(12) STANDARD PATENT (11) Application No. **AU 2008355461 B2**
(19) AUSTRALIAN PATENT OFFICE

(54) Title
Cyanobacteria saxitoxin gene cluster and detection of cyanotoxic organisms

(51) International Patent Classification(s)
C12Q 1/68 (2006.01) ***C12N 9/10*** (2006.01)
C12N 9/02 (2006.01) ***C12N 9/20*** (2006.01)
C12N 9/04 (2006.01) ***C12N 9/78*** (2006.01)

(21) Application No: **2008355461** (22) Date of Filing: **2008.12.05**

(87) WIPO No: **WO09/129558**

(30) Priority Data

(31) Number	(32) Date	(33) Country
2008902056	**2008.04.24**	**AU**

(43) Publication Date: **2009.10.29**
(44) Accepted Journal Date: **2015.07.30**

(71) Applicant(s)
NewSouth Innovations Pty Limited

(72) Inventor(s)
Kellmann, Ralf;Neilan, Brett A.;Jeon, Young Jae;Mihali, Troco Kaan

(74) Agent / Attorney
Spruson & Ferguson, L 35 St Martins Tower 31 Market St, Sydney, NSW, 2000

(56) Related Art
POMATI, F. et al., Nucleic Acids Research, 2004, Vol. 32, No. 1, e7

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

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
29 October 2009 (29.10.2009)

PCT

(10) International Publication Number
WO 2009/129558 A1

(51) International Patent Classification:
C12Q 1/68 (2006.01) *C12N 9/02* (2006.01)
C12N 9/04 (2006.01) *C12N 9/10* (2006.01)
C12N 9/20 (2006.01) *C12N 9/78* (2006.01)

(21) International Application Number:
PCT/AU2008/001805

(22) International Filing Date:
5 December 2008 (05.12.2008)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
2008902056 24 April 2008 (24.04.2008) AU

(71) Applicant *(for all designated States except US)*: **NEWSOUTH INNOVATIONS PTY LIMITED** [AU/AU]; Rupert Myers Building, Barker Street, University of New South Wales, NSW 2052 (AU).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: **NEILAN, Brett, A.** [AU/AU]; 2/15 McKeon Street, Maroubra, NSW 2035 (AU). **MIHALI, Troco, Kaan** [DE/AU]; 2/18 Carlisle Street, Tamarama, NSW 2026 (AU). **KELLMANN, Ralf** [DE/NO]; Gamle Kirkeveien 5, N-5222 Nesttun (NO). **JEON, Young, Jae** [KR/AU]; 2/11 Anzac Parade, Kensington, NSW 2033 (AU).

(74) Agent: **SPRUSON & FERGUSON**; GPO Box 3898, Syndey, NSW 2001 (AU).

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

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

Published:

— *with international search report (Art. 21(3))*

— *with sequence listing part of description (Rule 5.2(a))*

WO 2009/129558 A1

(54) **Title**: CYANOBACTERIA SAXITOXIN GENE CLUSTER AND DETECTION OF CYANOTOXIC ORGANISMS

(57) **Abstract**: The present invention relates to methods for the detection of cyanobacteria, dinoflagellates, and in particular, methods for the detection of cyanotoxic organisms. Kits for the detection of cyanobacteria, dinoflagellates, and cyanotoxic organisms are provided. The invention further relates to methods of screening for compounds that modulate the activity of polynucleotides and/or polypeptides of the saxitoxin and cylindrospermopsin biosynthetic pathways.

Cyanobacteria saxitoxin gene cluster and detection of cyanotoxic organisms

Technical Field

The present invention relates to methods for the detection of cyanobacteria, dinoflagellates, and in particular, methods for the detection of cyanotoxic organisms. Kits for the detection of cyanobacteria, dinoflagellates, and cyanotoxic organisms are provided. The invention further relates to methods of screening for compounds that modulate the activity of polynucleotides and/or polypeptides of the saxitoxin and cylindrospermopsin biosynthetic pathways.

Background

Cyanobacteria, also known as blue-green algae, are photosynthetic bacteria widespread in marine and freshwater environments. Of particular significance for water quality and human and animal health are those cyanobacteria which produce toxic compounds. Under eutrophic conditions cyanobacteria tend to form large blooms which drastically promote elevated toxin concentrations. Cyanobacterial blooms may flourish and expand in coastal waters, streams, lakes, and in drinking water and recreational reservoirs. The toxins they produce can pose a serious health risk for humans and animalsand this problem is internationally relevant since most toxic cyanobacteria have a global distribution.

A diverse range of cyanobacterial genera are well known for the formation of toxic blue-green algal blooms on water surfaces. Saxitoxin (*SXT*) and its analogues cause the paralytic shellfish poisoning (PSP) syndrome, which afflicts human health and impacts on coastal shellfish economies worldwide. PSP toxins are unique alkaloids, being produced by both prokaryotes and eukaryotes. PSP toxins are among the most potent and pervasive algal toxins and are considered a serious toxicological health-risk that may affect humans, animals and ecosystems worldwide. These toxins block voltage-gated sodium and calcium channels, and prolong the gating of potassium channels preventing the transduction of neuronal signals. It has been estimated that more than 2000 human cases of PSP occur globally every year. Moreover, coastal blooms of producing microorganisms result in millions of dollars of economic damage due to PSP toxin contamination of seafood and the continuous requirement for costly biotoxin monitoring programs. Early warning systems to anticipate paralytic shellfish toxin (PST)-producing

algal blooms, such as PCR and ELISA-based screening, are as yet unavailable due to the lack of data on the genetic basis of PST production.

SXT is a tricyclic perhydropurine alkaloid which can be substituted at various positions leading to more than 30 naturally occurring *SXT* analogues. Although *SXT* biosynthesis seems complex and unique, organisms from two kingdoms, including certain species of marine dinoflagellates and freshwater cyanobacteria, are capable of producing these toxins, apparently by the same biosynthetic route. In spite of considerable efforts none of the enzymes or genes involved in the biosynthesis and modification of *SXT* have been previously identified.

The occurrence of the cyanobacterial genus *Cylindrospermopsis* has been documented on all continents and therefore poses a significant public health threat on a global scale. The major toxin produced by *Cylindrospermopsis* is cylindrospermopsin (*CYR*). Besides posing a threat to human health, cylindrospermopsin also causes significant economic losses for farmers due to the poisoning of livestock with cylindrospermopsin-contaminated drinking water. Cylindrospermopsin has hepatotoxic, general cytotoxic and neurotoxic effects and is a potential carcinogen. Its toxicity is due to the inhibition of glutathione and protein synthesis as well as inhibiting cytochrome P450. Six cyanobacterial species have so far been identified to produce cylindrospermopsin; *Cylindrospermopsis raciborskii, Aphanizomenon ovalisporum, Aphanizomenon flos-aquae, Umezakia natans, Rhaphdiopsis curvata* and *Anabaena bergii*. Incidents of human poisoning with cylindrospermopsin have only been reported in sub-tropical Australia to date, however *C. raciborskii* and *A. flos-aquae* have recently been detected in areas with more temperate climates. The tendency of *C. raciborskii* to form dense blooms and the invasiveness of the producer organisms gives rise to global concerns for drinking water quality and necessitates the monitoring of drinking water reserves for the presence of cylindrospermopsin producers.

There is a need for rapid and accurate methods detecting cyanobacteria, and in particular those strains which are capable of producing cyanotoxins such as saxitoxin and cylindrospermopsin. Rapid and accurate methods for detecting cyanotoxic organisms are needed for assessing the potential health hazard of cyanobacterial blooms and for the implementation of effective water management strategies to minimize the effects of toxic bloom outbreaks.

2008355461 10 Jun 2015

Summary

In a first aspect, there is provided an isolated polynucleotide comprising a sequence according to SEQ ID NO: 1 or a variant or fragment thereof, wherein said fragment encodes a protein of a saxitoxin biosynthetic pathway.

In one embodiment of the first aspect, the fragment comprises a sequence selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, and variants and fragments thereof.

In a second aspect, there is provided an isolated ribonucleic acid or an isolated complementary DNA encoded by a sequence according to the first aspect.

In a third aspect, there is provided an isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, and variants and fragments thereof.

In one embodiment, there is provided a probe or primer that hybridises specifically with one or more of: a polynucleotide according to the first aspect, a ribonucleic acid or complementary DNA according to the second aspect, or a polypeptide according the third aspect.

In another embodiment, there is provided a vector comprising a polynucleotide according to the first aspect, or a ribonucleic acid or complementary DNA according the second aspect. The vector may be an expression vector.

In another embodiment, a host cell is provided comprising the vector.

In another embodiment, there is provided an isolated antibody capable of binding specifically to a polypeptide according to the third aspect.

2008355461 10 Jun 2015

In a fourth aspect, there is provided a method for the detection of cyanobacteria and/or dinoflagellates, the method comprising the steps of obtaining a sample for use in the method and analyzing the sample for the presence of one or more of:

(i) a polynucleotide comprising a sequence according to the first aspect

(ii) a ribonucleic acid or complementary DNA according to the second aspect

(iii) a polypeptide comprising a sequence according to third aspect

wherein said presence is indicative of cyanobacteria and/or dinoflagellates in the sample.

In a fifth aspect, there is provided a method for detecting a cyanotoxic organism, the method comprising the steps of obtaining a sample for use in the method and analyzing the sample for the presence of one or more of:

(i) a polynucleotide comprising a sequence selected from the group consisting of: SEQ ID NO: 14, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 36, and variants thereof sharing at least 80% sequence homology with SEQ ID NO: 14, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, or SEQ ID NO: 36,

(ii) a ribonucleic acid or complementary DNA encoded by a sequence according to (i)

(iii) a polypeptide comprising a sequence selected from the group consisting of: SEQ ID NO: 15, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 37, and variants thereof sharing at least 80% sequence homology with SEQ ID NO: 15, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, or SEQ ID NO: 37,

wherein said presence is indicative of cyanotoxic organisms in the sample.

In one embodiment of the fifth aspect, the cyanotoxic organism is a cyanobacteria or a dinoflagellate.

In one embodiment of the fourth and fifth aspects, analyzing the sample comprises amplification of DNA from the sample by polymerase chain reaction and detecting the amplified sequences. The polymerase chain reaction may utilise one or more primers comprising a sequence selected from the group consisting of SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 72, SEQ ID NO: 73, SEQ ID NO: 74, SEQ ID NO: 75, SEQ ID NO: 76, SEQ ID NO: 77, SEQ ID NO: 78, SEQ ID NO: 79, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO:

2008355461 10 Jun 2015

128, SEQ ID NO: 129, SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 132, SEQ ID NO: 133, SEQ ID NO: 134, and variants and fragments thereof.

In another embodiment of the fourth and fifth aspects, the method comprises further analyzing the sample for the presence of one or more of:

(i) a polynucleotide comprising a sequence selected from the group consisting of: SEQ ID NO: 80, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, and variants and fragments thereof,

(ii) a ribonucleic acid or complementary DNA encoded by a sequence according to (i),

(iii) a polypeptide comprising a sequence selected from the group consisting of: SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92 , SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, and SEQ ID NO: 110, and variants and fragments thereof.

The further analyis of the sample may comprise amplification of DNA from the sample by polymerase chain reaction. The polymerase chain reaction may utilise one or more primers comprising a sequence selected from the group consisting of SEQ ID NO: 111, SEQ ID NO: 112, or variants or fragments thereof.

Described herein is a method for the detection of dinoflagellates, the method comprising the steps of obtaining a sample for use in the method and analyzing the sample for the presence of one or more of:

(i) a polynucleotide comprising a sequence according to the first aspect,

(ii) a ribonucleic acid or complementary DNA according to the second aspect,

(iii) a polypeptide comprising a sequence according to the third aspect,

wherein said presence is indicative of dinoflagellates in the sample.

Analysing the sample may comprise amplification of DNA from the sample by polymerase chain reaction and detecting the amplified sequences.

In one embodiment of the fourth and fifth aspects, the detection comprises one or both of gel electrophoresis and nucleic acid sequencing. The sample may comprise one or more isolated or cultured organisms. The sample may be an environmental sample. The environmental sample may be derived from salt water, fresh water or a blue-green algal bloom.

2008355461 10 Jun 2015

In a sixth aspect, there is provided a kit for the detection of cyanobacteria and/or dinoflagellates, the kit comprising at least one agent for detecting the presence of one or more of:

(i) a polynucleotide comprising a sequence according to the first aspect,

(ii) a ribonucleic acid or complementary DNA according to the second aspect,

(iii) a polypeptide comprising a sequence according to the third aspect,

wherein said presence is indicative of cyanobacteria and/or dinoflagellates in the sample.

In a seventh aspect, there is provided a kit for the detection of cyanotoxic organisms, the kit comprising at least one agent for detecting the presence of one or more of:

(i) a polynucleotide comprising a sequence selected from the group consisting of: SEQ ID NO: 14, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 36, and variants thereof sharing at least 90% sequence homology with SEQ ID NO: 14, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, or SEQ ID NO: 36,

(ii) a ribonucleic acid or complementary DNA encoded by a sequence according to (i),

(iii) a polypeptide comprising a sequence selected from the group consisting of: SEQ ID NO: 15, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 37, and variants thereof sharing at least 90% sequence homology with SEQ ID NO: 15, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, or SEQ ID NO: 37,

wherein said presence is indicative of cyanotoxic organisms in the sample.

In one embodiment of the sixth and seventh aspects, the at least one agent is a primer, antibody or probe. The primer or probe may comprise a sequence selected from the group consisting of SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 72, SEQ ID NO: 73, SEQ ID NO: 74, SEQ ID NO: 75, SEQ ID NO: 76, SEQ ID NO: 77, SEQ ID NO: 78, SEQ ID NO: 79, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 132, SEQ ID NO: 133, SEQ ID NO: 134, and variants and fragments thereof.

In another embodiment of the sixth and seventh aspects, the kit further comprises at least one additional agent for detecting the presence of one or more of:

2008355461 10 Jun 2015

(i) a polynucleotide comprising a sequence selected from the group consisting of: SEQ ID NO: 80, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, and variants and fragments thereof,

(ii) a ribonucleic acid or complementary DNA encoded by a sequence according to (i),

(iii) a polypeptide comprising a sequence selected from the group consisting of: SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92 , SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, and SEQ ID NO: 110, and variants and fragments thereof.

The at least one additional agent may be a primer, antibody or probe. The primer or probe may comprise a sequence selected from the group consisting of SEQ ID NO: 109, SEQ ID NO: 110, and variants and fragments thereof.

Described herein is a kit for the detection of dinoflagellates, the kit comprising at least one agent for detecting the presence of one or more of:

(i) a polynucleotide comprising a sequence according to the first aspect,

(ii) a ribonucleic acid or complementary DNA according to the second aspect,

(iii) a polypeptide comprising a sequence according to the third aspect,

wherein said presence is indicative of dinoflagellates in the sample.

In an eighth aspect, there is provided a method of screening for a compound that modulates the expression or activity of one or more polypeptides according to the third aspect, the method comprising contacting the polypeptide with a candidate compound under conditions suitable to enable interaction of the candidate compound and the polypeptide, and assaying for activity of the polypeptide.

In one embodiment of the eighth aspect, modulating the expression or activity of one or more polypeptides comprises inhibiting the expression or activity of said polypeptide.

In another embodiment of the eighth aspect, modulating the expression or activity of one or more polypeptides comprises enhancing the expression or activity of said polypeptide.

Described herein is an isolated polynucleotide comprising a sequence according to SEQ ID NO: 80 or a variant or fragment thereof.

2008355461 10 Jun 2015

The fragment may comprise a sequence selected from the group consisting of SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO:107, SEQ ID NO: 109, and variants and fragments thereof.

Described herein is a ribonucleic acid or complementary DNA encoded by a sequence according to the present invention.

Described herein is an isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92 , SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, and variants and fragments thereof.

In one embodiment, there is provided a probe or primer that hybridises specifically with one or more of: a polynucleotide according to the present invention, a ribonucleic acid or complementary DNA according to the present invention, or a polypeptide according to the present invention.

In another embodiment, there is provided a vector comprising a polynucleotide according to the present invention, or a ribonucleic acid or complementary DNA according to the present invention. The vector may be an expression vector. In one embodiment, a host cell is provided comprising the vector.

In another embodiment, there is provided an isolated antibody capable of binding specifically to a polypeptide according to the present invention.

Described herein is a method for the detection of cyanobacteria, the method comprising the steps of obtaining a sample for use in the method and analyzing the sample for the presence of one or more of:

(i) a polynucleotide comprising a sequence according to the present invention,

(ii) a ribonucleic acid or complementary DNA according to the present invention,

(iii) a polypeptide comprising a sequence according to present invention,

wherein said presence is indicative of cyanobacteria in the sample.

Described herein is a method for detecting a cyanotoxic organism, the method comprising the steps of obtaining a sample for use in the method and analyzing the sample for the presence of one or both of:

(i) a polynucleotide comprising a sequence according to SEQ ID NO: 95 or a variant or fragment thereof,

2008355461 10 Jun 2015

(ii) a ribonucleic acid or complementary DNA encoded by a sequence according to (i),

(iii) a polypeptide comprising a sequence according to SEQ ID NO: 96, or a variant or fragment thereof,

wherein said presence is indicative of a cyanotoxic organism in the sample.

The cyanotoxic organism may be a cyanobacterium.

Analyzing the sample may comprise amplification of DNA from the sample by polymerase chain reaction and detecting the amplified sequences. The polymerase chain reaction may utilise one or more primers comprising a sequence selected from the group consisting of SEQ ID NO: 111, SEQ ID NO: 112 and variants and fragments thereof.

The method may comprise analyzing the sample for the presence of one or more of:

(i) a polynucleotide comprising a sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, and variants and fragments thereof,

(ii) a ribonucleic acid or complementary DNA encoded by a sequence according to (i),

(iii) a polypeptide comprising a sequence selected from the group consisting of: SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19 SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, and variants and fragments thereof.

The further analysis of the sample may comprise amplification of DNA from the sample by polymerase chain reaction. The polymerase chain reaction may utilise one or more primers comprising a sequence selected from the group consisting of SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 72, SEQ ID NO: 73, SEQ ID NO: 74, SEQ ID NO: 75,

2008355461 10 Jun 2015

SEQ ID NO: 76, SEQ ID NO: 77, SEQ ID NO: 78, SEQ ID NO: 79, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 132, SEQ ID NO: 133, SEQ ID NO: 134, and variants and fragments thereof.

Described herein is a method for detecting a cylindrospermopsin-producing organism, the method comprising the steps of obtaining a sample for use in the method and analyzing the sample for the presence of one or both of:

(i) a polynucleotide comprising a sequence according to SEQ ID NO: 95 or a variant or fragments thereof,

(ii) a ribonucleic acid or complementary DNA encoded by a sequence according to (i),

(iii) a polypeptide comprising a sequence according to SEQ ID NO: 96, or a variant or fragments thereof,

wherein said presence is indicative of a cylindrospermopsin-producing organism in the sample.

The cyanotoxic organism may be a cyanobacterium. Analyzing the sample may comprise amplification of DNA from the sample by polymerase chain reaction and detecting the amplified sequences. The polymerase chain reaction may utilise one or more primers comprising a sequence selected from the group consisting of SEQ ID NO: 111, SEQ ID NO: 112 and variants and fragments thereof.

The detection may comprise one or both of gel electrophoresis and nucleic acid sequencing. The sample may comprise one or more isolated or cultured organisms. The sample may be an environmental sample. The environmental sample may be derived from salt water, fresh water or a blue-green algal bloom.

Described herein is a kit for the detection of cyanobacteria, the kit comprising at least one agent for detecting the presence of one or more of:

(i) a polynucleotide comprising a sequence according to the present invention,

(ii) a ribonucleic acid or complementary DNA according to the present invention,

(iii) a polypeptide comprising a sequence according to the present invention,

wherein said presence is indicative of cyanobacteria in the sample.

Described herein is a kit for the detection of cyanotoxic organisms, the kit comprising at least one agent for detecting the presence of one or more of:

2008355461 10 Jun 2015

(i) a polynucleotide comprising a sequence according to SEQ ID NO: 95 or a variant or fragment thereof,

(ii) a ribonucleic acid or complementary DNA encoded by a sequence according to (i),

(iii) a polypeptide comprising a sequence according to SEQ ID NO: 96, or a variant or fragment thereof,

wherein said presence is indicative of cyanotoxic organisms in the sample.

The at least one agent may be a primer, antibody or probe. The primer or probe may comprise a sequence selected from the group consisting of SEQ ID NO: 111, SEQ ID NO: 112 and variants and fragments thereof.

The kit may further comprise at least one additional agent for detecting the presence of one or more nucleotide sequences selected from the group consisting of:

(i) a polynucleotide comprising a sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, and variants and fragments thereof,

(ii) a ribonucleic acid or complementary DNA encoded by a sequence according to (i),

(iii) a polypeptide comprising a sequence selected from the group consisting of: SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19 SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, and variants and fragments thereof.

The at least one additional agent may be a primer, antibody or probe. The primer or probe may comprise a sequence selected from the group consisting of SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 72, SEQ ID NO: 73, SEQ ID NO: 74, SEQ ID NO: 75,

2008355461 10 Jun 2015

SEQ ID NO: 76, SEQ ID NO: 77, SEQ ID NO: 78, SEQ ID NO: 79, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 132, SEQ ID NO: 133, SEQ ID NO: 134, and variants and fragments thereof.

Described herein is a kit for the detection of cylindrospermopsin-producing organisms, the kit comprising at least one agent for detecting the presence of one or more of:

(i) a polynucleotide comprising a sequence according to SEQ ID NO: 95 or a variant or fragment thereof,

(ii) a ribonucleic acid or complementary DNA encoded by a sequence according to (i),

(iii) a polypeptide comprising a sequence according to SEQ ID NO: 96, or a variant or fragment thereof,

wherein said presence is indicative of a cylindrospermopsin-producing organism in the sample.

