Val Leu Ser Phe Leu Asn
485 490 495

Phe Leu Asn Tyr Leu Phe Trp Ser Arg Arg Tyr Ser His Ala Pro Ser
500 505 510

Ala Leu Pro Gln Pro Asn Asn Ala Lys Glu Ile Asn Pro Tyr Ser Gln
515 520 525

Leu His Asp His His His Asn Asn Ile Ile Pro
530 535

<210> 259
<211> 332
<212> PRT
<213> Glycine max

<400> 259

Met Arg Gly Ser Cys Trp Trp Asn Arg Arg Thr Glu Gln Arg Phe Arg
1 5 10 15

Leu Leu Ala Ile Ser Thr Val Lys Ser Leu Lys Ile Lys Leu Leu Leu
20 25 30

Cys Cys Cys Val Ala Phe Thr Leu Leu Ala Phe Ser Thr Ser Ala Ser
35 40 45

Ser Phe Val Leu Trp Ile Asn Asn Gln Thr Pro Pro Pro Pro Pro Arg
50 55 60

Phe Pro Asp Ser Arg Lys Gly Tyr Ser Ile Val Met Asn Thr Trp Lys
65 70 75 80

Arg Tyr Asp Leu Leu Lys Gln Ser Ile Lys His Tyr Ser Ser Cys Pro
85 90 95

Arg Leu Glu Ser Val His Ile Val Trp Ser Glu Pro Asp Pro Pro Ser
100 105 110

Asp Asn Leu Leu Lys Phe Leu His His Val Val Lys Ser Lys Ser Lys
115 120 125

Asp Gly Arg Tyr Val Lys Leu Arg Phe Asp Ile Asn Lys Glu Asp Ser
130 135 140

Leu Asn Asn Arg Phe Lys Glu Ile Lys Asp Leu Glu Thr Asp Ala Val
145 150 155 160

Phe Ser Ile Asp Asp Asp Val Ile Phe Pro Cys Ser Thr Val Glu Phe
165 170 175

Ala Phe Asp Val Trp Gln Ser Ala Pro Asp Thr Met Val Gly Phe Val
180 185 190

Pro Arg Val His Trp Val Asp Ser Met Glu Gly Asn Asp Asn Lys Phe
195 200 205

Ile Tyr Gly Gly Trp Trp Ser Val Trp Trp Thr Gly Thr Tyr Ser Met
210 215 220

Val Leu Ser Lys Ala Ala Phe Phe His Lys Lys Tyr Phe Asn Ile Tyr
225 230 235 240

Thr Asn Glu Met Pro Ser Ser Ile Arg Glu Tyr Val Thr Lys Asn Arg
245 250 255

Asn Cys Glu Asp Ile Ala Met Ser Phe Leu Val Ala Asn Ala Thr Gly
260 265 270

Ala Pro Pro Ile Trp Val Lys Gly Lys Ile Phe Glu Ile Gly Ser Thr
275 280 285

Gly Ile Ser Ser Leu Gly Gly His Ser Glu Arg Arg Thr Glu Cys Val
290 295 300

Asn Arg Phe Ala Ala Val Tyr Gly Arg Met Pro Leu Val Ser Thr Ser
305 310 315 320

Val Lys Ala Val Asp Ser Arg Asn Ile Trp Phe Trp
325 330

<210> 260
<211> 334
<212> PRT
<213> Glycine max

<400> 260

Met Arg Gly Ser Cys Trp Cys Trp Asn Arg Arg Thr Glu Gln Arg Phe
1 5 10 15

Arg Leu Leu Ala Ile Ser Thr Val Lys Ser Leu Lys Ile Lys Leu Leu
20 25 30

Leu Phe Cys Cys Val Ala Phe Thr Leu Leu Ala Phe Ser Thr Ser Ala
35 40 45

Ser Ser Phe Val Leu Trp Ile Asn Asn Gln Thr Pro Pro Pro Pro Pro
50 55 60

Pro Arg Phe Pro Asp Ser Gly Lys Gly Tyr Ser Ile Val Met Asn Thr
65 70 75 80

Trp Lys Arg Tyr Asp Leu Leu Lys Gln Ser Ile Lys His Tyr Ser Ser
85 90 95

Cys Pro Arg Leu Glu Ser Val His Ile Val Trp Ser Glu Pro Asp Pro
100 105 110

Pro Ser Asp Ile Leu Leu Lys Phe Leu His His Val Val Lys Ser Lys
115 120 125

Ser Lys Asp Gly Arg Tyr Val Lys Leu Arg Phe Asp Ile Asn Lys Glu
130 135 140

Asp Ser Leu Asn Asn Arg Phe Lys Glu Ile Lys Asp Leu Glu Thr Asp
145 150 155 160

Ala Val Phe Ser Ile Asp Asp Asp Val Ile Phe Pro Cys Ser Thr Val
165 170 175

Glu Phe Ala Phe Asp Val Trp Gln Ser Ala Pro Asp Thr Met Val Gly
180 185 190

Phe Val Pro Arg Val His Trp Val Asp Ser Leu Glu Gly Asn Asp Ser
195 200 205

Lys Phe Ile Tyr Gly Gly Trp Trp Ser Val Trp Trp Thr Gly Thr Tyr
210 215 220

Ser Met Val Leu Ser Lys Ala Ala Phe Phe His Lys Lys Tyr Phe Asn
225 230 235 240

Ile Tyr Thr Asn Glu Met Pro Ser Ser Ile Arg Glu Tyr Val Thr Lys
245 250 255

Asn Arg Asn Cys Glu Asp Ile Ala Met Ser Phe Leu Val Ala Asn Ala
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RESUMEN

La invención se refiere a métodos y composiciones para incrementar la resistencia o la tolerancia frente a una plaga de nematodos que atacan plantas en una planta o una de sus partes. Se proporcionan secuencias de nucleótidos que confieren resistencia o tolerancia frente a plagas de nematodos que atacan plantas cuando se expresan en una planta, así como también composiciones que comprenden los polipéptidos codificados por las secuencias de nucleótidos, y plantas transgénicas y partes de estas que comprenden las secuencias de nucleótidos.