Described herein is a method of screening for a compound that modulates the expression or activity of one or more polypeptides according to the present invention, the method comprising contacting the polypeptide with a candidate compound under conditions suitable to enable interaction of the candidate compound and the polypeptide, and assaying for activity of the polypeptide.

Modulating the expression or activity of one or more polypeptides may comprise inhibiting the expression or activity of said polypeptide.

Modulating the expression or activity of one or more polypeptides may comprise enhancing the expression or activity of said polypeptide.

Definitions

As used in this application, the singular form "a", "an" and "the" include plural references unless the context clearly dictates otherwise. For example, the term "a stem cell" also includes a plurality of stem cells.

As used herein, the term "comprising" means "including." Variations of the word "comprising", such as "comprise" and "comprises," have correspondingly varied meanings. Thus, for example, a polynucleotide "comprising" a sequence encoding a protein may consist exclusively of that sequence or may include one or more additional sequences.

As used herein, the terms "antibody" and "antibodies" include IgG (including IgG1, IgG2, IgG3, and IgG4), IgA (including IgA1 and IgA2), IgD, IgE, or IgM, and IgY, whole antibodies, including single-chain whole antibodies, and antigen-binding fragments thereof. Antigen-binding antibody fragments include, but are not limited to, Fab, Fab' and F(ab')2, Fd, single-chain Fvs (scFv), single-chain antibodies, disulfide-linked Fvs (sdFv) and fragments comprising either a VL or VH domain. The antibodies may be from any animal origin. Antigen-binding antibody fragments, including single-chain antibodies, may comprise the variable region(s) alone or in combination with the entire or partial of the following: hinge region, CH1, CH2, and CH3 domains. Also included are any combinations of variable region(s) and hinge region, CH1, CH2, and CH3 domains. Antibodies may be monoclonal, polyclonal, chimeric, multispecific, humanized, and human monoclonal and polyclonal antibodies which specifically bind the biological molecule.

As used herein, the terms "polypeptide" and "protein" are used interchangeably and are taken to have the same meaning.

As used herein, the terms "nucleotide sequence" and "polynucleotide sequence" are used interchangeably and are taken to have the same meaning.

As used herein, the term "kit" refers to any delivery system for delivering materials. In the context of the detection assays described herein, such delivery systems include systems that allow for the storage, transport, or delivery of reaction reagents (for example labels, reference samples, supporting material, etc. in the appropriate containers) and/or supporting materials (for example, buffers, written instructions for performing the assay etc.) from one location to another. For example, kits include one or more enclosures, such as boxes, containing the relevant reaction reagents and/or supporting materials.

Any discussion of documents, acts, materials, devices, articles or the like which has been included in the present specification is solely for the purpose of providing a context for the present invention. It is not to be taken as an admission that any or all of these matters form part of the prior art base or were common general knowledge in the field relevant to the present invention before the priority date of this application.

For the purposes of description all documents referred to herein are incorporated by reference unless otherwise stated.

Brief Description of the Drawings

A preferred embodiment of the present invention will now be described, by way of an example only, with reference to the accompanying drawings wherein:

Figure 1A is a table showing the distribution of the *sxt* genes in toxic and non-toxic cyanobacteria. PSP, saxitoxin; CYLN, cylindrospermopsin; +, gene fragment amplified; - no gene detected.

Figure 1B is a table showing primer sequences used to amplify various *SXT* genes.

Figure 2 is a table showing *sxt* genes from the saxitoxin gene cluster of *C. raciborskii* T3, their putative length, their BLAST similarity match with similar protein sequences from other organisms, and their predicted function.

Figure 3 is a diagram showing the structural organisation of the *sxt* gene cluster from *C. raciborskii* T3. Abbreviations used are: IS4, insertion sequence 4; at, aminotransferase; dmt, drug metabolite transporter; ompR, transcriptional regulator of *ompR* family; penP, penicillin binding; smf, gene predicted to be involved in DNA uptake. The scale indicates the gene cluster length in base pairs.

Figure 4 is a flow diagram showing the pathway for *SXT* biosynthesis and the putative functions of *sxt* genes.

Figure 5 shows MS/MS spectra of selected ions from cellular extracts of *Cylindrospermopsis raciborskii* T3. The predicted fragmentation of ions and the corresponding *m/z* values are indicated. Figure 5A, arginine (*m/z* 175); Figure 5B, saxitoxin (*m/z* 300); Figure 5C, intermediate A' (*m/z* 187); Figure 5D, intermediate C' (*m/z* 211); Figure 5E, intermediate E' (*m/z* 225).

Figure 6 is a table showing the *cyr* genes from the cylindrospermopsin gene cluster of *C. raciborskii* AWT205, their putative length, their BLAST similarity match with similar protein sequences from other organisms, and their predicted function.

Figure 7 is a table showing the distribution of the sulfotransferase gene (*cyrJ*) in toxic and non-toxic cyanobacteria. 16S rRNA gene amplification is shown as a positive control. CYLN, cylindrospermopsin; SXT, saxitoxin; N.D., not detected; +, gene fragment amplified; -, no gene detected; NA, not available; AWQC, Australian Water Quality Center.

Figure 8 is a flow diagram showing the biosynthetic pathway of cylindrospermopsin biosynthesis.

Figure 9 is a diagram showing the structural organization of the cylindrospermopsin gene cluster from *C. raciborskii* AWT205. Scale indicates gene cluster length in base pairs.

Description

The inventors have identified a gene cluster responsible for saxitoxin biosynthesis (the *SXT* gene cluster) and a gene cluster responsible for cylindrospermopsin biosynthesis (the *CYR* gene cluster). The full sequence of each gene cluster has been determined and functional activities assigned to each of the genes identified therein. Based on this information, the inventors have elucidated the full saxitoxin and cylindrospermopsin biosynthetic pathways.

Accordingly, the invention provides polynucleotide and polypeptide sequences derived from each of the *SXT* and *CYR* gene clusters and in particular, sequences relating to the specific genes within each pathway. Methods and kits for the detection of cyanobacterial strains in a sample are provided based on the presence (or absence) in the sample of one or more of the sequences of the invention. The inventors have determined that certain open-reading frames present in the *SXT* gene cluster of saxitoxin-producing microorganisms are absent in the *SXT* gene cluster of microorganisms that do not produce saxitoxin. Similarly, it has been discovered that one open-reading frame present in the *CYR* gene cluster of cylindrospermopsin-producing microorganisms is absent in non-cylindrospermopsin-producing microorganisms. Accordingly, the invention provides methods and kits for the detection of toxin-producing microorganisms.

Also provided by the invention are screening methods for the identification of compounds capable of modulating the expression or activity of proteins in the saxitoxin and/or cylindrospermopsin biosynthetic pathways.

Polynucleotides and polypeptides

The inventors have determined the full polynucleotide sequence of the saxitoxin (*SXT*) gene cluster and the cylindrospermopsin (*CYR*) gene cluster.

In accordance with aspects and embodiments of the invention, the *SXT* gene cluster may have, but is not limited to, the polynucleotide sequence as set forth SEQ ID NO: 1 (GenBank accession number DQ787200), or display sufficient sequence identity thereto to hybridise to the sequence of SEQ ID NO: 1.

The *SXT* gene cluster comprises 31 genes and 30 intergenic regions.

Gene 1 of the *SXT* gene cluster is a 759 base pair (bp) nucleotide sequence set forth in SEQ ID NO: 4. The nucleotide sequence of *SXT* Gene 1 ranges from the nucleotide in position 1625 up to the nucleotide in position 2383 of SEQ ID NO: 1. The polypeptide sequence encoded by Gene 1 (*SXTD*) is set forth in SEQ ID NO: 5.

Gene 2 of the *SXT* gene cluster is a 396 bp nucleotide sequence set forth in SEQ ID NO: 6. The nucleotide sequence of *SXT* Gene 2 ranges from the nucleotide in position 2621 up to the nucleotide in position 3016 of SEQ ID NO: 1. The polypeptide sequence encoded by Gene 2 (*ORF3*) is set forth in SEQ ID NO: 7.

Gene 3 of the *SXT* gene cluster is a 360 bp nucleotide sequence set forth in SEQ ID NO: 8. The nucleotide sequence of *SXT* Gene 3 ranges from the nucleotide in position 2955 up to the nucleotide in position 3314 of SEQ ID NO: 1. The polypeptide sequence encoded by Gene 3 (*ORF4*) is set forth in SEQ ID NO: 9.

Gene 4 of the *SXT* gene cluster is a 354 bp nucleotide sequence set forth in SEQ ID NO: 10. The nucleotide sequence of *SXT* Gene 4 ranges from the nucleotide in position 3647 up to the nucleotide in position 4000 of SEQ ID NO: 1. The polypeptide sequence encoded by Gene 4 (*SXTC*) is set forth in SEQ ID NO: 11.

Gene 5 of the *SXT* gene cluster is a 957 bp nucleotide sequence set forth in SEQ ID NO: 12. The nucleotide sequence of *SXT* Gene 5 ranges from the nucleotide in position 4030 up to the nucleotide in position 4986 of SEQ ID NO: 1. The polypeptide sequence encoded by Gene 5 (*SXTB*) is set forth in SEQ ID NO: 13.

Gene 6 of the *SXT* gene cluster is a 3738 bp nucleotide sequence set forth in SEQ ID NO: 14. The nucleotide sequence of *SXT* Gene 6 ranges from the nucleotide in position 5047 up to the nucleotide in position 8784 of SEQ ID NO: 1. The polypeptide sequence encoded by Gene 6 (*SXTA*) is set forth in SEQ ID NO: 15.

Gene 7 of the *SXT* gene cluster is a 387 bp nucleotide sequence set forth in SEQ ID NO: 16. The nucleotide sequence of *SXT* Gene 7 ranges from the nucleotide in position

9140 up to the nucleotide in position 9526 of SEQ ID NO: 1. The polypeptide sequence encoded by Gene 7 (*SXTE*) is set forth in SEQ ID NO: 17.

Gene 8 of the *SXT* gene cluster is a 1416 bp nucleotide sequence set forth in SEQ ID NO: 18. The nucleotide sequence of *SXT* Gene 8 ranges from the nucleotide in position 9686 up to the nucleotide in position 11101 of SEQ ID NO: 1. The polypeptide sequence encoded by Gene 8 (*SXTF*) is set forth in SEQ ID NO: 19.

Gene 9 of the *SXT* gene cluster is an 1134 bp nucleotide sequence set forth in SEQ ID NO: 20. The nucleotide sequence of *SXT* Gene 9 ranges from the nucleotide in position 11112 up to the nucleotide in position 12245 of SEQ ID NO: 1. The polypeptide sequence encoded by *SXT* Gene 9 (*SXTG*) is set forth in SEQ ID NO: 21.

Gene 10 of the *SXT* gene cluster is a 1005 bp nucleotide sequence set forth in SEQ ID NO: 22. The nucleotide sequence of *SXT* Gene 10 ranges from the nucleotide in position 12314 up to the nucleotide in position 13318 of SEQ ID NO: 1. The polypeptide sequence encoded by Gene 10 (*SXTH*) is set forth in SEQ ID NO: 23.

Gene 11 of the *SXT* gene cluster is an 1839 bp nucleotide sequence set forth in SEQ ID NO: 24. The nucleotide sequence of *SXT* Gene 11 ranges from the nucleotide in position 13476 up to the nucleotide in position 15314 of SEQ ID NO: 1. The polypeptide sequence encoded by Gene 11 (*SXTI*) is set forth in SEQ ID NO: 25.

Gene 12 of the *SXT* gene cluster is a 444 bp nucleotide sequence set forth in SEQ ID NO: 26. The nucleotide sequence of *SXT* Gene 12 ranges from the nucleotide in position 15318 up to the nucleotide in position 15761 of SEQ ID NO: 1. The polypeptide sequence encoded by Gene 12 (*SXTJ*) is set forth in SEQ ID NO: 27.

Gene 13 of the *SXT* gene cluster is a 165 bp nucleotide sequence set forth in SEQ ID NO: 28. The nucleotide sequence of *SXT* Gene 13 ranges from the nucleotide in position 15761 up to the nucleotide in position 15925 of SEQ ID NO: 1. The polypeptide sequence encoded by Gene 13 (*SXTK*) is set forth in SEQ ID NO: 29.

Gene 14 of the *SXT* gene cluster is a 1299 bp nucleotide sequence set forth in SEQ ID NO: 30. The nucleotide sequence of *SXT* Gene 14 ranges from the nucleotide in position 15937 up to the nucleotide in position 17235 of SEQ ID NO: 1. The polypeptide sequence encoded by Gene 14 (*SXTL*) is set forth in SEQ ID NO: 31.

Gene 15 of the *SXT* gene cluster is a 1449 bp nucleotide sequence set forth in SEQ ID NO: 32. The nucleotide sequence of *SXT* Gene 15 ranges from the nucleotide in position 17323 up to the nucleotide in position 18771 of SEQ ID NO: 1. The polypeptide sequence encoded by Gene 16 (*SXTM*) is set forth in SEQ ID NO: 33.

Gene 16 of the *SXT* gene cluster is an 831 bp nucleotide sequence set forth in SEQ ID NO: 34. The nucleotide sequence of *SXT* Gene 16 ranges from the nucleotide in position 19119 up to the nucleotide in position 19949 of SEQ ID NO: 1. The polypeptide sequence encoded by Gene 16 (*SXTN*) is set forth in SEQ ID NO: 35.

Gene 17 of the *SXT* gene cluster is a 774 bp nucleotide sequence set forth in SEQ ID NO: 36. The nucleotide sequence of *SXT* Gene 17 ranges from the nucleotide in position 20238 up to the nucleotide in position 21011 of SEQ ID NO: 1. The polypeptide sequence encoded by Gene 17 (*SXTX*) is set forth in SEQ ID NO: 37.

Gene 18 of the *SXT* gene cluster is a 327 bp nucleotide sequence set forth in SEQ ID NO: 38. The nucleotide sequence of *SXT* Gene 18 ranges from the nucleotide in position 21175 up to the nucleotide in position 21501 of SEQ ID NO: 1. The polypeptide sequence encoded by Gene 18 (*SXTW*) is set forth in SEQ ID NO: 39.

Gene 19 of the *SXT* gene cluster is a 1653 bp nucleotide sequence set forth in SEQ ID NO: 40. The nucleotide sequence of *SXT* Gene 219 ranges from the nucleotide in position 21542 up to the nucleotide in position 23194 of SEQ ID NO: 1. The polypeptide sequence encoded by Gene 19 (*SXTV*) is set forth in SEQ ID NO: 41.

Gene 20 of the *SXT* gene cluster is a 750 bp nucleotide sequence set forth in SEQ ID NO: 42. The nucleotide sequence of *SXT* Gene 20 ranges from the nucleotide in position 23199 up to the nucleotide in position 23948 of SEQ ID NO: 1. The polypeptide sequence encoded by Gene 20 (*SXTU*) is set forth in SEQ ID NO: 43.

Gene 21 of the *SXT* gene cluster is a 1005 bp nucleotide sequence set forth in SEQ ID NO: 44. The nucleotide sequence of *SXT* Gene 21 ranges from the nucleotide in position 24091 up to the nucleotide in position 25095 of SEQ ID NO: 1. The polypeptide sequence encoded by Gene 21 (*SXTT*) is set forth in SEQ ID NO: 45.

Gene 22 of the *SXT* gene cluster is a 726 bp nucleotide sequence set forth in SEQ ID NO: 46. The nucleotide sequence of *SXT* Gene 22 ranges from the nucleotide in position 25173 up to the nucleotide in position 25898 of SEQ ID NO: 1. The polypeptide sequence encoded by Gene 22 (*SXTS*) is set forth in SEQ ID NO: 47.

Gene 23 of the *SXT* gene cluster is a 576 bp nucleotide sequence set forth in SEQ ID NO: 48. The nucleotide sequence of *SXT* Gene 23 ranges from the nucleotide in position 25974 up to the nucleotide in position 26549 of SEQ ID NO: 1. The polypeptide sequence encoded by Gene 23 (*ORF24*) is set forth in SEQ ID NO: 49.

Gene 24 of the *SXT* gene cluster is a 777 bp nucleotide sequence set forth in SEQ ID NO: 50. The nucleotide sequence of *SXT* Gene 24 ranges from the nucleotide in

position 26605 up to the nucleotide in position 27381 of SEQ ID NO: 1. The polypeptide sequence encoded by Gene 24 (*SXTR*) is set forth in SEQ ID NO: 51.

Gene 25 of the *SXT* gene cluster is a 777 bp nucleotide sequence set forth in SEQ ID NO: 52. The nucleotide sequence of *SXT* Gene 25 ranges from the nucleotide in position 27392 up to the nucleotide in position 28168 of SEQ ID NO: 1. The polypeptide sequence encoded by Gene 25 (*SXTQ*) is set forth in SEQ ID NO: 53.

Gene 26 of the *SXT* gene cluster is a 1227 bp nucleotide sequence set forth in SEQ ID NO: 54. The nucleotide sequence of *SXT* Gene 26 ranges from the nucleotide in position 28281 up to the nucleotide in position 29507 of SEQ ID NO: 1. The polypeptide sequence encoded by Gene 26 (*SXTP*) is set forth in SEQ ID NO: 55.

Gene 27 of the *SXT* gene cluster is a 603 bp nucleotide sequence set forth in SEQ ID NO: 56. The nucleotide sequence of *SXT* Gene 27 ranges from the nucleotide in position 29667 up to the nucleotide in position 30269 of SEQ ID NO: 1. The polypeptide sequence encoded by Gene 27 (*SXTO*) is set forth in SEQ ID NO: 57.

Gene 28 of the *SXT* gene cluster is a 1350 bp nucleotide sequence set forth in SEQ ID NO: 58. The nucleotide sequence of *SXT* Gene 28 ranges from the nucleotide in position 30612 up to the nucleotide in position 31961 of SEQ ID NO: 1. The polypeptide sequence encoded by Gene 28 (*ORF29*) is set forth in SEQ ID NO: 59.

Gene 29 of the *SXT* gene cluster is a 666 bp nucleotide sequence set forth in SEQ ID NO: 60. The nucleotide sequence of *SXT* Gene 29 ranges from the nucleotide in position 32612 up to the nucleotide in position 33277 of SEQ ID NO: 1. The polypeptide sequence encoded by Gene 29 (*SXTY*) is set forth in SEQ ID NO: 61.

Gene 30 of the *SXT* gene cluster is a 1353 bp nucleotide sequence set forth in SEQ ID NO: 62. The nucleotide sequence of *SXT* Gene 30 ranges from the nucleotide in position 33325 up to the nucleotide in position 34677 of SEQ ID NO: 1. The polypeptide sequence encoded by Gene 30 (*SXTZ*) is set forth in SEQ ID NO: 63.

Gene 31 of the *SXT* gene cluster is an 819 bp nucleotide sequence set forth in SEQ ID NO: 64. The nucleotide sequence of *SXT* Gene 31 ranges from the nucleotide in position 35029 up to the nucleotide in position 35847 of SEQ ID NO: 1. The polypeptide sequence encoded by Gene 31 (*OMPR*) is set forth in SEQ ID NO: 65.

The 5' border region of *SXT* gene cluster comprises a 1320 bp gene (*orf1*), the sequence of which is set forth in SEQ ID NO: 2. The nucleotide sequence of *orf1* ranges from the nucleotide in position 1 up to the nucleotide in position 1320 of SEQ ID NO: 1. The polypeptide sequence encoded by *orf1* is set forth in SEQ ID NO: 3.

The 3' border region of *SXT* gene cluster comprises a 774 bp gene *(hisA)*, the sequence of which is set forth in SEQ ID NO: 66. The nucleotide sequence of *hisA* ranges from the nucleotide in position 35972 up to the nucleotide in position 36745 of SEQ ID NO: 1. The polypeptide sequence encoded by *hisA* is set forth in SEQ ID NO: 67.

The 3' border region of *SXT* gene cluster also comprises a 396 bp gene *(orfA)*, the sequence of which is set forth in in SEQ ID NO: 68. The nucleotide sequence of *orfA* ranges from the nucleotide in position 37060 up to the nucleotide in position 37455 of SEQ ID NO: 1. The polypeptide sequence encoded by *orfA* is set forth in SEQ ID NO: 69.

In accordance with other aspects and embodiments of the invention, the *CYR* gene cluster may have, but is not limited to, the nucleotide sequence as set forth SEQ ID NO: 80 (GenBank accession number EU140798), or display sufficient sequence identity thereto to hybridise to the sequence of SEQ ID NO: 80.

The *CYR* gene cluster comprises 15 genes and 14 intergenic regions.

Gene 1 of the *CYR* gene cluster is a 5631 bp nucleotide sequence set forth in SEQ ID NO: 81. The nucleotide sequence of *CYR* Gene 1 ranges from the nucleotide in position 444 up to the nucleotide in position 6074 of SEQ ID NO: 80. The polypeptide sequence encoded by Gene 1 (*CYRD*) is set forth in SEQ ID NO: 82.

Gene 2 of the *CYR* gene cluster is a 4074 bp nucleotide sequence set forth in SEQ ID NO: 83. The nucleotide sequence of *CYR* Gene 2 ranges from the nucleotide in position 6130 up to the nucleotide in position 10203 of SEQ ID NO: 80. The polypeptide sequence encoded by Gene 2 (*CYRF*) is set forth in SEQ ID NO: 84.

Gene 3 of the *CYR* gene cluster is a 1437 bp nucleotide sequence set forth in SEQ ID NO: 85. The nucleotide sequence of *CYR* Gene 3 ranges from the nucleotide in position 10251 up to the nucleotide in position 11687 of SEQ ID NO: 80. The polypeptide sequence encoded by Gene 3 (*CYRG*) is set forth in SEQ ID NO: 86.

Gene 4 of the *CYR* gene cluster is an 831 bp nucleotide sequence set forth in SEQ ID NO: 87. The nucleotide sequence of *CYR* Gene 4 ranges from the nucleotide in position 11741 up to the nucleotide in position 12571 of SEQ ID NO: 80. The polypeptide sequence encoded by Gene 4 (*CYRI*) is set forth in SEQ ID NO: 88.

Gene 5 of the *CYR* gene cluster is a 1398 bp nucleotide sequence set forth in SEQ ID NO: 89. The nucleotide sequence of *CYR* Gene 5 ranges from the nucleotide in position 12568 up to the nucleotide in position 13965 of SEQ ID NO: 80. The polypeptide sequence encoded by Gene 5 (*CYRK*) is set forth in SEQ ID NO: 90.

Gene 6 of the *CYR* gene cluster is a 750 bp nucleotide sequence set forth in SEQ ID NO: 91. The nucleotide sequence of *CYR* Gene 6 ranges from the nucleotide in position 14037 up to the nucleotide in position 14786 of SEQ ID NO: 80. The polypeptide sequence encoded by Gene 6 (*CYRL*) is set forth in SEQ ID NO: 92.

Gene 7 of the *CYR* gene cluster is a 1431 bp nucleotide sequence set forth in SEQ ID NO: 93. The nucleotide sequence of *CYR* Gene 7 ranges from the nucleotide in position 14886 up to the nucleotide in position 16316 of SEQ ID NO: 80. The polypeptide sequence encoded by Gene 7 (*CYRH*) is set forth in SEQ ID NO: 94.

Gene 8 of the *CYR* gene cluster is a 780 bp nucleotide sequence set forth in SEQ ID NO: 95. The nucleotide sequence of *CYR* Gene 8 ranges from the nucleotide in position 16893 up to the nucleotide in position 17672 of SEQ ID NO: 80. The polypeptide sequence encoded by Gene 8 (*CYRJ*) is set forth in SEQ ID NO: 96.

Gene 9 of the *CYR* gene cluster is an 1176 bp nucleotide sequence set forth in SEQ ID NO: 97. The nucleotide sequence of *CYR* Gene 9 ranges from the nucleotide in position 18113 up to the nucleotide in position 19288 of SEQ ID NO: 80. The polypeptide sequence encoded by Gene 9 (*CYRA*) is set forth in SEQ ID NO: 98.

Gene 10 of the *CYR* gene cluster is an 8754 bp nucleotide sequence set forth in SEQ ID NO: 99. The nucleotide sequence of *CYR* Gene 10 ranges from the nucleotide in position 19303 up to the nucleotide in position 28056 of SEQ ID NO: 80. The polypeptide sequence encoded by Gene 10 (*CYRB*) is set forth in SEQ ID NO: 100.

Gene 11 of the *CYR* gene cluster is a 5667 bp nucleotide sequence set forth in SEQ ID NO: 101. The nucleotide sequence of *CYR* Gene 11 ranges from the nucleotide in position 28061 up to the nucleotide in position 33727 of SEQ ID NO: 80. The polypeptide sequence encoded by Gene 11 (*CYRE*) is set forth in SEQ ID NO: 102.

Gene 12 of the *CYR* gene cluster is a 5004 bp nucleotide sequence set forth in SEQ ID NO: 103. The nucleotide sequence of *CYR* Gene 12 ranges from the nucleotide in position 34299 up to the nucleotide in position 39302 of SEQ ID NO: 80. The polypeptide sequence encoded by Gene 12 (*CYRC*) is set forth in SEQ ID NO: 104.

Gene 13 of the *CYR* gene cluster is a 318 bp nucleotide sequence set forth in SEQ ID NO: 105. The nucleotide sequence of *CYR* Gene 13 ranges from the nucleotide in position 39366 up to the nucleotide in position 39683 of SEQ ID NO: 80. The polypeptide sequence encoded by Gene 13 (*CYRM*) is set forth in SEQ ID NO: 106.

Gene 14 of the *CYR* gene cluster is a 600 bp nucleotide sequence set forth in SEQ ID NO: 107. The nucleotide sequence of *CYR* Gene 14 ranges from the nucleotide in

position 39793 up to the nucleotide in position 40392 of SEQ ID NO: 80. The polypeptide sequence encoded by Gene 14 (*CYRN*) is set forth in SEQ ID NO: 108.

Gene 15 of the *CYR* gene cluster is a 1548 bp nucleotide sequence set forth in SEQ ID NO: 109. The nucleotide sequence of *CYR* Gene 15 ranges from the nucleotide in position 40501 up to the nucleotide in position 42048 of SEQ ID NO: 80. The polypeptide sequence encoded by Gene 15 (*CYRO*) is set forth in SEQ ID NO: 110.

In general, the nucleic acids and polypeptides of the invention are of an isolated or purified form.

In addition to the *SXT* and *CYR* polynucleotides and polypeptide sequences set forth herein, also included within the scope of the present invention are variants and fragments thereof.

SXT and *CYR* polynucleotides disclosed herein may be deoxyribonucleic acids (DNA), ribonucleic acids (RNA) or complementary deoxyribonucleic acids (cDNA).

RNA may be derived from RNA polymerase-catalyzed transcription of a DNA sequence. The RNA may be a primary transcript derived transcription of a corresponding DNA sequence. RNA may also undergo post-transcriptional processing. For example, a primary RNA transcript may undergo post-transcriptional processing to form a mature RNA. Messenger RNA (mRNA) refers to RNA derived from a corresponding open reading frame that may be translated into protein by the cell. cDNA refers to a double-stranded DNA that is complementary to and derived from mRNA. Sense RNA refers to RNA transcript that includes the mRNA and so can be translated into protein by the cell. Antisense RNA refers to an RNA transcript that is complementary to all or part of a target primary transcript or mRNA and may be used to block the expression of a target gene.

The skilled addresse will recognise that RNA and cDNA sequences encoded by the *SXT* and *CYR* DNA sequences disclosed herein may be derived using the genetic code. An RNA sequence may be derived from a given DNA sequence by generating a sequence that is complementary the particular DNA sequence. The complementary sequence may be generated by converting each cytosine ('C') base in the DNA sequence to a guanine ('G') base, each guanine ('G') base in the DNA sequence to a cytosine ('C') base, each thymidine ('T') base in the DNA sequence to an adenine ('A') base, and each adenine ('A') base in the DNA sequence to a uracil ('U') base.

A complementary DNA (cDNA) sequence may be derived from a DNA sequence by deriving an RNA sequence from the DNA sequence as above, then converting the RNA sequence into a cDNA sequence. An RNA sequence can be converted into a cDNA

sequence by converting each cytosine ('C') base in the RNA sequence to a guanine ('G') base, each guanine ('G') base in the RNA sequence to a cytosine ('C') base, each uracil ('U') base in the RNA sequence to an adenine ('A') base, and each adeneine ('A') base in the RNA sequence to a thymidine ('T') base.

The term "variant" as used herein refers to a substantially similar sequence. In general, two sequences are "substantially similar" if the two sequences have a specified percentage of amino acid residues or nucleotides that are the same (percentage of "sequence identity"), over a specified region, or, when not specified, over the entire sequence. Accordingly, a "variant" of a polynucleotide and polypeptide sequence disclosed herein may share at least 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 83% 85%, 88%, 90%, 93%, 95%, 96%, 97%, 98% or 99% sequence identity with the reference sequence.

In general, polypeptide sequence variants possess qualitative biological activity in common. Polynucleotide sequence variants generally encode polypeptides which generally possess qualitative biological activity in common. Also included within the meaning of the term "variant" are homologues of polynucleotides and polypeptides of the invention. A polynucleotide homologue is typically from a different bacterial species but sharing substantially the same biological function or activity as the corresponding polynucleotide disclosed herein. A polypeptide homologue is typically from a different bacterial species but sharing substantially the same biological function or activity as the corresponding polypeptide disclosed herein. For example, homologues of the polynucleotides and polypeptides disclosed herein include, but are not limited to those from different species of cyanobacteria.

Further, the term "variant" also includes analogues of the polypeptides of the invention. A polypeptide "analogue" is a polypeptide which is a derivative of a polypeptide of the invention, which derivative comprises addition, deletion, substitution of one or more amino acids, such that the polypeptide retains substantially the same function. The term "conservative amino acid substitution" refers to a substitution or replacement of one amino acid for another amino acid with similar properties within a polypeptide chain (primary sequence of a protein). For example, the substitution of the charged amino acid glutamic acid (Glu) for the similarly charged amino acid aspartic acid (Asp) would be a conservative amino acid substitution.

In general, the percentage of sequence identity between two sequences may be determined by comparing two optimally aligned sequences over a comparison window.

The portion of the sequence in the comparison window may, for example, comprise deletions or additions (*i.e.* gaps) in comparison to the reference sequence (for example, a polynucleotide or polypeptide sequence disclosed herein), which does not comprise deletions or additions, in order to align the two sequences optimally. A percentage of sequence identity may then be calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison, and multiplying the result by 100 to yield the percentage of sequence identity.

In the context of two or more nucleic acid or polypeptide sequences, the percentage of sequence identity refers to the specified percentage of amino acid residues or nucleotides that are the same over a specified region, (or, when not specified, over the entire sequence), when compared and aligned for maximum correspondence over a comparison window, or designated region as measured using one of the following sequence comparison algorithms or by manual alignment and visual inspection.

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. Default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters. Methods of alignment of sequences for comparison are well known in the art. Optimal alignment of sequences for comparison can be determined conventionally using known computer programs, including, but not limited to: CLUSTAL in the PC/Gene program (available from Intelligenetics, Mountain View, California); the ALIGN program (Version 2.0) and GAP, BESTFIT, BLAST, FASTA, and TFASTA in the GCG Wisconsin Genetics Software Package, Version 10 (available from Accelrys Inc., 9685 Scranton Road, San Diego, California, USA).

The BESTFIT program (Wisconsin Sequence Analysis Package, for Unix, Genetics Computer Group, University Research Park, 575 Science Drive, Madison, Wis. 53711) uses the local homology algorithm of Smith and Waterman to find the best segment of homology between two sequences (Smith and Waterman, Advances in Applied Mathematics 2:482-489 (1981)). When using BESTFIT or any other sequence alignment

program to determine the degree of homology between sequences, the parameters may be set such that the percentage of identity is calculated over the full length of the reference nucleotide sequence and that gaps in homology of up to 5% of the total number of nucleotides in the reference sequence are allowed.

GAP uses the algorithm described in Needleman and Wunsch (1970) J. Mol. Biol. 48:443-453, to find the alignment of two complete sequences that maximizes the number of matches and minimizes the number of gaps. GAP considers all possible alignments and gap positions and creates the alignment with the largest number of matched bases and the fewest gaps. It allows for the provision of a gap creation penalty and a gap extension penalty in units of matched bases. GAP presents one member of the family of best alignments.

Another method for determining the best overall match between a query sequence and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag and colleagues (Comp. App. Biosci. 6:237-245 (1990)). In a sequence alignment the query and subject sequences are both DNA sequences. An RNA sequence can be compared by converting U's to T's. The result of said global sequence alignment is in percent identity.

The BLAST and BLAST 2.0 algorithms, may be used for determining percent sequence identity and sequence similarity. These are described in Altschul et al. (1977) Nuc. Acids Res. 25:3389-3402, and Altschul et al (1990) J. Mol. Biol. 215:403-410, respectively. 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, supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are 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) or 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) Proc. Natl, Acad. Sci USA 89:10915) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands. [0028] The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin and Altschul (1993) Proc. Natl. Acad. Sci. USA 90:5873-5787). 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 nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001.

The invention also contemplates fragments of the polypeptides disclosed herein. A polypeptide "fragment" is a polypeptide molecule that encodes a constituent or is a constituent of a polypeptide of the invention or variant thereof. Typically the fragment possesses qualitative biological activity in common with the polypeptide of which it is a constituent. The peptide fragment may be between about 5 to about 3000 amino acids in length, between about 5 to about 2750 amino acids in length, between about 5 to about 2500 amino acids in length, between about 5 to about 2250 amino acids in length, between about 5 to about 2000 amino acids in length, between about 5 to about 1750 amino acids in length, between about 5 to about 1500 amino acids in length, between about 5 to about 1250 amino acids in length, between about 5 to about 1000 amino acids in length, between about 5 to about 900 amino acids in length, between about 5 to about 800 amino acids in length, between about 5 to about 700 amino acids in length, between about 5 to about 600 amino acids in length, between about 5 to about 500 amino acids in length, between about 5 to about 450 amino acids in length, between about 5 to about 400 amino acids in length, between about 5 to about 350 amino acids in length, between about 5 to about 300 amino acids in length, between about 5 to about 250 amino acids in length, between about 5 to about 200 amino acids in length, between about 5 to about 175 amino acids in length, between about 5 to about 150 amino acids in length, between about 5 to

about 125 amino acids in length, between about 5 to about 100 amino acids in length, between about 5 to about 75 amino acids in length, between about 5 to about 50 amino acids in length, between about 5 to about 40 amino acids in length, between about 5 to about 30 amino acids in length, between about 5 to about 20 amino acids in length, and between about 5 to about 15 amino acids in length. Alternatively, the peptide fragment may be between about 5 to about 10 amino acids in length.

Also contemplated are fragments of the polynucleotides disclosed herein. A polynucleotide "fragment" is a polynucleotide molecule that encodes a constituent or is a constituent of a polynucleotide of the invention or variant thereof. Fragments of a polynucleotide do not necessarily need to encode polypeptides which retain biological activity. The fragment may, for example, be useful as a hybridization probe or PCR primer. The fragment may be derived from a polynucleotide of the invention or alternatively may be synthesized by some other means, for example by chemical synthesis.

Certain embodiments of the invention relate to fragments of SEQ ID NO: 1. A fragment of SEQ ID NO: 1 may comprise, for example, a constituent of SEQ ID NO: 1 in which the 5' gene border region gene *orf1* is absent. Alternatively, a fragment of SEQ ID NO: 1 may comprise, for example, a constituent of SEQ ID NO: 1 in which the 3' gene border region gene *hisA* is absent. Alternatively, a fragment of SEQ ID NO: 1 may comprise, for example, a constituent of SEQ ID NO: 1 in which the 3' gene border region gene *orfA* is absent. Alternatively, a fragment of SEQ ID NO: 1 may comprise, for example, a constituent of SEQ ID NO: 1 in which the 5' gene border region gene *orf1* is absent and the 3' border region gene *orfA* is absent. Alternatively, a fragment of SEQ ID NO: 1 may comprise, for example, a constituent of SEQ ID NO: 1 in which the 5' gene border region gene *orf1* is absent and the 3' border region genes *hisA* and *orfA* are absent.

In other embodiments, a fragment of SEQ ID NO: 1 may comprise one or more *SXT* open reading frames. The *SXT* open reading frame may be selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID

NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, and variants thereof.

Additional embodiments of the invention relate to fragments of SEQ ID NO: 80. The fragment of SEQ ID NO: 80 may comprise one or more *CYR* open reading frames. The *CYR* open reading frame may be selected from the group consisting of of SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO:107, SEQ ID NO: 109, and variants thereof.

In particular embodiments, the polynucleotides of the invention may be cloned into a vector. The vector may comprise, for example, a DNA, RNA or complementary DNA (cDNA) sequence. The vector may be a plasmid vector, a viral vector, or any other suitable vehicle adapted for the insertion of foreign sequences, their introduction into cells and the expression of the introduced sequences. Typically the vector is an expression vector and may include expression control and processing sequences such as a promoter, an enhancer, ribosome binding sites, polyadenylation signals and transcription termination sequences. The invention also contemplates host cells transformed by such vectors. For example, the polynucleotides of the invention may be cloned into a vector which is transformed into a bacterial host cell, for example *E. coli*. Methods for the construction of vectors and their transformation into host cells are generally known in the art, and described in, for example, *Molecular Cloning: A Laboratory Manual* (2nd ed., Cold Spring Harbor Laboratory Press, Plainview, New York, and, Ausubel F. M. et al. (Eds) *Current Protocols in Molecular* Biology (2007), John Wiley and Sons, Inc.

Nucleotide Probes, Primers and Antibodies

The invention contemplates nucleotides and fragments based on the sequences of the polynucleotides disclosed herein for use as primers and probes for the identification of homologous sequences.

The nucleotides and fragments may be in the form of oligonucleotides. Oligonucleotides are short stretches of nucleotide residues suitable for use in nucleic acid amplification reactions such as PCR, typically being at least about 5 nucleotides to about 80 nucleotides in length, more typically about 10 nucleotides in length to about 50 nucleotides in lenght, and even more typically about 15 nucleotides in length to about 30 nucleotides in length.

Probes are nucleotide sequences of variable length, for example between about 10 nucleotides and several thousand nucleotides, for use in detection of homologous sequences, typically by hybridization. Hybridization probes may be genomic DNA fragments, cDNA fragments, RNA fragments, or other oligonucleotides.

Methods for the design and/or production of nucleotide probes and/or primers are generally known in the art, and are described in Sambrook et al. (1989) *Molecular Cloning: A Laboratory Manual* (2nd ed., Cold Spring Harbor Laboratory Press, Plainview, New York; Itakura K. et al. (1984) Annu. Rev. Biochem. 53:323; Innis *et al.*, (Eds) (1990) *PCR Protocols: A Guide to Methods and Applications* (Academic Press, New York); Innis and Gelfand, (Eds) (1995) *PCR Strategies* (Academic Press, New York); and Innis and Gelfand, (Eds) (1999) *PCR Methods Manual* (Academic Press, New York). Nucleotide primers and probes may be prepared, for example, by chemical synthesis techniques for example, the phosphodiester and phosphotriester methods (see for example Narang S. A. et al. (1979) Meth. Enzymol. 68:90; Brown, E. L. (1979) et al. Meth. Enzymol. 68:109; and U.S. Patent No. 4356270), the diethylphosphoramidite method (see Beaucage S.L et al. (1981) Tetrahedron Letters, 22:1859-1862). A method for synthesizing oligonucleotides on a modified solid support is described in U.S. Patent No. 4458066.

The nucleic acids of the invention, including the above-mentioned probes and primers, may be labelled by incorporation of a marker to facilitate their detection. Techniques for labelling and detecting nucleic acids are described, for example, in Ausubel F. M. et al. (Eds) *Current Protocols in Molecular* Biology (2007), John Wiley and Sons, Inc. Examples of suitable markers include fluorescent molecules (*e.g.* acetylaminofluorene, 5-bromodeoxyuridine, digoxigenin, fluorescein) and radioactive isotopes (*e.g.* 32P, 35S, 3H, 33P). Detection of the marker may be achieved, for example, by chemical, photochemical, immunochemical, biochemical, or spectroscopic techniques.

The probes and primers of the invention may be used, for example, to detect or isolate cyanobacteria and/or dinoflagellates in a sample of interest. Additionally or alternatively, the probes and primers of the invention may be used to detect or isolate a cyanotoxic organism and/or a cylindrospermopisn-producing organism in a sample of interest. Additionally or alternatively, the probes or primers of the invention may be used to isolate corresponding sequences in other organisms including, for example, other bacterial species. Methods such as the polymerase chain reaction (PCR), hybridization, and the like can be used to identify such sequences based on their sequence homology to

the sequences set forth herein. Sequences that are selected based on their sequence identity to the entire sequences set forth herein or to fragments thereof are encompassed by the embodiments. Such sequences include sequences that are orthologs of the disclosed sequences. The term "orthologs" refers to genes derived from a common ancestral gene and which are found in different species as a result of speciation. Genes found in different species are considered orthologs when their nucleotide sequences and/or their encoded protein sequences share substantial identity as defined elsewhere herein. Functions of orthologs are often highly conserved among species.

In hybridization techniques, all or part of a known nucleotide sequence is used to generate a probe that selectively hybridizes to other corresponding nucleic acid sequences present in a given sample. The hybridization probes may be genomic DNA fragments, cDNA fragments, RNA fragments, or other oligonucleotides, and may be labelled with a detectable marker. Thus, for example, probes for hybridization can be made by labelling synthetic oligonucleotides based on the sequences of the invention.

The level of homology (sequence identity) between probe and the target sequence will largely be determined by the stringency of hybridization conditions. In particular the nucleotide sequence used as a probe may hybridize to a homologue or other variant of a polynucleotide disclosed herein under conditions of low stringency, medium stringency or high stringency. There are numerous conditions and factors, well known to those skilled in the art, which may be employed to alter the stringency of hybridization. For instance, the length and nature (DNA, RNA, base composition) of the nucleic acid to be hybridized to a specified nucleic acid; concentration of salts and other components, such as the presence or absence of formamide, dextran sulfate, polyethylene glycol etc; and altering the temperature of the hybridization and/or washing steps.

Typically, stringent hybridization conditions will be those in which the salt concentration is less than about 1.5 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 at least about 30°C for short probes (*e.g.*, 10 to 50 nucleotides) and at least about 60°C for long probes (*e.g.*, greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. Exemplary low stringency conditions include hybridization with a buffer solution of 30% to 35% formamide, 1 M NaCl, 1% SDS (sodium dodecyl sulfate) at 37 °C, and a wash in 1X to 2X SSC (20X SSC = 3.0 M NaCl/0.3 M trisodium citrate) at 50°C to 55 °C. Exemplary moderate stringency conditions include hybridization in 40% to 45% formamide, 1.0 M NaCl, 1% SDS at

37 °C, and a wash in 0.5X to 1X SSC at 55°C to 60 °C. Exemplary high stringency conditions include hybridization in 50% formamide, 1 M NaCl, 1% SDS at 37 °C, and a final wash in 0.1X SSC at 60°C to 65 °C for at least about 20 minutes. Optionally, wash buffers may comprise about 0.1% to about 1% SDS. The duration of hybridization is generally less than about 24 hours, usually about 4 to about 12 hours.

Under a PCR approach, oligonucleotide primers can be designed for use in PCR reactions to amplify corresponding DNA sequences from cDNA or genomic DNA extracted from any organism of interest. Methods for designing PCR primers and PCR cloning are generally known in the art and are disclosed in Sambrook *et al.* (1989) *Molecular Cloning: A Laboratory Manual* (2nd ed., Cold Spring Harbor Laboratory Press, Plainview, New York); Ausubel F. M. et al. (Eds) *Current Protocols in Molecular* Biology (2007), John Wiley and Sons, Inc; Maniatis et al. *Molecular Cloning* (1982), 280-281; Innis et al. (Eds) (1990) *PCR Protocols: A Guide to Methods and Applications* (Academic Press, New York); Innis and Gelfand, (Eds) (1995) *PCR Strategies* (Academic Press, New York); and Innis and Gelfand, (Eds) (1999) *PCR Methods Manual* (Academic Press, New York). Known methods of PCR include, but are not limited to, methods using paired primers, nested primers, single specific primers, degenerate primers, gene-specific primers, vector-specific primers, partially-mismatched primers, and the like.

The skilled addressee will recognise that the primers described herein for use in PCR or RT-PCR may also be used as probes for the detection of *SXT* or *CYR* sequences.

Also contemplated by the invention are antibodies which are capable of binding specifically to the polypeptides of the invention. The antibodies may be used to qualitatively or quantitatively detect and analyse one or more *SXT* or *CYR* polypeptides in a given sample. By "binding specifically" it will be understood that the antibody is capable of binding to the target polypeptide or fragment thereof with a higher affinity than it binds to an unrelated protein. For example, the antibody may bind to the polypeptide or fragment thereof with a binding constant in the range of at least about 10^{-4}M to about 10^{-10}M. Preferably the binding constant is at least about 10^{-5}M, or at least about 10^{-6}M, more preferably the binding constant of the antibody to the *SXT* or *CYR* polypeptide or fragment thereof is at least about 10^{-7}M, at least about 10^{-8}M, or at least about 10^{-9}M or more.

Antibodies of the invention may exist in a variety of forms, including for example as a whole antibody, or as an antibody fragment, or other immunologically active fragment thereof, such as complementarity determining regions. Similarly, the antibody

may exist as an antibody fragment having functional antigen-binding domains, that is, heavy and light chain variable domains. Also, the antibody fragment may exist in a form selected from the group consisting of, but not limited to: Fv, F_{ab}, $F(ab)_2$, scFv (single chain Fv), dAb (single domain antibody), chimeric antibodies, bi-specific antibodies, diabodies and triabodies.

An antibody 'fragment' may be produced by modification of a whole antibody or by synthesis of the desired antibody fragment. Methods of generating antibodies, including antibody fragments, are known in the art and include, for example, synthesis by recombinant DNA technology. The skilled addressee will be aware of methods of synthesising antibodies, such as those described in, for example, US Patent No. 5296348 and Ausubel F. M. et al. (Eds) *Current Protocols in Molecular* Biology (2007), John Wiley and Sons, Inc.

Preferably antibodies are prepared from discrete regions or fragments of the *SXT* or *CYR* polypeptide of interest. An antigenic portion of a polypeptide of interest may be of any appropriate length, such as from about 5 to about 15 amino acids. Preferably, an antigenic portion contains at least about 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 amino acid residues.

In the context of this specification reference to an antibody specific to a *SXT* or *CYR* polypeptide of the invention includes an antibody that is specific to a fragment of the polypeptide of interest.

Antibodies that specifically bind to a polypeptide of the invention can be prepared, for example, using the purified *SXT* or *CYR* polypeptides or their nucleic acid sequences using any suitable methods known in the art. For example, a monoclonal antibody, typically containing Fab portions, may be prepared using hybridoma technology described in Harlow and Lane (Eds) *Antibodies - A Laboratory Manual*, (1988), Cold Spring Harbor Laboratory, N.Y; Coligan, *Current Protocols in Immunology* (1991); Goding, *Monoclonal Antibodies: Principles and Practice* (1986) 2nd ed; and Kohler & Milstein, (1975) Nature 256: 495-497. Such techniques include, but are not limited to, antibody preparation by selection of antibodies from libraries of recombinant antibodies in phage or similar vectors, as well as preparation of polyclonal and monoclonal antibodies by immunizing rabbits or mice (see, for example, Huse et al. (1989) Science 246: 1275-1281; Ward et al. (1989) Nature 341: 544-546).

It will also be understood that antibodies of the invention include humanised antibodies, chimeric antibodies and fully human antibodies. An antibody of the invention

may be a bi-specific antibody, having binding specificity to more than one antigen or epitope. For example, the antibody may have specificity for one or more *SXT* or *CYR* polypeptide or fragments thereof, and additionally have binding specificity for another antigen. Methods for the preparation of humanised antibodies, chimeric antibodies, fully human antibodies, and bispecific antibodies are known in the art and include, for example as described in United States Patent No. 6995243 issued February 7, 2006 to Garabedian, et al. and entitled "Antibodies that recognize and bind phosphorylated human glucocorticoid receptor and methods of using same".

Generally, a sample potentially comprising *SXT* or *CYR* polypeptides can be contacted with an antibody that specifically binds the *SXT* or *CYR* polypeptide or fragment thereof. Optionally, the antibody can be fixed to a solid support to facilitate washing and subsequent isolation of the complex, prior to contacting the antibody with a sample. Examples of solid supports include, for example, microtitre plates, beads, ticks, or microbeads. Antibodies can also be attached to a ProteinChip array or a probe substrate as described above.

Detectable labels for the identification of antibodies bound to the *SXT* or *CYR* polypeptides of the invention include, but are not limited to fluorochromes, fluorescent dyes, radiolabels, enzymes such as horse radish peroxide, alkaline phosphatase and others commonly used in the art, and colorimetric labels including colloidal gold or coloured glass or plastic beads. Alternatively, the marker in the sample can be detected using an indirect assay, wherein, for example, a second, labelled antibody is used to detect bound marker-specific antibody.

Methods for detecting the presence of or measuring the amount of, an antibody-marker complex include, for example, detection of fluorescence, chemiluminescence, luminescence, absorbance, birefringence, transmittance, reflectance, or refractive index such as surface plasmon resonance, ellipsometry, a resonant mirror method, a grating coupler wave guide method or interferometry. Radio frequency methods include multipolar resonance spectroscopy. Electrochemical methods include amperometry and voltametry methods. Optical methods include imaging methods and non-imaging methods and microscopy.

Useful assays for detecting the presence of or measuring the amount of, an antibody-marker complex include, include, for example, enzyme-linked immunosorbent assay (ELISA), a radioimmune assay (RIA), or a Western blot assay. Such methods are described in, for example, Clinical Immunology (Stites & Terr, eds., 7th ed. 1991);

Methods in Cell Biology: Antibodies in Cell Biology, volume 37 (Asai, ed. 1993); and Harlow & Lane, supra.

Methods and kits for detection

The invention provides methods and kits for the detection and/or isolation of *SXT* nucleic acids and polypeptides. Also provided are methods and kits for the detection and/or isolation *CYR* nucleic acids and polypeptides.

In one aspect, the invention provides a method for the detection of cyanobacteria. The skilled addressee will understand that the detection of "cyanobacteria" encompasses the detection of one or more cyanobacteria. The method comprises obtaining a sample for use in the method, and detecting the presence of one or more *SXT* polynucleotides or polypeptides as disclosed herein, or a variant or fragment thereof. The presence of *SXT* polynucleotides, polypeptides, or variants or fragments thereof, is indicative of cyanobacteria in the sample.

The *SXT* polynucleotide may comprise a sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, and variants and fragments thereof.

Alternatively, the *SXT* polynucleotide may be an RNA or cDNA encoded by a sequence selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66,

SEQ ID NO: 68, and variants and fragments thereof and/or polypeptides as disclosed herein, or a variant or fragment thereof.

The *SXT* polypeptide may comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, and variants and fragments thereof.

The inventors have determined that several genes of the *SXT* gene cluster exist in saxitoxin-producing organisms, and are absent in organisms with the *SXT* gene cluster that do not produce saxitoxin. Specifically, the inventors have identified that gene 6 (*sxtA*) (SEQ ID NO: 14), gene 9 (*sxtG*) (SEQ ID NO: 20), gene 10 (*sxtH*) (SEQ ID NO: 22), gene 11 (*sxtI*) (SEQ ID NO: 24) and gene 17 (*sxtX*) (SEQ ID NO: 36) of the *SXT* gene cluster are present only in organisms that produce saxitoxin.

Accordingly, in another aspect the invention provides a method of detecting a cyanotoxic organism. The method comprises obtaining a sample for use in the method, and detecting a cyanotoxic organism based on the detection of one or more *SXT* polynucleotides comprising a sequence set forth in SEQ ID NO: 14 (*sxtA*, gene 6), SEQ ID NO: 20 (*sxtG*, gene 9), SEQ ID NO: 22 (*sxtH*, gene 10), SEQ ID NO: 24 (*sxtI*, gene 11), SEQ ID NO: 36 (*sxtX*, gene 17), or variants or fragments thereof. Additionally or alternatively, a cyanotoxic organism may be detected based on the detection of an RNA or cDNA comprising a sequence encoded by SEQ ID NO: 14 (*sxtA*, gene 6), SEQ ID NO: 20 (*sxtG*, gene 9), SEQ ID NO: 22 (*sxtH*, gene 10), SEQ ID NO: 24 (*sxtI*, gene 11), SEQ ID NO: 36 (*sxtX*, gene 17), or variants or fragments thereof. Additionally or alternatively, a cyanotoxic organism may be detected based on the detection of one or more polypeptides comprising a sequence set forth in SEQ ID NO: 15 (*SXTA*), SEQ ID NO: 21 (*SXTG*), SEQ ID NO: 23 (*SXTH*), SEQ ID NO: 25 (*SXTI*), SEQ ID NO: 37 (*SXTX*), or variants or fragments thereof, in a sample suspected of comprising one or more cyanotoxic organisms. The cyanotoxic organism may be any organism capable of producing saxitoxin. In a preferred embodiment of the invention, the cyanotoxic organism is a cyanobacteria or a dinoflagellate.

In certain embodiments of the invention, the methods for detecting cyanobacteria or the methods for detecting cyanotoxic organisms may further comprise the detection of one or more *CYR* polynucleotides or *CYR* polypeptides as disclosed herein, or a variant or fragment thereof. The *CYR* polynucleotide may comprise a sequence selected from the group consisting of SEQ ID NO: 80, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, and variants or fragments thereof.

Alternatively, the *CYR* polynucleotide may be an RNA or cDNA encoded by a polynucleotide sequence selected from the group consisting of SEQ ID NO: 80, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, and variants or fragments thereof.

The *CYR* polypeptide may comprise a sequence selected from the group consisting of SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92 , SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, and SEQ ID NO: 110, and variants or fragments thereof.

The inventors have determined gene 8 (*cyrJ*) (SEQ ID NO: 95) of the *CYR* gene cluster exists in cylindrospermopsin-producing organisms, and is absent in organisms with the *CYR* gene cluster that do not produce cylindrospermopsin. Accordingly, the methods for detecting cyanobacteria or the methods for detecting cyanotoxic organisms may further comprise the detection of a cylindrospermopsin-producing organism based on the detection of a *CYR* polynucleotide comprising a sequence set forth in SEQ ID NO: 95, or a variant or fragment thereof. Additionally or alternatively, the methods for detecting cyanobacteria or the methods for detecting cyanotoxic organisms may further comprise the detection of a cylindrospermopsin-producing organism based on the detection of an RNA or cDNA comprising a sequence encoded by SEQ ID NO: 95, or a variant or fragment thereof. Additionally or alternatively, the methods for detecting cyanobacteria or the methods for detecting cyanotoxic organisms may further comprise the detection of a cylindrospermopsin-producing organism based on the detection of a *CYR* polypeptide comprising a sequence set forth in SEQ ID NO: 96, or a variant or fragment thereof.

In another aspect, the invention provides a method for the detection of cyanobacteria. The skilled addressee will understand that the detection of "cyanobacteria" encompasses the detection of one or more cyanobacteria. The method comprises obtaining a sample for use in the method, and detecting the presence of one or more *CYR* polynucleotides or polypeptides as disclosed herein, or a variant or fragment thereof. The presence of *CYR* polynucleotides, polypeptides, or variants or fragments thereof, is indicative of cyanobacteria in the sample.

The *CYR* polynucleotide may comprise a sequence selected from the group consisting of SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO:107, SEQ ID NO: 109 and variants and fragments thereof.

Alternatively, the *CYR* polynucleotide may be an RNA or cDNA encoded by a sequence selected from the group consisting of SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO:107, SEQ ID NO: 109 and variants and fragments thereof.

The *CYR* polypeptide may comprise a sequence selected from the group consisting of SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92 , SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, and SEQ ID NO: 110, and variants or fragments thereof.

In another aspect of the invention there is provided a method of detecting a cylindrospermopsin-producing organism based on the detection of *CYR* gene 8 (*cyrJ*). The method comprises obtaining a sample for use in the method, and detecting the presence of a *CYR* polynucleotide comprising a sequence set forth in SEQ ID NO: 95, or a variant or fragment thereof. Additionally or alternatively, the method for detecting a cylindrospermopsin-producing organism based on the detection of *CYR* gene 8 (*cyrJ*) may comprise the detection of an RNA or cDNA comprising a sequence encoded by SEQ ID NO: 95, or a variant or fragment thereof. Additionally or alternatively, the method for detecting a cylindrospermopsin-producing organism based on the detection of *CYR* gene 8 (*cyrJ*) may comprise the detection of a *CYR* polypeptide comprising a sequence set forth in SEQ ID NO: 96, or a variant or fragment thereof.

In certain embodiments of the invention, the methods for detecting cyanobacteria comprising the detection of *CYR* sequences or variants or fragments thereof further comprise the detection of one or more *SXT* polynucleotides or *SXT* polypeptides as disclosed herein, or a variant or fragment thereof.

The *SXT* polynucleotide may comprise a sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, and variants and fragments thereof.

Alternatively, the *SXT* polynucleotide may be an RNA or cDNA encoded by a sequence selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, and variants and fragments thereof and/or polypeptides as disclosed herein, or a variant or fragment thereof.

The *SXT* polypeptide may comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, and variants and fragments thereof.

In another aspect, the invention provides a method for the detection of dinoflagellates. The skilled addressee will understand that the detection of

"dinoflagellates" encompasses the detection of one or more dinoflagellates. The method comprises obtaining a sample for use in the method, and detecting the presence of one or more *SXT* polynucleotides or polypeptides as disclosed herein, or a variant or fragment thereof. The presence of *SXT* polynucleotides, polypeptides, or variants or fragments thereof, is indicative of dinoflagellates in the sample.

The *SXT* polynucleotide may comprise a sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, and variants and fragments thereof.

Alternatively, the *SXT* polynucleotide may be an RNA or cDNA encoded by a sequence selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, and variants and fragments thereof and/or polypeptides as disclosed herein, or a variant or fragment thereof.

The *SXT* polypeptide may comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, and variants and fragments thereof.

A sample for use in accordance with the methods described herein may be suspected of comprising one or more cyanotoxic organisms. The cyanotoxic organisms may be one or more cyanobacteria and/or one or more dinoflagellates. Additionally or alternatively, a sample for use in accordance with the methods described herein may be suspected of comprising one more cyanobacteria and/or one or more dinoflagellates. A sample for use in accordance with the methods described herein may be a comparative or control sample, for example, a sample comprising a known concentration or density of a cyanobacteria and/or dinoflagellates, or a sample comprising one or more known species or strains of cyanobacteria and/or dinoflagellates.

A sample for use in accordance with the methods described herein may be derived from any source. For example, a sample may be an environmental sample. The environmental sample may be derived, for example, from salt water, fresh water or a blue-green algal bloom. Alternatively, the sample may be derived from a laboratory source, such as a culture, or a commercial source.

It will be appreciated by those in the art that the methods and kits disclosed herein are generally suitable for detecting any organisms in which the *SXT* and/or *CYR* gene clusters are present. Suitable cyanobacteria to which the methods of the invention are applicable may be selected from the orders Oscillatoriales, Chroococcales, Nostocales and Stigonematales. For example, the cyanobacteria may be selected from the genera *Anabaena*, *Nostoc*, *Microcystis*, *Planktothrix*, *Oscillatoria*, *Phormidium*, and *Nodularia*. For example, the cyanobacteria may be selected from the species *Cylindrospermopsis raciborskii* T3, *Cylindrospermopsis raciborskii* AWT205, *Aphanizomenon ovalisporum*, *Aphanizomenon flos-aquae*, *Aphanizomenon sp.*, *Umezakia natans*, *Raphidiopsis curvata*, *Anabaena bergii*, *Lyngbya wollei*, and *Anabaena* circinalis. Examples of suitable dinoflagellates to which the methods and kits of the invention are applicable may be selected from the genera *Alexandrium*, *Pyrodinium* and *Gymnodinium*. The methods and kits of the invention may also be employed for the discovery of novel hepatotoxic species or genera in culture collections or from environmental samples. The methods and kits of the invention may also be employed to detect cyanotoxins that accumulate in other animals, for example, fish and shellfish.

Detection of *SXT* and *CYR* polynucleotides and polypeptides disclosed herein may be performed using any suitable method. For example, methods for the detection of *SXT* and *CYR* polynucleotides and/or polypeptides disclosed herein may involve the use of a primer, probe or antibody specific for one or more *SXT* and *CYR* polynucleotides and

polypeptides. Suitable techniques and assays in which the skilled addressee may utilise a primer, probe or antibody specific for one or more *SXT* and *CYR* polynucleotides and polypeptides include, for example, the polymerase chain reaction (and related variations of this technique), antibody based assays such as ELISA and flow cytometry, and fluorescent microscopy. Methods by which the *SXT* and *CYR* polypeptides disclosed herein may be identified are generally known in the art, and are described for example in Coligan J. E. et al. (Eds) *Current Protocols in Protein Science* (2007), John Wiley and Sons, Inc; Walker, J. M., (Ed) (1988) *New Protein Techniques: Methods in Molecular Biology*, Humana Press, Clifton, N.J; and Scopes, R. K. (1987) *Protein Purification: Principles and Practice,* 3rd. Ed., Springer-Verlag, New York, N.Y. For example, *SXT* and *CYR* polypeptides disclosed herein may be detected by western blot or spectrophotometric analysis. Other examples of suitable methods for the detection of *SXT* and *CYR* polypeptides are described, for example, in US Patent No. 4683195, US Patent No. 6228578, US Patent No. 7282355, US Patent No. 7348147 and PCT publication No. WO/2007/056723.

In a preferred embodiment of the invention, the detection of *SXT* and *CYR* polynucleotides and polypeptides is achieved by amplification of DNA from the sample of interest by polymerase chain reaction, using primers that hybridise specifically to the *SXT* and/or *CYR* sequence, or a variant or fragment thereof, and detecting the amplified sequence.

Nucleic acids and polypeptides for analysis using methods and kits disclosed herein may be extracted from organisms either in mixed culture or as individual species or genus isolates. Accordingly, the organisms may be cultured prior to nucleic acid and/or polypeptide isolation or alternatively nucleic acid and/or polypeptides may be extracted directly from environmental samples, such as water samples or blue-green algal blooms.

Suitable methods for the extraction and purification of nucleic acids for analysis using the methods and kits invention are generally known in the art and are described, for example, in Ausubel F. M. et al. (Eds) *Current Protocols in Molecular* Biology (2007), John Wiley and Sons, Inc; Neilan (1995) Appl. Environ. Microbiol. 61:2286-2291; and Neilan et al. (2002) Astrobiol. 2:271-280. The skilled addressee will readily appreciate that the invention is not limited to the specific methods for nucleic acid isolation described therein and other suitable methods are encompassed by the invention. The invention may be performed without nucleic acid isolation prior to analysis of the nucleic acid.

Suitable methods for the extraction and purification of polypeptides for the purposes of the invention are generally known in the art and are described, for example, in Coligan J. E. et al. (Eds) *Current Protocols in Protein Science* (2007), John Wiley and Sons, Inc; Walker, J. M., (Ed) (1988) *New Protein Techniques: Methods in Molecular Biology*, Humana Press, Clifton, N.J; and Scopes, R. K. (1987) *Protein Purification: Principles and Practice,* 3rd. Ed., Springer-Verlag, New York, N.Y. Examples of suitable techniques for protein extraction include, but are not limited to dialysis, ultrafiltration, and precipitation. Protein purification techniques suitable for use include, but are not limited to, reverse-phase chromatography, hydrophobic interaction chromatography, centrifugation, gel filtration, ammonium sulfate precipitation, and ion exchange.

In accordance with the methods and kits of the invention, *SXT* and *CYR* polynucleotides or variants or fragments thereof may be detected by any suitable means known in the art. In a preferred embodiment of the invention, *SXT* and *CYR* polynucleotides are detected by PCR amplification. Under the PCR approach, oligonucleotide primers can be designed for use in PCR reactions to amplify *SXT* and *CYR* polynucleotides of the invention. Also encompassed by the invention is the PCR amplification of complementary DNA (cDNA) amplified from messenger RNA (mRNA) derived from reverse-transcription of *SXT* and *CYR* sequences (RT-PCR). Known methods of PCR include, but are not limited to, methods using paired primers, nested primers, single specific primers, degenerate primers, gene-specific primers, vector-specific primers, partially-mismatched primers, and the like. Methods for designing PCR and RT-PCR primers are generally known in the art and are disclosed, for example, in Ausubel F. M. et al. (Eds) *Current Protocols in Molecular* Biology (2007), John Wiley and Sons, Inc; Maniatis et al. *Molecular Cloning* (1982), 280-281; Innis et al. (Eds) (1990) *PCR Protocols: A Guide to Methods and Applications* (Academic Press, New York); Innis and Gelfand, (Eds) (1995) *PCR Strategies* (Academic Press, New York); Innis and Gelfand, (Eds) (1999) *PCR Methods Manual* (Academic Press, New York); and Sambrook *et al.* (1989) *Molecular Cloning: A Laboratory Manual* (2nd ed., Cold Spring Harbor Laboratory Press, Plainview, New York.

The skilled addressee will readily appreciate that various parameters of PCR and RT-PCR procedures may be altered without affecting the ability to achieve the desired product. For example, the salt concentration may be varied or the time and/or temperature of one or more of the denaturation, annealing and extension steps may be varied. Similarly, the amount of DNA, cDNA, or RNA template may also be varied depending on

the amount of nucleic acid available or the optimal amount of template required for efficient amplification. The primers for use in the methods and kits of the present invention are typically oligonucleotides typically being at least about 5 nucleotides to about 80 nucleotides in length, more typically about 10 nucleotides in length to about 50 nucleotides in length, and even more typically about 15 nucleotides in length to about 30 nucleotides in length. The skilled addressee will recognise that the primers described herein may be useful for a number of different applications, including but not limited to PCR, RT-PCR, and use of probes for the detection of *SXT* or *CYR* sequences.

Such primers can be prepared by any suitable method, including, for example, direct chemical synthesis or cloning and restriction of appropriate sequences. Not all bases in the primer need reflect the sequence of the template molecule to which the primer will hybridize, the primer need only contain sufficient complementary bases to enable the primer to hybridize to the template. A primer may also include mismatch bases at one or more positions, being bases that are not complementary to bases in the template, but rather are designed to incorporate changes into the DNA upon base extension or amplification. A primer may include additional bases, for example in the form of a restriction enzyme recognition sequence at the 5' end, to facilitate cloning of the amplified DNA.

The invention provides a method of detecting a cyanotoxic organism based on the detection of one or more of *SXT* gene 6 (*sxtA*), *SXT* gene 9 (*sxtG*), *SXT* gene 10 (*sxtH*), *SXT* gene 11 (*sxtI*) and *SXT* gene 17 (*sxtX*) (SEQ ID NOS: 14, 20, 22, 24, and 36 respectively), or fragments or variants thereof. Additionally or alternatively, a cyanotoxic organism may be detected based on the detection of one or more of the following *SXT* polypeptides: *SXTA* (SEQ ID NO: 15), *SXTG* (SEQ ID NO: 21), *SXTH* (SEQ ID NO: 23), *SXTI* (SEQ ID NO: 25), *SXTX* (SEQ ID NO: 37), or fragments or variants thereof.

The skilled addressee will recognise that any primers capable of the amplifying the stated *SXT* and/or *CYR* sequences, or variants or fragments thereof, are suitable for use in the methods of the invention. For example, suitable oligonucleotide primer pairs for the PCR amplification of *SXT* gene 6 (*sxtA*) may comprise a first primer comprising the sequence of SEQ ID NO: 70 and a second primer comprising the sequence of SEQ ID NO: 71, a first primer comprising the sequence of SEQ ID NO: 72 and a second primer comprising the sequence of SEQ ID NO: 73, a first primer comprising the sequence of SEQ ID NO: 74 and a second primer comprising the sequence of SEQ ID NO: 75, a first primer comprising the sequence of SEQ ID NO: 76 and a second primer comprising the

sequence of SEQ ID NO: 77, a first primer comprising the sequence of SEQ ID NO: 78 and a second primer comprising the sequence of SEQ ID NO: 79, a first primer comprising the sequence of SEQ ID NO: 113 and a second primer comprising the sequence of SEQ ID NO: 114, or a first primer comprising the sequence of SEQ ID NO: 115 or SEQ ID NO:116 and a second primer comprising the sequence of SEQ ID NO: 117.

Suitable oligonucleotide primer pairs for the amplification of *SXT* gene 9 (*sxtG*) may comprise a first primer comprising the sequence of SEQ ID NO: 118 and a second primer comprising the sequence of SEQ ID NO: 119, or a first primer comprising the sequence of SEQ ID NO: 120 and a second primer comprising the sequence of SEQ ID NO: 121.

Suitable oligonucleotide primer pairs for the amplification of *SXT* gene 10 (*sxtH*) may comprise a first primer comprising the sequence of SEQ ID NO: 122 and a second primer comprising the sequence of SEQ ID NO: 123.

Suitable oligonucleotide primer pairs for the amplification of *SXT* gene 11 (*sxtI*) may comprise a first primer comprising the sequence of SEQ ID NO: 124 or SEQ ID NO: 125 and a second primer comprising the sequence of SEQ ID NO: 126, or a first primer comprising the sequence of SEQ ID NO: 127 and a second primer comprising the sequence of SEQ ID NO: 128.

Suitable oligonucleotide primer pairs for the amplification of *SXT* gene 17 (*sxtX*) may comprise a first primer comprising the sequence of SEQ ID NO: 129 and a second primer comprising the sequence of SEQ ID NO: 130, or a first primer comprising the sequence of SEQ ID NO: 131 and a second primer comprising the sequence of SEQ ID NO: 132.

The skilled addressee will recognise that fragments and variants of the above-mentioned primer pairs may also efficiently amplify *SXT* gene 6 (*sxtA*), *SXT* gene 9 (*sxtG*), *SXT* gene 10 (*sxtH*), *SXT* gene 11 (*sxtI*) or *SXT* gene 17 (*sxtX*) sequences.

In certain embodiments of the invention, polynucleotide sequences derived from the *CYR* gene are detected based on the detection of *CYR* gene 8 (*cyrJ*) (SEQ ID NO: 95). Suitable oligonucleotide primer pairs for the PCR amplification of *CYR* gene 8 (*cyrJ*) may comprise a first primer having the sequence of SEQ ID NO: 111 or a fragment or variant thereof and a second primer having the sequence of SEQ ID NO: 112 or a fragment thereof.

Also included within the scope of the present invention are variants and fragments of the exemplified oligonucleotide primers. The skilled addressee will also recognise that the invention is not limited to the use of the specific primers exemplified, and alternative primer sequences may also be used, provided the primers are designed appropriately so as to enable the amplification of *SXT* and/or *CYR* sequences. Suitable primer sequences can be determined by those skilled in the art using routine procedures without undue experimentation. The location of suitable primers for the amplification of *SXT* and/or *CYR* sequences may be determined by such factors as G+C content and the ability for a sequence to form unwanted secondary structures.

Suitable methods of analysis of the amplified nucleic acids are well known to those skilled in the art and are described for example, in, Sambrook *et al.* (1989) *Molecular Cloning: A Laboratory Manual* (2nd ed., Cold Spring Harbor Laboratory Press, Plainview, New York); Ausubel F. M. et al. (Eds) *Current Protocols in Molecular* Biology (2007), John Wiley and Sons, Inc; and Maniatis et al. *Molecular Cloning* (1982), 280-281. Suitable methods of analysis of the amplified nucleic acids include, for example, gel electrophoresis which may or may not be preceded by restriction enzyme digestion, and/or nucleic acid sequencing. Gel electrophoresis may comprise agarose gel electrophoresis or polyacrylamide gel electrophoresis, techniques commonly used by those skilled in the art for separation of DNA fragments on the basis of size. The concentration of agarose or polyacrylamide in the gel in large part determines the resolution ability of the gel and the appropriate concentration of agarose or polyacrylamide will therefore depend on the size of the DNA fragments to be distinguished.

In other embodiments of the invention, *SXT* and *CYR* polynucleotides and variants or fragments thereof may be detected by the use of suitable probes. The probes of the invention are based on the sequences of *SXT* and/or *CYR* polynucleotides disclosed herein. Probes are nucleotide sequences of variable length, for example between about 10 nucleotides and several thousand nucleotides, for use in detection of homologous sequences, typically by hybridization. Hybridization probes of the invention may be genomic DNA fragments, cDNA fragments, RNA fragments, or other oligonucleotides.

Methods for the design and/or production of nucleotide probes are generally known in the art, and are described, for example, in Robinson P. J.. et al. (Eds) *Current Protocols in Cytometry* (2007), John Wiley and Sons, Inc; Ausubel F. M. et al. (Eds) *Current Protocols in Molecular* Biology (2007), John Wiley and Sons, Inc; Sambrook et

al. (1989) *Molecular Cloning: A Laboratory Manual* (2nd ed., Cold Spring Harbor Laboratory Press, Plainview, New York; and Maniatis et al. *Molecular Cloning* (1982), 280-281. Nucleotide probes may be prepared, for example, by chemical synthesis techniques, for example, the phosphodiester and phosphotriester methods (see for example Narang S. A. et al. (1979) Meth. Enzymol. 68:90; Brown, E. L. (1979) et al. Meth. Enzymol. 68:109; and U.S. Patent No. 4356270), the diethylphosphoramidite method (see Beaucage S.L et al. (1981) Tetrahedron Letters, 22:1859-1862). A method for synthesizing oligonucleotides on a modified solid support is described in U.S. Patent No. 4458066.

The probes of the invention may be labelled by incorporation of a marker to facilitate their detection. Techniques for labelling and detecting nucleic acids are described, for example, in Ausubel F. M. et al. (Eds) *Current Protocols in Molecular* Biology (2007), John Wiley and Sons, Inc. Examples of suitable markers include fluorescent molecules (*e.g.* acetylaminofluorene, 5-bromodeoxyuridine, digoxigenin, fluorescein) and radioactive isotopes (*e.g.* 32P, 35S, 3H, 33P). Detection of the marker may be achieved, for example, by chemical, photochemical, immunochemical, biochemical, or spectroscopic techniques.

The methods and kits of the invention also encompass the use of antibodies which are capable of binding specifically to the polypeptides of the invention. The antibodies may be used to qualitatively or quantitatively detect and analyse one or more *SXT* or *CYR* polypeptides in a given sample. Methods for the generation and use of antibodies are generally known in the art and described in, for example, Harlow and Lane (Eds) *Antibodies - A Laboratory Manual*, (1988), Cold Spring Harbor Laboratory, N.Y: Coligan, *Current Protocols in Immunology* (1991); Goding, *Monoclonal Antibodies: Principles and Practice* (1986) 2nd ed; and Kohler & Milstein, (1975) Nature 256: 495-497. The antibodies may be conjugated to a fluorochrome allowing detection, for example, by flow cytometry, immunohistochemisty or other means known in the art. Alternatively, the antibody may be bound to a substrate allowing colorimetric or chemiluminescent detection. The invention also contemplates the use of secondary antibodies capable of binding to one or more antibodies capable of binding specifically to the polypeptides of the invention.

The invention also provides kits for the detection of cyanotoxic organisms and/or cyanobacteria, and/or dinoflagellates. In general, the kits of the invention comprise at least one agent for detecting the presence of one or more *SXT* and/or *CYR* polynucleotide

or polypeptides disclosed herein, or a variant or fragment thereof. Any suitable agent capable of detecting *SXT* and/or *CYR* sequences of the invention may be included in the kit. Non-limiting examples include primers, probes and antibodies.

In one aspect, the invention provides a kit for the detection of cyanobacteria, the kit comprising at least one agent for detecting the presence the presence of one or more *SXT* polynucleotides or polypeptides as disclosed herein, or a variant or fragment thereof.

The *SXT* polynucleotide may comprise a sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, and variants and fragments thereof.

Alternatively, the *SXT* polynucleotide may be an RNA or cDNA encoded by a sequence selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, and variants and fragments thereof and/or polypeptides as disclosed herein, or a variant or fragment thereof.

The *SXT* polypeptide may comprise an amino acid sequence selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, and variants and fragments thereof.

Also provided is a kit for the detection of cyanotoxic organisms. The kit comprises at least one agent for detecting the presence of one or more *SXT* polynucleotides or polypeptides as disclosed herein, or a variant or fragment thereof.

The *SXT* polynucleotide may comprise a sequence selected from the group consisting of SEQ ID NO: 14, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 36, and variants and fragments thereof.

Alternatively, the *SXT* polynucleotide may be an RNA or cDNA encoded by a sequence selected from the group consisting of SEQ ID NO: 14, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 36, and variants and fragments thereof.

The *SXT* polypeptide may comprising an amino acid sequence selected from the group consisting of consisting of SEQ ID NO: 15, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 37, and variants and fragments thereof.

The at least one agent may be any suitable reagent for the detection of *SXT* polynucleotides and/or polypeptides disclosed herein. For example, the agent may be a primer, an antibody or a probe. By way of exemplification only, the primers or probes may comprise a sequence selected from the group consisting of SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 72, SEQ ID NO: 73, SEQ ID NO: 74, SEQ ID NO: 75, SEQ ID NO: 76, SEQ ID NO: 77, SEQ ID NO: 78, SEQ ID NO: 79, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 132, SEQ ID NO: 133, SEQ ID NO: 134, and variants and fragments thereof.

In certain embodiments of the invention, the kits for the detection of cyanobacteria or cyanotoxic organisms may further comprise at least one additional agent capable of detecting one or more CYR polynucleotide and/or *CYR* polypeptide sequences as disclosed herein, or a variant or fragment thereof.

The *CYR* polynucleotide may comprise a polynucleotide comprising a sequence selected from the group consisting of: SEQ ID NO: 80, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, and variants and fragments thereof.

Alternatively, the *CYR* polynucleotide may comprise a ribonucleic acid or complementary DNA encoded by a sequence selected from the group consisting of: SEQ ID NO: 80, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, and variants and fragments thereof.

The *CYR* polypeptide may comprise a polypeptide comprising a sequence selected from the group consisting of: SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92 , SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, and SEQ ID NO: 110, and variants and fragments thereof.

The at least one additional agent may be selected, for example, from the group consisting of primers, antibodies and probes. A suitable primer or probe may comprise a sequence selected from the group consisting of SEQ ID NO: 111, SEQ ID NO: 112, and variants and fragments thereof.

In another aspect, the invention provides a kit for the detection of cyanobacteria, the kit comprising at least one agent for detecting the presence the presence of one or more *CYR* polynucleotides or polypeptides as disclosed herein, or a variant or fragment thereof.

The *CYR* polynucleotide may comprise a sequence selected from the group consisting of SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO:107, SEQ ID NO: 109, and variants and fragments thereof.

Alternatively, the *CYR* polynucleotide may be an RNA or cDNA encoded by a sequence selected from the group consisting of SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO:107, SEQ ID NO: 109, and variants and fragments thereof.

The *CYR* polypeptide may comprise a sequence selected from the group consisting of SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92 , SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, and SEQ ID NO: 110, and variants or fragments thereof.

In certain embodiments of the invention, the kits for detecting cyanobacteria comprising one or more agents for the detection of *CYR* sequences or variants or fragments thereof, may further comprise at least one additional agent capable of detecting one or more of the *SXT* polynucleotides and/or *SXT* polypeptides disclosed herein, or variants or fragments thereof.

The *SXT* polynucleotide may comprise a sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, and variants and fragments thereof.

Alternatively, the *SXT* polynucleotide may be an RNA or cDNA encoded by a sequence selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, and variants and fragments thereof and/or polypeptides as disclosed herein, or a variant or fragment thereof.

The at least one agent may be any suitable reagent for the detection of *CYR* polynucleotides and/or polypeptides disclosed herein. For example, the agent may be a primer, an antibody or a probe. By way of exemplification only, the primers or probes may comprise a sequence selected from the group consisting of SEQ ID NO: 111, SEQ ID NO: 112, and variants and fragments thereof.

Also provided is a kit for the detection of dinoflagellates, the kit comprising at least one agent for detecting the presence one or more *SXT* polynucleotides or polypeptides as disclosed herein, or a variant or fragment thereof.

The *SXT* polynucleotide may comprise a sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID

NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, and variants and fragments thereof.

Alternatively, the *SXT* polynucleotide may be an RNA or cDNA encoded by a sequence selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, and variants and fragments thereof and/or polypeptides as disclosed herein, or a variant or fragment thereof.

The *SXT* polypeptide may comprise an amino acid sequence selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, and variants and fragments thereof.

In general, the kits of the invention may comprise any number of additional components. By way of non-limiting examples the additional components may include, reagents for cell culture, reference samples, buffers, labels, and written instructions for performing the detection assay.

Methods of screening

The polypeptides and polynucleotides of the present invention, and fragments and analogues thereof are useful for the screening and identification of compounds and agents that interact with these molecules. In particular, desirable compounds are those that modulate the activity of these polypeptides and polynucleotides. Such compounds may exert a modulatory effect by activating, stimulating, increasing, inhibiting or preventing expression or activity of the polypeptides and/or polynucleotides. Suitable compounds may exert their effect by virtue of either a direct (for example binding) or indirect interaction.

Compounds which bind, or otherwise interact with the polypeptides and polynucleotides of the invention, and specifically compounds which modulate their activity, may be identified by a variety of suitable methods. Non limiting methods include the two-hybrid method, co-immunoprecipitation, affinity purification, mass spectroscopy, tandem affinity purification, phage display, label transfer, DNA microarrays/gene coexpression and protein microarrays.

For example, a two-hybrid assay may be used to determine whether a candidate agent or plurality of candidate agents interacts or binds with a polypeptide of the invention or a variant or fragment thereof. The yeast two-hybrid assay system is a yeast-based genetic assay typically used for detecting protein-protein interactions (Fields and Song., *Nature* 340: 245-246 (1989)). The assay makes use of the multi-domain nature of transcriptional activators. For example, the DNA-binding domain of a known transcriptional activator may be fused to a polypeptide of the invention or a variant or fragment thereof, and the activation domain of the transcriptional activator fused to the candidate agent. Interaction between the candidate agent and the polypeptide of the invention or a variant or fragment thereof, will bring the DNA-binding and activation domains of the transcriptional activator into close proximity. Subsequent transcription of a specific reporter gene activated by the transcriptional activator allows the detection of an interaction.

In a modification of the technique above, a fusion protein may be constructed by fusing the polypeptide of the invention or a variant or fragment thereof to a detectable tag, for example alkaline phosphatase, and using a modified form of immunoprecipitation as described by Flanagan and Leder (Flanagan and Leder, *Cell* 63:185–194 (1990))

Alternatively, co-immunoprecipation may be used to to determine whether a candidate agent or plurality of candidate agents interacts or binds with polypeptide of the invention or a variant or fragment thereof. Using this technique, cyanotoxic organisms,

cyanobacteria and/or dinoflagellates may be lysed under nondenaturing conditions suitable for the preservation of protein-protein interactions. The resulting solution can then be incubated with an antibody specific for a polypeptide of the invention or a variant or fragment thereof and immunoprecipitated from the bulk solution, for example by capture with an antibody-binding protein attached to a solid support. Immunoprecipitation of the polypeptide of the invention or a variant or fragment thereof by this method facilitates the co-immunoprecipation of an agent associated with that protein. The identification an associated agent can be established using a number of methods known in the art, including but not limited to SDS-PAGE, western blotting, and mass spectrometry.

Alternatively, the phage display method may be used to to determine whether a candidate agent or plurality of candidate agents interacts or binds with a polypeptide of the invention or a variant or fragment thereof. Phage display is a test to screen for protein interactions by integrating multiple genes from a gene bank into phage. Under this method, recombinant DNA techniques are used to express numerous genes as fusions with the coat protein of a bacteriophage such the peptide or protein product of each gene is displayed on the surface of the viral particle. A whole library of phage-displayed peptides or protein products of interest can be produced in this way. The resulting libraries of phage-displayed peptides or protein products may then be screened for the ability to bind a polypeptide of the invention or a variant or fragment thereof. DNA extracted from interacting phage contains the sequences of interacting proteins.

Alternatively, affinity chromatography may be used to to determine whether a candidate agent or plurality of candidate agents interacts or binds with a polypeptide of the invention or a variant or fragment thereof. For example, a polypeptide of the invention or a variant or fragment thereof, may be immobilised on a support (such as sepharose) and cell lysates passed over the column. Proteins binding to the immobilised polypeptide of the invention or a variant or fragment thereof may then be eluted from the column and identified, for example by N-terminal amino acid sequencing.

Potential modulators of the activity of the polypeptides of the invention may be generated for screening by the above methods by a number of techniques known to those skilled in the art. For example, methods such as X-ray crystallography and nuclear magnetic resonance spectroscopy may be used to model the structure of polypeptide of the invention or a variant or fragment thereof, thus facilitating the design of potential modulating agents using computer-based modeling. Various forms of combinatorial chemistry may also be used to generate putative modulators.

Polypeptides of the invention and appropriate variants or fragments thereof can be used in high-throughput screens to assay candidate compounds for the ability to bind to, or otherwise interact therewith. These candidate compounds can be further screened against functional polypeptides to determine the effect of the compound on polypeptide activity.

The present invention also contemplates compounds which may exert their modulatory effect on polypeptides of the invention by altering expression of the polypeptide. In this case, such compounds may be identified by comparing the level of expression of the polypeptide in the presence of a candidate compound with the level of expression in the absence of the candidate compound.

It will be appreciated that the methods described above are merely examples of the types of methods that may be utilised to identify agents that are capable of interacting with, or modulating the activity of polypeptides of the invention or variants or fragments thereof. Other suitable methods will be known by persons skilled in the art and are within the scope of this invention.

Using the methods described above, an agent may be identified that is an agonist of a polypeptide of the invention or a variant or fragment thereof. Agents which are agonists enhance one or more of the biological activities of the polypeptide. Alternatively, the methods described above may identify an agent that is an antagonist of a polypeptide of the invention or a variant or fragment thereof. Agents which are antagonists retard one or more of the biological activities of the polypeptide.

Antibodies may act as agonists or antagonists of a polypeptide of the invention or a variant or fragment thereof. Preferably suitable antibodies are prepared from discrete regions or fragments of the polypeptides of the invention or variants or fragments thereof. An antigenic portion of a polynucleotide of interest may be of any appropriate length, such as from about 5 to about 15 amino acids. Preferably, an antigenic portion contains at least about 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 amino acid residues.

Methods for the generation of suitable antibodies will be readily appreciated by those skilled in the art. For example, monoclonal antibody specific for a polypeptide of the invention or a variant or fragment thereof typically containing Fab portions, may be prepared using hybridoma technology described in *Antibodies-A Laboratory Manual*, Harlow and Lane, eds., Cold Spring Harbor Laboratory, N.Y. (1988).

In essence, in the preparation of monoclonal antibodies directed toward polypeptide of the invention or a variant or fragment thereof, any technique that provides for the

production of antibody molecules by continuous cell lines in culture may be used. These include the hybridoma technique originally developed by Kohler *et al.*, *Nature,* 256:495-497 (1975), as well as the trioma technique, the human B-cell hybridoma technique (Kozbor *et al., Immunology Today*, 4:72 (1983)), and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole *et al.*, in Monoclonal Antibodies and Cancer Therapy, pp. 77- 96, Alan R. Liss, Inc., (1985)). Immortal, antibody-producing cell lines can be created by techniques other than fusion, such as direct transformation of B lymphocytes with oncogenic DNA, or transfection with Epstein-Barr virus. See, for example, M. Schreier *et al., "Hybridoma Techniques"* Cold Spring Harbor Laboratory, (1980); Hammerling *et al., "Monoclonal Antibodies and T-cell Hybridomas"* Elsevier/North-Holland Biochemical Press, Amsterdam (1981); and Kennett *et al., "Monoclonal Antibodies"*, Plenum Press (1980).

In brief, a means of producing a hybridoma from which the monoclonal antibody is produced, a myeloma or other self-perpetuating cell line is fused with lymphocytes obtained from the spleen of a mammal hyperimmunised with a recognition factor-binding portion thereof, or recognition factor, or an origin-specific DNA-binding portion thereof. Hybridomas producing a monoclonal antibody useful in practicing this invention are identified by their ability to immunoreact with the present recognition factors and their ability to inhibit specified transcriptional activity in target cells.

A monoclonal antibody useful in practicing the invention can be produced by initiating a monoclonal hybridoma culture comprising a nutrient medium containing a hybridoma that secretes antibody molecules of the appropriate antigen specificity. The culture is maintained under conditions and for a time period sufficient for the hybridoma to secrete the antibody molecules into the medium. The antibody-containing medium is then collected. The antibody molecules can then be further isolated by well-known techniques.

Similarly, there are various procedures known in the art which may be used for the production of polyclonal antibodies. For the production of polyclonal antibodies against a polypeptide of the invention or a variant or fragment thereof, various host animals can be immunized by injection with a polypeptide of the invention, or a variant or fragment thereof, including but not limited to rabbits, chickens, mice, rats, sheep, goats, etc. Further, the polypeptide variant or fragment thereof can be conjugated to an immunogenic carrier (e.g., bovine serum albumin (BSA) or keyhole limpet hemocyanin (KLH)). Also, various adjuvants may be used to increase the immunological response, including but not

limited to Freund's (complete and incomplete), mineral gels such as aluminium hydroxide, surface active substances such as rysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanins, dinitrophenol, and potentially useful human adjuvants such as BCG (bacille Calmette-Guerin) and Corynebacterium parvum.

Screening for the desired antibody can also be accomplished by a variety of techniques known in the art. Assays for immunospecific binding of antibodies may include, but are not limited to, radioimmunoassays, ELISAs (enzyme-linked immunosorbent assay), sandwich immunoassays, immunoradiometric assays, gel diffusion precipitation reactions, immunodiffusion assays, in situ immunoassays, Western blots, precipitation reactions, agglutination assays, complement fixation assays, immunofluorescence assays, protein A assays, and immunoelectrophoresis assays, and the like (see, for example, Ausubel *et al.*, Current Protocols in Molecular Biology, Vol. 1, John Wiley & Sons, Inc., New York (1994)). Antibody binding may be detected by virtue of a detectable label on the primary antibody. Alternatively, the antibody may be detected by virtue of its binding with a secondary antibody or reagent which is appropriately labelled. A variety of methods are known in the art for detecting binding in an immunoassay and are included in the scope of the present invention.

The antibody (or fragment thereof) raised against a polypeptide of the invention or a variant or fragment thereof, has binding affinity for that protein. Preferably, the antibody (or fragment thereof) has binding affinity or avidity greater than about $10^5 M^{-1}$, more preferably greater than about $10^6 M^{-1}$, more preferably still greater than about $10^7 M^{-1}$ and most preferably greater than about $10^8 M^{-1}$.

In terms of obtaining a suitable amount of an antibody according to the present invention, one may manufacture the antibody(s) using batch fermentation with serum free medium. After fermentation the antibody may be purified via a multistep procedure incorporating chromatography and viral inactivation/removal steps. For instance, the antibody may be first separated by Protein A affinity chromatography and then treated with solvent/detergent to inactivate any lipid enveloped viruses. Further purification, typically by anion and cation exchange chromatography may be used to remove residual proteins, solvents/detergents and nucleic acids. The purified antibody may be further purified and formulated into 0.9% saline using gel filtration columns. The formulated bulk preparation may then be sterilised and viral filtered and dispensed.

Embodiments of the invention may utilise antisense technology to inhibit the expression of a nucleic acid of the invention or a fragment or variant thereof by blocking translation of the encoded polypeptide. Antisense technology takes advantage of the fact that nucleic acids pair with complementary sequences. Suitable antisense molecules can be manufactured by chemical synthesis or, in the case of antisense RNA, by transcription *in vitro* or *in vivo* when linked to a promoter, by methods known to those skilled in the art.

For example, antisense oligonucleotides, typically of 18-30 nucleotides in length, may be generated which are at least substantially complementary across their length to a region of the nucleotide sequence of the polynucleotide of interest. Binding of the antisense oligonucleotide to their complementary cellular nucleotide sequences may interfere with transcription, RNA processing, transport, translation and/or mRNA stability. Suitable antisense oligonucleotides may be prepared by methods well known to those of skill in the art and may be designed to target and bind to regulatory regions of the nucleotide sequence or to coding (gene) or non-coding (intergenic region) sequences. Typically antisense oligonucleotides will be synthesized on automated synthesizers. Suitable antisense oligonucleotides may include modifications designed to improve their delivery into cells, their stability once inside a cell, and/or their binding to the appropriate target. For example, the antisense oligonucleotide may be modified by the addition of one or more phosphorothioate linkages, or the inclusion of one or morpholine rings into the backbone (so-called 'morpholino' oligonucleotides).

An alternative antisense technology, known as RNA interference (RNAi), may be used, according to known methods in the art (see for example WO 99/49029 and WO 01/70949), to inhibit the expression of a polynucleotide. RNAi refers to a means of selective post-transcriptional gene silencing by destruction of specific mRNA by small interfering RNA molecules (siRNA). The siRNA is generated by cleavage of double stranded RNA, where one strand is identical to the message to be inactivated. Double-stranded RNA molecules may be synthesised in which one strand is identical to a specific region of the p53 mRNA transcript and introduced directly. Alternatively corresponding dsDNA can be employed, which, once presented intracellularly is converted into dsRNA. Methods for the synthesis of suitable molecule for use in RNAi and for achieving post-transcriptional gene silencing are known to those of skill in the art.

A further means of inhibiting expression may be achieved by introducing catalytic antisense nucleic acid constructs, such as ribozymes, which are capable of cleaving

mRNA transcripts and thereby preventing the production of wild type protein. Ribozymes are targeted to and anneal with a particular sequence by virtue of two regions of sequence complementarity to the target flanking the ribozyme catalytic site. After binding the ribozyme cleaves the target in a site-specific manner. The design and testing of ribozymes which specifically recognise and cleave sequences of interest can be achieved by techniques well known to those in the art (see for example Lieber and Strauss, 1995, *Molecular and Cellular Biology*, 15:540-551.

The invention will now be described with reference to specific examples, which should not be construed as in any way limiting the scope of the invention.

Examples

The invention will now be described with reference to specific examples, which should not be construed as in any way limiting the scope of the invention.

Example 1: Cyanobacterial cultures and characterisation of the *SXT* gene cluster.

Cyanobacterial strains used in the present study (Figure 1) were grown in Jaworski medium in static batch culture at 26°C under continuous illumination (10 μmol m^{-2} s^{-1}). Total genomic DNA was extracted from cyanobacterial cells by lysozyme/SDS/proteinase K lysis following phenol-chloroform extraction as described in Neilan, B. A. 1995.. Appl Environ Microbiol 61:2286-2291. DNA in the supernatant was precipitated with 2 volumes - 20°C ethanol, washed with 70% ethanol, dissolved in TE-buffer (10:1), and stored at - 20°C. PCR primer sequences used for the amplification of *sxt* ORFs are shown in Figure 1B).

PCR amplicons were separated by agarose gel electrophoresis in TAE buffer (40 mM Tris-acetate, 1 mM EDTA, pH 7.8), and visualised by UV translumination after staining in ethidium bromide (0.5 μg/ml). Sequencing of unknown regions of DNA was performed by adaptor-mediated PCR as described in Moffitt et al. (2004) Appl. Environ. Microbiol. 70:6353-6362. Automated DNA sequencing was performed using the PRISM Big Dye cycle sequencing system and a model 373 sequencer (Applied Biosystems). Sequence data were analysed using ABI Prism-Autoassembler software, and percentage similarity and identity to other translated sequences determined using BLAST in

conjunction with the National Center for Biotechnology Information (NIH), Fugue blast (http://www-cryst.bioc.cam.ac.uk/fugue/) was used to identify distant homologs via sequence-structure comparisons. The *sxt* gene clusters were assembled using the software Phred, Phrap, and Consed (http://www.phrap.org/phredphrapconsed.html), and open reading frames manually identified. GenBank accession numbers for the *sxt* gene cluster from *C. raciborskii* T3 is DQ787200.

Example 2: Mass spectrometric analysis of *SXT* intermediates.

Bacterial extracts and *SXT* standards were analysed by HPLC (Thermo Finnigan Surveyor HPLC and autosampler) coupled to an ion trap mass spectrometer (Thermo Finnigan LCQ Deca XP Plus) fitted with an electrospray source. Separation of analytes was obtained on a 2.1 mm x 150 mm Phenomenex Luna 3 micron C18 column at 100 mL/min. Analysis was performed using a gradient starting at 5% acetonitrile in10 mM heptafluorobutyric acid (HFBA) This was maintained for 10 min, then ramped to 100% acetonitrile, over 30 min. Conditions were held at 100% acetonitrile for 10 min to wash the column and then returned to 5% acetonitrile in10 mM HFBA and again held for 10 min to equilibrate the column for the next sample. This resulted in a runtime of 60 min per sample. Sample volumes of 10-100 mL were injected for each analysis. The HPLC eluate directly entered the electrospray source, which was programmed as follows: electrospray voltage 5 kV, sheath gas flow rate 30 arbitrary units, auxiliary gas flow rate 5 arbitrary units. The capillary temperature was 200°C and had a voltage of 47 V. Ion optics were optimised for maximum sensitivity before sample analysis using the instruments autotune function with a standard toxin solution. Mass spectra were acquired in the centroid mode over the m/z range 145-650. Mass range setting was 'normal', with 200 ms maximum ion injection time and automatic gain control (AGC) on. Tandem mass spectra were obtained over a m/z range relevant to the precursor ion. Collision energy was typically 20-30 ThermoFinnigan arbitrary units, and was optimised for maximal information using standards where available.

Example 3: Identification and sequencing of the *SXT* gene cluster in *Cylindrospermopsis raciborskii* T3

O-carbamoyltransferase was initially detected in *C. raciborskii* T3 via degenerate PCR, and later named *sxtI*. Further investigation showed that homologues of *sxtI* were exclusively present in *SXT* toxin-producing strains of four cyanobacterial genera (Table

1), thus representing a good candidate gene in *SXT* toxin biosynthesis. The sequence of the complete putative *SXT* biosynthetic gene cluster (*sxt*) was then obtained by genome walking up- and downstream of *sxtI* in *C. raciborskii* T3 (Figure 3). In *C. raciborskii* T3, this *sxt* gene cluster spans approximately 35000 bp, encoding 31 open reading frames (Figure 2). The cluster also included other genes encoding *SXT*-biosynthesis enzymes, including a methyltransferase (*sxtA1*), a class II aminotransferase (*sxtA4*), an amidinotransferase (*sxtG*), dioxygenases (*sxtH*), in addition to the Ocarbamoyltransferase (*sxtI*). PCR screening of selected *sxt* open reading frames in toxic and non-toxic cyanobacteria strains showed that they were exclusively present in *SXT* toxin-producing isolates (Figure 1A), indicating the association of these genes with the toxic phenotype. In the following passages we describe the open reading frames in the putative *sxt* gene cluster and their predicted functions, based on bioinformatic analysis, LCMS/ MS data on biosynthetic intermediates and *in vitro* biosynthesis, when applicable.

Example 4: Functional prediction of the parent molecule *SXT* biosynthetic genes

Bioinformatic analysis of the *sxt* gene cluster revealed that it contains a previously undescribed example of a polyketide synthase (PKS) like structure, named *sxtA*. SxtA possesses four catalytic domains, SxtA1 to SxtA4. An iterated PSI-blast search revealed low sequence homology of SxtA1 to S-adenosylmethionine (SAM)-dependent methyltransferases. Further analysis revealed the presence of three conserved sequence motifs in SxtA1 (278-ITDMGCGDG- 286, 359-DPENILHI-366, and 424-VVNKHGLMIL-433) that are specific for SAMdependent methyltransferases. SxtA2 is related to GCN5-related N-acetyl transferases (GNAT). GNAT catalyse the transfer of acetate from acetyl-CoA to various heteroatoms, and have been reported in association with other unconventional PKSs, such as PedI, where they load the acyl carrier protein (ACP) with acetate. SxtA3 is related to an ACP, and provides a phosphopantetheinyl-attachment site. SxtA4 is homologous to class II aminotransferases and was most similar to 8-amino-7-oxononanoate synthase (AONS). Class II aminotransferases are a monophyletic group of pyridoxal phosphate (PLP)-dependent enzymes, and the only enzymes that are known to perform Claisen-condensations of amino acids. We therefore reasoned that *sxtA* performs the first step in SXT biosynthesis, involving a Claisen-condensation.

The predicted reaction sequence of SxtA, based on its primary structure, is the loading of the ACP (SxtA3) with acetate from acetyl-CoA, followed by the SxtA1-

catalysed methylation of acetyl-ACP, converting it to propionyl-ACP. The class II aminotransferase domain, SxtA4, would then perform a Claisen-condensation between propionyl-ACP and arginine (Figure 4). The putative product of SxtA is thus 4-amino-3-oxoguanidinoheptane which is here designated as Compound A', (Figure 4). To verify this pathway for SXT biosynthesis based on comparative gene sequence analysis, cell extracts of *C. raciborskii* T3 were screened by LC-MS/MS for the presence of compound A' (Figure 5) as well as arginine and SXT as controls. Arginine and SXT were readily detected (Figure 5) and produced the expected fragment ions. On the other hand, LC-MS/MS data obtained from *m/z* 187 was consistent with the presence of structure A from *C. raciborskii* T3 (Figure 5). MS/MS spectra showed the expected fragment ion (m/z 170, m/z 128) after the loss of ammonia and guanidine from A'. LC-MS/MS data strongly supported the predicted function of SxtA and thus a revised initiating reaction in the SXT biosynthesis pathway.

sxtG encodes a putative amidinotransferase, which had the highest amino acid sequence similarity to L-arginine:lysine amidinotransferases. It is proposed that the product of SxtA is the substrate for the amidinotransferase SxtG, which transfers an amidino group from arginine to the a-amino group A' (Figure 4), thus producing 4,7-diguanidino-3-oxoheptane designated compound B' (Figure 3). This hypothetical sequence of reactions was also supported by the detection of C' by LC-MS/MS (Figure 4). Cell extracts from *C. raciborskii* T3, however, did not contain any measurable levels of B' (4,7-diguanidino-3- oxoheptane). A likely explanation for the failure to detect the intermediate B' is its rapid cyclisation to form C' via the action of SxtB.

The *sxt* gene cluster encodes an enzyme, sxtB, similar to the cytidine deaminase-like enzymes from g-proteobacteria. The catalytic mechanism of cytidine deaminase is a retro-aldol cleavage of ammonia from cytidine, which is the same reaction mechanism in the reverse direction as the formation of the first heterocycle in the conversion from B' to C' (Figure 4). It is therefore suggested that SxtB catalyses this retroaldol- like condensation (step 4, Figure 4).

The incorporation of methionine methyl into SXT, and its hydroxylation was studied. Only one methionine methyl-derived hydrogen is retained in SXT, and a 1,2-H shift has been observed between acetate-derived C-5 and C-6 of SXT. Hydroxylation of the methyl side-chain of the SXT precursor proceeds via epoxidation of a double-bond between the SAM-derived methyl group and the acetate derived C-6. This incorporation pattern may result from an electrophilic attack of methionine methyl on the double bond

between C-5 and C-6, which would have formed during the preceding cyclisation. Subsequently, the new methylene side-chain would be epoxidated, followed by opening to an aldehyde, and subsequent reduction to a hydroxyl. Retention of only one methionine methyl-derived hydrogen, the 1,2-H shift between C-5 and C-6, and the lacking 1,2-H shift between C-1 and C-5 is entirely consistent with the results of this study, whereby the introduction of methionine methyl precedes the formation of the three heterocycles.

sxtD encodes an enzyme with sequence similarity to sterol desaturase and is the only candidate desaturase present in the *sxt* gene cluster, SxtD is predicted to introduce a double bond between C-1 and C-5 of C', and cause a 1,2-H shift between C-5 and C-6 (compound D', Figure 3). The gene product of *sxtS* has sequence homology to non-heme iron 2-oxoglutaratedependent (2OG) dioxygenases. These are multifunctional enzymes that can perform hydroxylation, epoxidation, desaturation, cyclisation, and expansion reactions. 2OG dioxygenases have been reported to catalyse the oxidative formation of heterocycles. SxtS could therefore perform the consecutive epoxidation of the new double bond, and opening of the epoxide to an aldehyde with concomitant bicyclisation. This explains the retention of only one methionine methyl-derived hydrogen, and the lack of a 1,2-H shift between C-1 and C-5 of SXT (steps 5 to 7, Figure 4). SxtU has sequence similarity to short-chain alcohol dehydrogenases. The most similar enzyme with a known function is clavaldehyde dehydrogenase (AAF86624), which reduces the terminal aldehyde of clavulanate-9-aldehyde to an alcohol. SxtU is therefore predicted to reduce the terminal aldehyde group of the SXT precursor in step 8 (Figure 4), forming compound E'.

The concerted action of SxtD, SxtS and SxtU is therefore the hydroxylation and bicyclisation of compound C' to E' (Figure 4). In support for this proposed pathway of SXT biosynthesis, LC-MS/MS obtained from *m/z* 211 and *m/z* 225 allowed the detection of compounds C' and E' from *C. raciborskii* T3 (Figure 5). On the other hand, no evidence could be found by LC-MS/MS for intermediates B (*m/z* 216), and C (*m/z* 198). MS/MS spectra showed the expected fragment ions after the loss of ammonia and guanidine from C', as well as the loss of water in the case of E'.

The detection of E' indicated that the final reactions leading to the complete SXT molecule are the O-carbamoylation of its free hydroxyl group and a oxidation of C-12. The actual sequence of these final reactions, however, remains uncertain. The gene product of *sxtI* is most similar to a predicted Ocarbamoyltransferase from *Trichodesmium erythraeum* (accession ABG50968) and other predicted O-carbamoyltransferases from

cyanobacteria. O-carbamoyltransferases invariably transfer a carbamoyl group from carbamoylphosphate to a free hydroxyl group. Our data indicate that SxtI may catalyse the transfer of a carbamoyl group from carbamoylphosphate to the free hydroxy group of E'. Homologues of *sxtJ* and *sxtK* with a known function were not found in the databases, however it was noted that *sxtJ* and *sxtK* homologues were often encoded adjacent to O-carbamoyltransferase genes.

The *sxt* gene cluster contains two genes, *sxtH* and *sxtT*, each encoding a terminal oxygenase subunit of bacterial phenyl-propionate and related ring-hydroxylating dioxygenases. The closest homologue with a predicted function was capreomycidine hydroxylase from *Streptomyces vinaceus*, which hydroxylates a ringcarbon (C-6) of capreomycidine. SxtH and SxtT may therefore perform a similar function in SXT biosynthesis, that is, the oxidation or hydroxylation and oxidation of C-12, converting F' into *SXT*.

Members belonging to bacterial phenylpropionate and related ring-hydroxylating dioxygenases are multi-component enzymes, as they require an oxygenase reductase for their regeneration after each catalytic cycle. The *sxt* gene cluster provides a putative electron transport system, which would fulfill this function. *sxtV* encodes a 4Fe-4S ferredoxin with high sequence homology to a ferredoxin from *Nostoc punctiforme*. *sxtW* was most similar to fumarate reductase/succinate dehydrogenase-like enzymes from *A. variabilis* and *Nostoc punctiforme,* followed by AsfA from *Pseudomonas putida*. AsfA and AsfB are enzymes involved in the transport of electrons resulting from the catabolism of aryl sulfonates. SxtV could putatively extract an electron pair from succinate, converting it to fumarate, and then transfer the electrons via ferredoxin (SxtW) to SxtH and SxtT.

Example 5: Comparative sequence analysis and functional assignment of *SXT* tailoring genes

Following synthesis of the parent molecule SXT, modifying enzymes introduce various functional groups. In addition to SXT, *C. raciborskii* T3 produces N-1 hydroxylated (neoSXT), decarbamoylated (dcSXT), and N-sulfurylated (GTX-5) toxins, whereas *A. circinalis* AWQC131C produces decarbamoylated (dcSXT), O-sulfurylated (GTX-3/2, dcGTX-3/2), as well as both O-and N-sulfurylated toxins (C- 1/2), but no N-1 hydroxylated toxins.

sxtX encodes an enzyme with homology to cephalosporin hydroxylase. *sxtX* was only detected in *C. raciborskii* T3, *A. flos-aquae* NH- 5, and *Lyngbya wollei*, which produce N-1 hydroxylated analogues of *SXT*, such as neoSXT. This component of the gene cluster was not present in any strain of *A. circinalis*, and therefore probably the reason why this species does not produce N-1 hydroxylated *PSP* toxins (Figure 1A). The predicted function of SxtX is therefore the N-1 hydroxylation of *SXT*.

A. circinalis AWQC131C and *C. raciborskii* T3 also produces N- and O-sulfated analogues of SXT (GTX-5, C-2/3, (dc)GTX- 3/4). The activity of two 3'-phosphate 5'-phosphosulfate (PAPS)-dependent sulfotransferases, which were specific for the N- 21 of SXT and GTX-3/2, and O-22 of 11- hydroxy *SXT*, respectively, has been described from the *SXT* toxin-producing dinoflagellate *Gymnodinium catenatum*. The *sxt* gene cluster from *C. raciborskii* T3 encodes a putative sulfotransferase, SxtN. A PSI-BLAST search with SxtN identified only 25 hypothetical proteins of unknown function with an E value above the threshold (0.005). A profile library search, however, revealed significant structural relatedness of SxtN to estrogen sulfotransferase (1AQU) (Z-score=24.02) and other sulfotransferases. SxtN has a conserved N-terminal region, which corresponds to the adenosine 3'-phosphate 5'-phosphosulfate (PAPS) binding region in 1AQU. It is not known, however, whether SxtN transfers a sulfate group to N-21 or O-22. Interestingly, the *sxt* gene cluster encodes an adenylylsulfate kinase (APSK), SxtO, homologues of which are involved in the formation of PAPS (Figure 2). APKS phosphorylates the product of ATPsulfurylase, adenylylsulfate, converting it to PAPS. Other biosynthetic gene clusters that result in sulfated secondary metabolites also contain genes required for the production of PAPS.

Decarbamoylated analogues of *SXT* could be produced via either of two hypothetical scenarios. Enzymes that act downstream of the carbamoyltransferase, SxtI, in the biosynthesis of PSP toxins are proposed to have broad substrate specificity, processing both carbamoylated and decarbamoylated precursors of *SXT*. Alternatively, hydrolytic cleavage of the carbamoyl moiety from *SXT* or its precursors may occur. SxtL is related to GDSL-lipases, which are multifunctional enzymes with thioesterase, arylesterase, protease and lysophospholipase activities. The function of SxtL could therefore include the hydrolytic cleavage of the carbamoyl group from *SXT* analogues.

Example 6: Cluster-associated *SXT* genes involved in metabolite transport

sxtF and *sxtM* encoded two proteins with high sequence similarity to sodium-driven multidrug and toxic compound extrusion (MATE) proteins of the NorM family. Members of the NorM family of MATE proteins are bacterial sodium-driven antiporters, that export cationic substances. All of the PSP toxins are cationic substances, except for the C-toxins which are zwitterionic. It is therefore probable that SxtF and SxtM are also involved in the export of PSP toxins. A mutational study of NorM from *V. parahaematolyticus* identified three conserved negatively charged residues (D32, E251, and D367) that confer substrate specificity, however the mechanism of substrate recognition remains unknown. In SxtF, the residue corresponding to E251 of NorM is conserved, whereas those corresponding to D32 and D367 are replaced by the neutral amino acids asparagine and tyrosine, respectively. Residues corresponding to D32 and E251 are conserved in SxtM, but D367 is replaced by histidine. The changes in substrate-binding residues may reflect the differences in PSP toxin substrates transported by these proteins.

Example 7: Putative transcriptional regulators of saxitoxin synthase

Environmental factors, such as nitrogen and phosphate availability have been reported to regulate the production of PSP toxins in dinoflagellates and cyanobacteria. Two transcriptional factors, *sxtY* and *sxtZ*, related to PhoU and OmpR, respectively, as well as a two component regulator histidine kinase were identified proximal to the 3'-end of the *sxt* gene cluster in *C. raciborskii* T3. PhoU-related proteins are negative regulators of phosphate uptake whereas OmpR-like proteins are involved in the regulation of a variety of metabolisms, including nitrogen and osmotic balance. It is therefore likely that PSP toxin production in *C. raciborskii* T3 is regulated at the transcriptional level in response to the availability of phosphate, as well as, other environmental factors.

Example 8: Phylogenetic origins of the *SXT* genes

The *sxt* gene cluster from *C. raciborskii* T3 has a true mosaic structure. Approximately half of the *sxt* genes of *C. raciborskii* T3 were most similar to counterparts from other cyanobacteria, however the remaining genes had their closest matches with homologues from proteobacteria, actinomycetes, sphingobacteria, and firmicutes. There is an increasing body of evidence that horizontal gene transfer (HGT) is a major driving force behind the evolution of prokaryotic genomes, and cyanobacterial genomes are known to be greatly affected by HGT, often involving transposases and

phages. The fact that the majority of *sxt* genes are most closely related to homologues from other cyanobacteria, suggests that *SXT* biosynthesis may have evolved in an ancestral cyanobacterium that successively acquired the remaining genes from other bacteria via HGT. The structural organisation of the investigated *sxt* gene cluster, as well as the presence of several transposases related to the IS4-family, suggests that small cassettes of *sxt* genes are mobile.

Example 9: Cyanobacterial cultures and characterisation of the *CYR* gene cluster.

Cyanobacterial strains were grown in Jaworski medium as described in Example 1 above. Total genomic DNA was extracted from cyanobacterial cells by lysozyme/SDS/proteinase K lysis following phenol-chloroform extraction as described previously Neilan, B. A. 1995.. Appl Environ Microbiol 61:2286-2291. DNA in the supernatant was precipitated with 2 volumes -20°C ethanol, washed with 70% ethanol, dissolved in TE-buffer (10:1), and stored at -20°C.

Characterization of unknown regions of DNA flanking the putative cylindrospermopsin biosynthesis genes was performed using an adaptor-mediated PCR as described in Moffitt et al. (2004) Appl. Environ. Microbiol. 70:6353-6362. PCRs were performed in 20 µl reaction volumes containing 1 x *Taq* polymerase buffer 2.5 mM $MgCl_2$, 0.2 mM deoxynucleotide triphosphates, 10 pmol each of the forward and reverse primers, between 10 and 100 ng genomic DNA and 0.2 U of *Taq* polymerase (Fischer Biotech, Australia). Thermal cycling was performed in a GeneAmp PCR System 2400 Thermal cycler (Perkin Elmer Corporation, Norwalk, CT). Cycling began with a denaturing step at 94°C for 3 min followed by 30 cycles of denaturation at 94°C for 10 s, primer annealing between 55° and 65°C for 20 s and a DNA strand extension at 72°C for 1-3 min. Amplification was completed by a final extension step at 72°C for 7 min. Amplified DNA was separated by agarose gel electrophoresis in TAE buffer (40 mM Tris-acetate, 1 mM EDTA, pH 7.8), and visualized by UV transillumination after staining with ethidium bromide (0.5 µg/ml).

Automated DNA sequencing was performed using the PRISM Big Dye cycle sequencing system and a model 373 sequencer (Applied Biosystems, Foster City, CA). Sequence data were analyzed using ABI Prism-Autoassembler software, while identity/similarity values to other translated sequences were determined using BLAST in conjunction with the National Center for Biotechnology Information (NIH, Bethesda,

MD). Fugue blast (http://www-cryst.bioc.cam.ac.uk/fugue/) was used to identify distant homologs via sequence-structure comparisons. The gene clusters were assembled using the software Phred, Phrap, and Consed (http://www.phrap.org/phredphrapconsed.html), open reading frames were manually identified. Polyketide synthase and non-ribosomal peptide synthetase domains were determined using the specialized databases based on crystal structures (http://www-ab.informatik.uni-tuebingen.de/software/NRPSpredictor; http://www.tigr.org/jravel/nrps/, http://www.nii.res.in/nrps-pks.html).

Example 10: Genetic screening of Cylindrospermopsin-producing and non-producing cyanobacterial strains

Cylindrospermopsin-producing and non-producing cyanobacterial strains were screened for the presence of the sulfotransferase gene cyrJ using the primer set cynsulfF (5' ACTTCTCTCCTTTCCCTATC 3') (SEQ ID NO: 111) and cylnamR (5' GAGTGAAAATGCGTAGAACTTG 3') (SEQ ID NO: 112). Genomic DNA was tested for positive amplification using the 16S rRNA gene primers 27F and 809 as described in Neilan et al. (1997) Int. J. Syst. Bacteriol. 47:693-697. Amplicons were sequenced, as described in Example 9 above, to verify the identity of the gene fragment.

The biosynthesis of cylindrospermopsin involves an amidinotransferase, a NRPS, and a PKS (AoaA, AoaB and AoaC, respectively). In order to obtain the entire sequence of the cylindrospermopsin biosynthesis gene cluster, we used adaptor-mediated 'gene-walking' technology, initiating the process from a partial sequence of the amidinotransferase gene from *C. raciborskii* AWT205. Successive outward facing primers were designed and the entire gene cluster spanning 43 kb was sequenced, together with a further 3.5 kb on either side of the toxin gene cluster.

These flanking regions encode putative accessory genes (*hyp* genes), which include molecular chaperons involved in the maturation of hydrogenases. Due to the fact that these genes are flanking the cylindrospermopsin gene cluster at both ends, we postulate that the toxin gene cluster was inserted into this area of the genome thus interrupting the HYP gene cluster. This genetic rearrangement is mechanistically supported by the presence of transposase-like sequences within the cylindrospermopsin cluster.

Bioinformatic analysis of the toxin gene cluster was performed and based on gene function inference using sequence alignments (NCBI BLAST), predicted structural homologies (Fugue Blast), and analysis of PKS and NRPS domains using specialized blast servers based on crystal structures. The cylindrospermopsin biosynthesis cluster

contains 15 ORFs, which encode all the functions required for the biosynthesis, regulation and export of the toxin cylindrospermopsin (Figure 6).

Example 11: Formation of the *CYR* carbon skeleton

The first step in formation of the carbon skeleton of cylindrospermopsin involves the synthesis of guanidinoacetate via transamidination of glycine. CyrA, the AoaA homolog, which encodes an amidinotransferase similar to the human arginine:glycine amidinotransferase GATM, transfers a guanidino group from a donor molecule, most likely arginine, onto an acceptor molecule of glycine thus forming guanidinoacetate (Figure 8, step 1).

The next step (Figure 8, step 2) in the biosynthesis is carried out by CyrB (AoaB homolog), a mixed NRPS-PKS. CyrB spans 8.7 kb and encodes the following domains; adenylation domain (A domain) and a peptidyl carrier protein (PCP) of an NRPS followed by a βketosynthase domain (KS), acyltransferase domain (AT), dehydratase domain (DH), methyltransferase domain (MT), ketoreductase domain (KR), and an acyl carrier protein (ACP) of PKS origin. CyrB therefore must catalyse the second reaction since it is the only gene containing an A domain that could recruit a starter unit for subsequent PKS extensions. The specific amino acid activated by the CyrB A domain cannot be predicted as its substrate specificity conferring residues do not match any in the available databases (http://www-ab.informatik.uni-tuebingen.de/software/NRPSpredictor; http://www.tigr.org/jravel/nrps/, http://www.nii.res.in/nrps-pks.html). So far, no other NRPS has been described that utilizes guanidinoacetate as a substrate. The A domain is thought to activate guanidinoacetate, which is then transferred via the swinging arm of the peptidyl carrier protein (PCP) to the KS domain. The AT domain activates malonyl-CoA and attaches it to the ACP. This is followed by a condensation reaction between the activated guanidinoacetate and malonyl-CoA in the KS domain. CyrB contains two reducing modules, KR and DH. Their concerted reaction reduces the keto group to a hydroxyl followed by elimination of H_2O, resulting in a double bond between C13 and C14. The methyl transferase (MT) domain identified in CyrB via the NRPS/PKS databases (Example 9 above), is homologous to S-adenosylmethionine (SAM) dependent MT. It is therefore suggested that the MT methylates C13. It is proposed that a nucleophilic attack of the amidino group at N19 onto the newly formed double bond between C13 and C14 occurs via a 'Michael addition'. The cyclization follows Baldwin's rules for ring closure (Baldwin et al. (1997) J. Org. Chem 42;3846-3852), resulting in the

formation of the first ring in cylindrospermopsin. This reaction could be spontaneous and may not require enzymatic catalysis, as it is energetically favourable. This is the first of three ring formations.

The third step (Figure 8, step 3) in the biosynthesis involves CyrC (AoaC homolog), which encodes a PKS with KS, AT, KR, and ACP domains. The action of these domains results in the elongation of the growing chain by an acetate via activation of malonyl-CoA by the AT domain, its transfer to ACP and condensation at the KS domain with the product of CyrB. The elongated chain is bound to the ACP of CyrC and the KR domain reduces the keto group to a hydroxyl group on C12. The PKS module carrying out this step contains a KR domain and does not contain a DH domain, this corresponds only to CyrC.

Following the catalysis of enzyme CyrC is CyrD (Figure 8, step 4), a PKS with five modules; KS, AT, DH, KR, and an ACP. The action of this PKS module on the product of CyrC results in the addition of one acetate and the reduction of the keto group on C10 to a hydroxyl and dehydration to a double bond between C9 and C10. This double bond is the site of a nucleophilic attack by the amidino group N19 via another Michael addition that again follows Baldwin's rules of ring closure, resulting in the formation of the second ring, the first 6-membered ring made in cylindrospermopsin.

The product of CyrD is the substrate for CyrE (step 5 in Figure 8), a PKS containing a KS, AT, DH, KR domains and an ACP. Since this sequence of domains is identical to that of CyrD, it is not possible at this stage to ascertain which PKS acts first, but as their action is proposed to be identical it is immaterial at this point. CyrE catalyzes the addition of one acetate and the formation of a double bond between C7 and C8. This double bond is attacked by N18 via a Michael addition and the third cyclisation occurs, resulting in the second 6-member ring.

CyrF is the final PKS module (step 6 of Figure 8) and is a minimal PKS containing only a KS, AT, and ACP. CyrF acts on the product of CyrE and elongates the chain by an acetate, leaving C4 and C6 unreduced.

Step 7 in the pathway (Figure 8) involves the formation of the uracil ring, a reaction that is required for the toxicity of the final cylindrospermopsin compound. The cylindrospermopsin gene cluster encodes two enzymes with high sequence similarity (87%) that have been denoted CyrG and CyrH. A Psi-blast search (NCBI) followed by a Fugue profile library search (see materials and methods) revealed that CyrG and CyrH are most similar to the enzyme family of amidohydrolases/ureases/dihydroorotases, whose

members catalyze the formation and cleavage of N-C bonds. It is proposed that these enzymes transfer a second guanidino group from a donor molecule, such as arginine or urea, onto C6 and C4 of cylindrospermopsin resulting in the formation of the uracil ring. These enzymes carry out two or three reactions depending on the guanidino donor. The first reaction consists of the formation of a covalent bond between the N of the guanidino donor and C6 of cylindrospermopsin followed by an elimination of H_2O forming a double bond between C5 and C6. The second reaction catalyses the formation of a bond between the second N on the guanidino donor and C4 of cylindrospermopsin, co-committently with the breaking of the thioester bond between the acyl carrier protein of CyrE and cylindrospermopsin, causing the release of the molecule from the enzyme complex. Feeding experiments with labeled acetate have shown that the oxygen at C4 is of acetate origin and is not lost during biosynthesis, therefore requiring the *de novo* formation of the uracil ring. The third reaction - if required - would catalyze the cleavage of the guanidino group from a donor molecule other than urea. The action of CyrG and CyrH in the formation of the uracil ring in cylindrospermopsin describes a novel biosynthesis pathway of a pyrimidine.

One theory suggest a linear polyketide which readily assumes a favorable conformation for the formation of the rings. Cyclization may thus be spontaneous and not under enzymatic control. These analyses show that this may happen step-wise, with successive ring formation of the appropriate intermediate as it is synthesized. This mechanism also explains the lack of a thioesterase or cyclization domain, which are usually associated with NRPS/PKS modules and catalyze the release and cyclization of the final product from the enzyme complex.

Example 12: *CYR* tailoring reactions

Cylindrospermopsin biosynthesis requires the action of tailoring enzymes in order to complete the biosynthesis, catalyzing the sulfation at C12 and hydroxylation at C7. Analysis of the cylindrospermopsin gene cluster revealed three candidate enzymes for the tailoring reactions involved in the biosynthesis of cylindrospermopsin, namely CyrI, CyrJ, and CyrN. The sulfation of cylindrospermopsin at C12 is likely to be carried out by the action of a sulfotransferase. CyrJ encodes a protein that is most similar to human 3'-phosphoadenylyl sulfate (PAPS) dependent sulfotransferases. The cylindrospermopsin gene cluster also encodes an adenylsulfate kinase (ASK), namely CyrN. ASKs are enzymes that catalyze the formation of PAPS, which is the sulfate donor for

sulfotransferases. It is proposed that CyrJ sulfates cylindrospermopsin at C12 while CyrN creates the pool of PAPS required for this reaction. Screening of cylindrospermopsin producing and non-producing strains revealed that the sulfotransferase genes were only present in cylindrospermopsin producing strains, further affirming the involvement of this entire cluster in the biosynthesis of cylindrospermopsin (Figure 7). The *cyrJ* gene might therefore be a good candidate for a toxin probe, as it is more unique than NRPS and PKS genes and would presumably have less cross-reactivity with other gene clusters containing these genes, which are common in cyanobacteria. The final tailoring reaction is carried out by CyrI. A Fugue search and an iterated Psi-Blast revealed that CyrI is similar to a hydroxylase belonging to the 2-oxoglutarate and Fe(II)-dependent oxygenase superfamily, which includes the mammalian Prolyl 4-hydroxylase alpha subunit that catalyze the hydroxylation of collagen. It is proposed that CyrI catalyzes the hydroxylation of C7, a residue that, along with the uracil ring, seems to confer much of the toxicity of cylindrospermopsin. The hydroxylation at C7 by CyrI is probably the final step in the biosynthesis of cylindrospermopsin.

Example 13: *CYR* toxin transport

Cylindrospermopsin and other cyanobacterial toxins appear to be exported out of the producing cells. The cylindrospermopsin gene cluster contains an ORF denoted CyrK, the product of which is most similar to sodium ion driven multi-drug and toxic compound extrusion proteins (MATE) of the NorM family. It is postulated that CyrK is a transporter for cylindrospermopsin, based on this homology and its central location in the cluster. Heterologous expression and characterization of the protein are currently being undertaken to verify its putative role in cylindrospermopsin export.

Example 14: Transcriptional regulation of the toxin gene cluster

Cylindrospermopsin production has been shown to be highest when fixed nitrogen is eliminated from the growth media (Saker et al. (1999) J. Phycol 35:599-606). Flanking the cylindrospermopsin gene cluster are "*hyp*" gene homologs involved in the maturation of hydrogenases. In the cyanobacterium *Nostoc* PCC73102 they are under the regulation of the global nitrogen regulator NtcA, that activates transcription of nitrogen assimilation genes. It is plausible that the cylindrospermopsin gene cluster is under the same regulation, as it is located wholly within the "*hyp*" gene cluster in *C. raciborskii*

AWT205, and no obvious promoter region in the cylindrospermopsin gene cluster could be identified.

Finally, the cylindrospermopsin cluster also includes an ORF at its 3' -end designated CyrO. By homology, it encodes a hypothetical protein that appears to possess an ATP binding cassette, and is similar to WD repeat proteins, which have diverse regulatory and signal transduction roles. CyrO may also have a role in transcriptional regulation and DNA binding. It also shows homology to AAA family proteins that often perform chaperone-like functions and assist in the assembly, operation, or disassembly of protein complexes. Further insights into the role of CyrO are hindered due to low sequence homology with other proteins in databases.

The foregoing describes preferred forms of the present invention. It is to be understood that the present invention should not be restricted to the particular embodiment(s) shown above. Modifications and variations, obvious to those skilled in the art can be made thereto without departing from the scope of the present invention.

Related Application

This application claims benefit from Australian Provisional Application Number 2008902056 entitled "Detection of Cyanotoxic Organisms" which was filed on 24 April 2008, the entire contents of which are incorporated herein by reference.

CLAIMS:

1. An isolated polynucleotide comprising a nucleotide sequence sharing at least 90% sequence homology with SEQ ID NO: 1 or a fragment thereof, wherein said fragment encodes a protein of a saxitoxin biosynthetic pathway.

2. The polynucleotide according to claim 1, wherein said fragment comprises a nucleotide sequence sharing at least 90% sequence homology with a sequence selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, and SEQ ID NO: 68.

3. An isolated ribonucleic acid or an isolated complementary DNA encoded by a sequence according to claim 1 or claim 2.

4. An isolated saxitoxin biosynthetic pathway polypeptide comprising an amino acid sequence sharing at least 90% sequence homology with a sequence selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, and SEQ ID NO: 69.

5. A probe or primer that hybridises specifically with one or more of:

(i) a polynucleotide according to claim 1 or 2,

(ii) a ribonucleic acid or complementary DNA according to claim 3,

(iii) a polypeptide according to claim 4.

6. A vector comprising a polynucleotide according to claim 1 or claim 2, or a ribonucleic acid or complementary DNA according to claim 3.

7. A host cell comprising the vector according to claim 6.

8. A method for the detection of cyanobacteria and/or dinoflagellates, the method comprising the steps of obtaining a sample for use in the method and analyzing the sample for the presence of one or more of:

(i) a polynucleotide comprising a sequence according to claim 1 or 2,

2008355461 10 Jun 2015

(ii) a ribonucleic acid or complementary DNA according to claim 3,

(iii) a polypeptide comprising a sequence according to claim 4,

wherein said presence is indicative of cyanobacteria and/or dinoflagellates in the sample.

9. A method for detecting a cyanotoxic organism, the method comprising the steps of obtaining a sample for use in the method and analyzing the sample for the presence of one or more of:

(i) a polynucleotide comprising a sequence selected from the group consisting of: SEQ ID NO: 14, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 36, and variants thereof sharing at least 80% sequence homology with SEQ ID NO: 14, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, or SEQ ID NO: 36,

(ii) a ribonucleic acid or complementary DNA encoded by a sequence according to (i),

(iii) a polypeptide comprising a sequence selected from the group consisting of: SEQ ID NO: 15, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 37, and variants thereof sharing at least 80% sequence homology with SEQ ID NO: 15, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, or SEQ ID NO: 37,

wherein said presence is indicative of cyanotoxic organisms in the sample.

10. The method according to claim 9, wherein said cyanotoxic organism is a cyanobacterium or a dinoflagellate.

11. The method according to any one of claims 8 to 10, further comprising analyzing the sample for the presence of one or more of:

(i) a polynucleotide comprising a sequence selected from the group consisting of: SEQ ID NO: 80, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, and variants and fragments thereof,

(ii) a ribonucleic acid or complementary DNA encoded by a sequence according to (i),

(iii) a polypeptide comprising a sequence selected from the group consisting of: SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92 , SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, and SEQ ID NO: 110, and variants and fragments thereof.

12. The method according to any one of claims 8 to 11, wherein said analyzing comprises amplification of DNA from the sample by polymerase chain reaction.

2008355461 10 Jun 2015

13. The method according to claim 12, wherein said polymerase chain reaction utilises:

(i) one or more primers comprising a sequence selected from the group consisting of SEQ ID NO: 111, SEQ ID NO: 112, and variants and fragments thereof; and/or

(ii) one or more primers comprising a sequence selected from the group consisting of SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 72, SEQ ID NO: 73, SEQ ID NO: 74, SEQ ID NO: 75, SEQ ID NO: 76, SEQ ID NO: 77, SEQ ID NO: 78, SEQ ID NO: 79, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 132, SEQ ID NO: 133, SEQ ID NO: 134, and variants and fragments thereof.

14. An isolated antibody capable of binding specifically to a polypeptide according to claim 4.

15. A kit for the detection of cyanobacteria and/or dinoflagellates, the kit comprising at least one agent for detecting the presence of one or more of:

(i) a polynucleotide comprising a sequence according to claim 1 or 2,

(ii) a ribonucleic acid or complementary DNA according to claim 3,

(iii) a polypeptide comprising a sequence according to claim 4,

wherein said presence is indicative of cyanobacteria and/or dinoflagellates in the sample.

16. A kit for the detection of cyanotoxic organisms, the kit comprising at least one agent for detecting the presence of one or more of:

(i) a polynucleotide comprising a sequence selected from the group consisting of: SEQ ID NO: 14, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 36, and variants thereof sharing at least 90% sequence homology with SEQ ID NO: 14, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, or SEQ ID NO: 36,

(ii) a ribonucleic acid or complementary DNA encoded by a sequence according to (i),

(iii) a polypeptide comprising a sequence selected from the group consisting of: SEQ ID NO: 15, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 37, and variants thereof sharing at least 90% sequence homology with SEQ ID NO: 15, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, or SEQ ID NO: 37,

wherein said presence is indicative of cyanotoxic organisms in the sample.

17. The kit according to claim 15 or claim 16, further comprising at least one additional agent for detecting the presence of one or more of:

(i) a polynucleotide comprising a sequence selected from the group consisting of: SEQ ID NO: 80, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, and variants and fragments thereof,

(ii) a ribonucleic acid or complementary DNA encoded by a sequence according to (i),

(iii) a polypeptide comprising a sequence selected from the group consisting of: SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92 , SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, and SEQ ID NO: 110, and variants and fragments thereof.

18. The kit according to any one of claims 15 to 17, wherein said at least one additional agent is a primer, antibody or probe.

19. The kit according to claim 18, wherein said primer or probe comprises:

(i) a sequence selected from the group consisting of SEQ ID NO: 109, SEQ ID NO: 110, and variants and fragments thereof; or

(ii) a sequence selected from the group consisting of SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 72, SEQ ID NO: 73, SEQ ID NO: 74, SEQ ID NO: 75, SEQ ID NO: 76, SEQ ID NO: 77, SEQ ID NO: 78, SEQ ID NO: 79, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 132, SEQ ID NO: 133, SEQ ID NO: 134, and variants and fragments thereof.

20. A method of screening for a compound that modulates the expression or activity of one or more polypeptides according to claim 4, the method comprising:

contacting the polypeptide with a candidate compound under conditions suitable to enable interaction of the candidate compound and the polypeptide; and

assaying for activity of the polypeptide.

NewSouth Innovations UNSW AUSTRALIA

Patent Attorneys for the Applicant/Nominated Person

SPRUSON & FERGUSON

Cyanobacteria Strains	Toxicity (Ref)	*sxtA*	*sxtG*	*sxtH*	*sxtI*	*sxtX*
A. circinalis AWQC118C	PSP (54)	+	+	+	+	-
A. circinalis AWQC131C	PSP (25)	+	+	+	+	-
A. circinalis AWQC134C	PSP (54)	+	+	+	+	-
A. circinalis AWQC150E	PSP (54)	+	+	+	+	-
A. circinalis AWQC173A	PSP (54)	+	+	+	+	-
A. circinalis AWQC271C	- (54)	-	-	-	-	-
A. circinalis AWQC306A	- (54)	-	-	-	-	-
A. circinalis AWQC310F	- (54)	-	-	-	-	-
A. circinalis AWQC342D	- (54)	-	-	-	-	-
Aph. flos-aquaea NH-5	PSP (26)	+	+	+	+	+
Aph. ovalisporum APH028A	CYLN (46)	-	-	-	-	-
C. raciborskii T3	PSP (23)	+	+	+	+	+
C. raciborskii 23B	CYLN (58)	-	-	-	-	-
C. raciborskii GOON	CYLN (43)	-	-	-	-	-
C. raciborskii GERM1	- (30)	-	-	-	-	-
C. raciborskii MARAU1	- (30)	-	-	-	-	-
L. wollei	PSP (7)	+	+	+	+	+

FIGURE 1A

Primer	From	To	Direction	Sequence	Gene	
SEQ ID NO:133	1917	1937	-->	GCAAATTTTGCAGGAGTAATG	sterole desaturase	sxtD
SEQ ID NO:134	2744	2763	-->	AGAGATGCTATGCTTTTCAA	InsB	orf3
SEQ ID NO:135	2889	2911	-->	TTTTGGGTAAACTTTTATAGCCAT	InsB	orf3
SEQ ID NO:136	3020	3041	<--	TGGGTCTGGACAGTTGTAGATA	InsA	orf4
SEQ ID NO:137	3306	3328	<--	AAGGGGAAAACAAAATTATCAAT	InsA	orf4
SEQ ID NO:138	3396	3415	-->	GGCGATCGCCTGCTAAAAAT	InsA	orf4
SEQ ID NO:139	3717	3739	-->	CCTCATTTTCATTTCTAGACGTT	SPUR	sxtC
SEQ ID NO:140	4201	4220	-->	CCACTTCAACTAAAACAGCA	cytidine deaminase	sxtB
SEQ ID NO:141	4362	4381	<--	AAAAATTTTGGAGGGGTAGC	cytidine deaminase	sxtB
SEQ ID NO:142	4932	4951	-->	ATCCAAGATGCGACAACACT	cytidine deaminase	sxtB
SEQ ID NO: 70	5193	5212	-->	TTAATTGCTTGGTCTAICTC	PKS	sxtA
SEQ ID NO: 71	5206	5225	<--	CAATACCGAAGAGGAGATAG	PKS	sxtA
SEQ ID NO: 72	5345	5364	<--	TAGGCGTGTTAGTGGGAGAT	PKS	sxtA
SEQ ID NO: 73	5415	5434	-->	TGTGTAACCAATTTGTGAGT	PKS	sxtA
SEQ ID NO: 74	5478	5497	<--	TTAGCCGGATTACAGGTGAA	PKS	sxtA
SEQ ID NO: 75	6136	6155	<--	CTGGACTCGGCTTGTTGCTT	PKS	sxtA
SEQ ID NO: 76	6933	6952	-->	CAGCGAGTTACACCCACCAC	PKS	sxtA
SEQ ID NO: 76	7035	7054	<--	CTCGCACTAAAATATTCTACC	PKS	sxtA
SEQ ID NO: 78	7434	7452	-->	AAAACCTCAGCTTCCACAA	PKS	sxtA
SEQ ID NO: 79	7537	7558	<--	ATGATTTTGGAGGTCCATTGTT	PKS	sxtA
SEQ ID NO: 113	7820	7841	-->	CCCAATATCTCCCTGTAAAACT	PKS	sxtA
SEQ ID NO: 114	8170	8189	<--	TGGCAATTGTCTCTCCGTAT	PKS	sxtA
SEQ ID NO: 115	8742	8761	<--	CTCGCCGATGAAAGTCCTCT	PKS	sxtA
SEQ ID NO: 116	8772	8791	<--	GCGTGTCGAGAAAAAGGTGT	PKS	sxtA
SEQ ID NO: 117	8782	8801	-->	CTCGACACGCAAGAATATACG	PKS	sxtA
SEQ ID NO: 143	9390	9410	-->	GGTCCTTGCGCAGATAGAGTG	chaperon-like	sxtE
SEQ ID NO: 144	9390	9410	<--	CACTCTAICTGCGCAAGGACC	chaperon-like	sxtE
SEQ ID NO: 145	9856	9876	<--	TGACTGCAITTCGCTGTATAAA	MATE1	sxtF
SEQ ID NO: 118	10080	10100	-->	ATGCTTCTGCTTTGGCAIGGC	amidinotransferase	sxtG
SEQ ID NO: 119	11468	11488	<--	TAACTCGACGAACTTTGACCC	amidinotransferase	sxtG

FIGURE 1B

Primer	From	To	Direction	Sequence	Gene	
SEQ ID NO: 120	11551	11569	-->	GCCGCCAATCCTCGCGATG	amidinotransferase	sxtG
SEQ ID NO: 121	12256	12277	<--	GAACGTCTAATGTTGCACAGTG	amidinotransferase	sxtG
SEQ ID NO: 122	12410	12432	-->	CTGGTACGTAGTCGCAAAGGTGG	dioxygenase I	sxtH
SEQ ID NO: 123	13292	13317	-->	CTGACGGTACATGTATTTCCTGTGAC	dioxygenase I	sxtH
SEQ ID NO: 124	13540	13561	-->	cgtctcatATGCAGATCTTAGGAATTTCAG	carbamoyltransferase	sxtI
SEQ ID NO: 125	13561	13585	-->	GCTTACTACCACGATAGTGCTGCCG	carbamoyltransferase	sxtI
SEQ ID NO: 126	14451	14472	-->	TCTATGTTTAGCAGGTGGTGTC	carbamoyltransferase	sxtI
SEQ ID NO: 127	14735	14754	<--	TTCTGCAAGACGAGCCATAA	carbamoyltransferase	sxtI
SEQ ID NO: 128	15211	15230	<--	GGTTCGCCGCGGACATTAAA	carbamoyltransferase	sxtI
SEQ ID NO: 146	15709	15730	-->	TTCATAAGACGGCTGTTGAATC	hypothetical protein	sxtJ
SEQ ID NO: 147	15966	15989	<--	ctcgagTTAAAAAAGAGTGTAAATGAAAGG	hypothetical protein	sxtK
SEQ ID NO: 148	16326	16348	<--	TTCTATAACTGCTGCCAAATTTT	GDSL-lipase	sxtL
SEQ ID NO: 149	16400	16422	-->	AATTTTGGAGTGACTGGTTATGG	GDSL-lipase	sxtL
SEQ ID NO: 150	16400	16422	<--	CCATAACCAGTCACTCCAAAATT	GDSL-lipase	sxtL
SEQ ID NO: 151	16929	16949	-->	TTTTAGTTGTTACTTTTGGCG	GDSL-lipase	sxtL
SEQ ID NO: 152	17215	17234	-->	ACAGCAGATGAGAGAAAGTA	GDSL-lipase	sxtL
SEQ ID NO: 153	18054	18073	-->	GGGTTGTCTTGCTGATTTTC	MATE II	sxtM
SEQ ID NO: 154	18721	18742	<--	CATTAAAATAAGTCCGGACAGG	MATE II	sxtM
SEQ ID NO: 155	19133	19152	<--	TTAAACAGAATGAGGAGCAA	MATE II	sxtM
SEQ ID NO: 156	19260	19279	<--	AAACAACACACCCATCTAAG	sulfotransferase	sxtN
SEQ ID NO: 157	19531	19550	-->	TTAATAAGGCATCCCCAAGA	sulfotransferase	sxtN
SEQ ID NO: 158	19728	19747	<--	GAAATGGCTGTGTAAAAACT	sulfotransferase	sxtN
SEQ ID NO: 129	20584	20603	<--	ATGCTAATGCGGTGGGAGTA	cephalosporin hydroxylase	sxtX
SEQ ID NO: 130	20643	20662	-->	AAAGCAGTTCCGACGACATT	cephalosporin hydroxylase	sxtX
SEQ ID NO: 131	20831	20853	-->	CCTATTTCGATTATTGTTTTCGG	cephalosporin hydroxylase	sxtX
SEQ ID NO: 132	21252	21271	<--	GATACCGATCATAAACTACG	cephalosporin hydroxylase	sxtX
SEQ ID NO: 159	21290	21309	-->	TCTGCCATATCCCCAACCTA	ferredoxin	sxtW
SEQ ID NO: 160	21445	21464	<--	GATCGCCCGACAGGAAGACT	ferredoxin	sxtW
SEQ ID NO: 161	22020	22039	-->	TCCGGCTTGACCTGCTGGAC	succinate dehydrogenase	sxtV

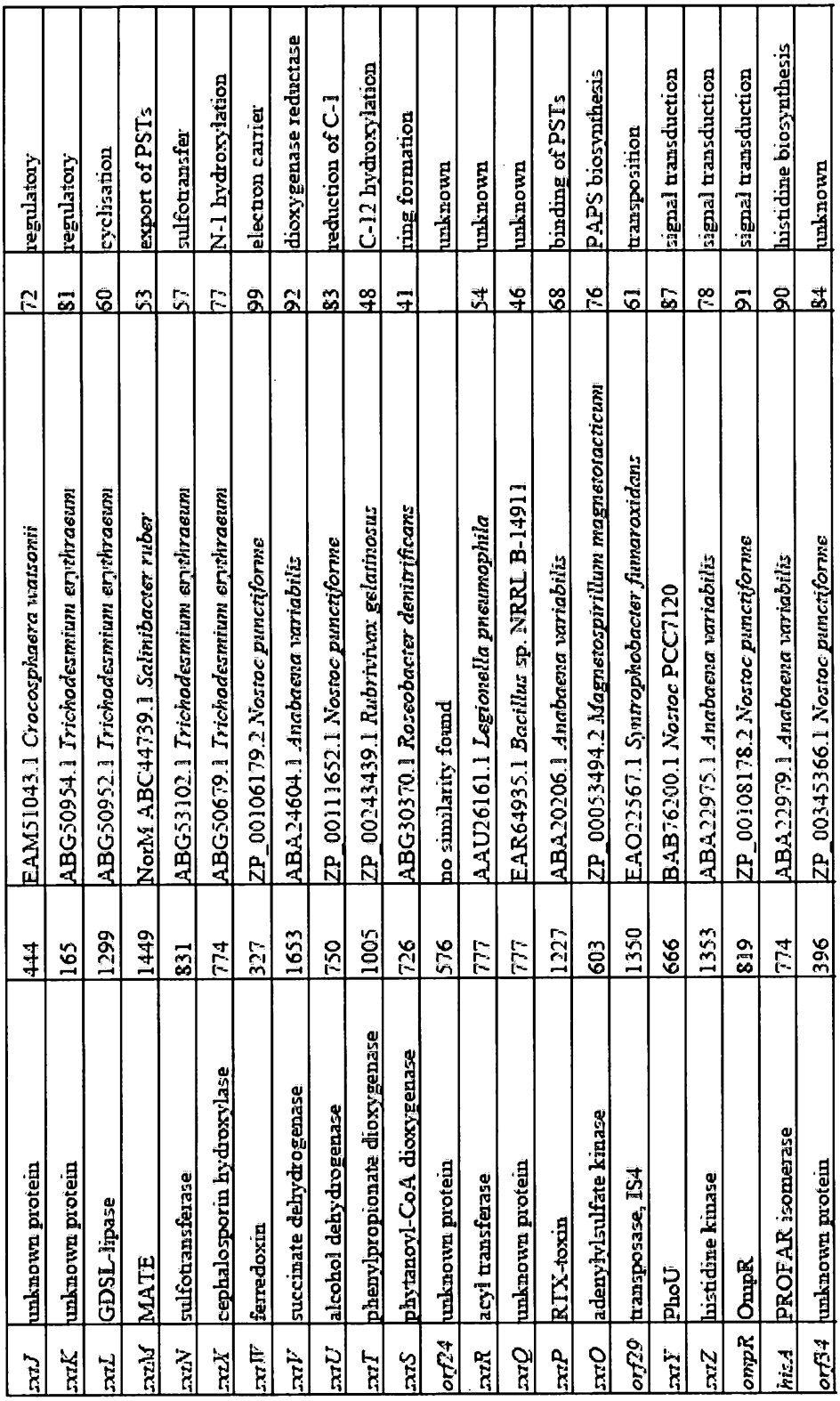
FIGURE 1B (cont)

Primer	From	To	Direction	Sequence	Gene	
SEQ ID NO: 162	22715	22734	-->	TGCGATGATTTTGCCTCTGT	succinate dehydrogenase	sxtV
SEQ ID NO: 163	22801	22820	-->	AAAATTTGCACACCCACACG	succinate dehydrogenase	sxtV
SEQ ID NO: 164	22942	22968	-->	TTGGATTGAACGTGTAATTGAAAAAGC	succinate dehydrogenase	sxtV
SEQ ID NO: 186	22942	22968	<--	GCTTTTTCAATTACACGTTCAATCCAA	succinate dehydrogenase	sxtV
SEQ ID NO: 165	23434	23453	<--	GTTTAGTCGATACGCCATTT	succinate dehydrogenase	sxtV
SEQ ID NO: 166	23434	23453	-->	AAATGGCGTATCGACTAAC	succinate dehydrogenase	sxtV
SEQ ID NO: 167	24095	24115	-->	ATATAGGAGCGCATAAAGTGC	succinate dehydrogenase	sxtV
SEQ ID NO: 168	24728	24747	-->	CTTGGTATAAGTCTTGTGAT	dioxygenase II	sxtT
SEQ ID NO: 169	25426	25445	<--	AACACTCATTAGATTCATCT	phytanoyl-CoA dioxygenase	sxtS
SEQ ID NO: 170	25979	25999	<--	TCCACTAAATCCTTTGAATTG	phytanoyl-CoA dioxygenase	sxtS
SEQ ID NO: 171	26279	26299	-->	TGTTTGTCTGGATGCGATCCT	unknown protein	orf24
SEQ ID NO: 172	26451	26470	-->	GCAGTTCAGGTCCATGAAAC	unknown protein	orf25
SEQ ID NO: 173	27155	27174	-->	AGCCCAGTCACAACCTTCGT	GNAT transferase	sxtR
SEQ ID NO: 174	27508	27528	-->	TCTGGAAGTACTTGCACTGTC	unknown protein	sxtQ
SEQ ID NO: 175	28197	28218	-->	TGTAACTCCGTCAGGACATAAA	unknown protein	sxtQ
SEQ ID NO: 176	28395	28417	<--	TGCAAATTTTAGTAGCAATAACG	RTX-toxin like	sxtP
SEQ ID NO: 177	29532	29558	<--	CTTTACTAATTATAGCGGGGGATATTAT	RTX-toxin like	sxtP
SEQ ID NO: 178	29868	29887	<--	CAGTGGGGAAATAGATGGAT	adenylylsulphate kinase	sxtO
SEQ ID NO: 179	30249	30268	<--	TGGTCATAAAAGCGGGATTC	adenylylsulphate kinase	sxtO
SEQ ID NO: 180	31745	31762	-->	GGATCTTGGCGCAATTTA	IS4	orf29
SEQ ID NO: 181	33031	33053	<--	GTTAGAGACTTGGAACGTATTGG	PhoU	sxtY
SEQ ID NO: 182	34711	34729	-->	CCAAACCCAGAAGAAATCC	histidine kinase	sxtZ
SEQ ID NO: 183	35100	35121	-->	AATCTATAGCCAAAACCCCTAA	ribotide isomerase	
SEQ ID NO: 184	36447	36465	-->	ACTGTGTGAACAATTCCCC	ribotide isomerase	
SEQ ID NO: 185	36652	36680	-->	GCAACAAGACTACATTTAGTAGATTTAGA	ribotide isomerase	

FIGURE 1B (cont)

Name	Enzyme Family	Size (bp)	Blast Similarity Match	(%)	Putative Function
orf1	unknown protein	1320	BAB76734.1 *Nostoc* PCC7120	82	unknown
orf2	sterole desaturase-like	759	ABG52264.1 *Trichodesmium erythraeum*	63	desaturation
orf3	transposase InsB	392	CAE11915.2 *Microcystis aeruginosa*	86	transposition
orf4	transposase InsA	360	CAE11914.1 *Microcystis aeruginosa*	71	transposition
orfC	unknown protein	354	no similarity found		regulatory
orfB	cytidine deaminase	957	EAS64681.1 *Vibrio angustum*	62	cyclisation
orfA	methyltransferase	1506	ABF89568.1 *Myxococcus xanthus*	64	methylation
	GNAT	633	AAT70096.1 CurA *Lyngbya majuscula*	64	loading of ACP
	acyl carrier protein	324	AAV97870 OmnB *Theonella swinhoei*	59	ACP
	AONS	1275	ABD13093.1 *Frankia* sp. CcI3	61	Claisen condensation
orfE	unknown protein	387	ABE53436.1 *Shewanella denitrificans*	52	unknown
orfF	MATE	1416	NorM ABC44739.1 *Salinibacter ruber*	52	export of PSTs
orfG	amidinotransferase	1134	ABA05575.1 *Nitrobacter winogradskyi*	71	amidinotransfer
orfH	phenylpropionate dioxygenase	1005	ZP_00243439.1 *Rubrivivax gelatinosus*	50	C-12 hydroxylation
orfI	carbamoyltransferase	1839	ABG50968.1 *Trichodesmium erythraeum*	82	carbamoylation

FIGURE 2



nrJ	unknown protein	444	EAM51043.1 *Crocosphaera watsonii*	72	regulatory
nrK	unknown protein	165	ABG50954.1 *Trichodesmium erythraeum*	81	regulatory
nrL	GDSL-lipase	1299	ABG50952.1 *Trichodesmium erythraeum*	60	cyclisation
nrM	MATE	1449	NorM ABC44739.1 *Salinibacter ruber*	53	export of PSTs
nrN	sulfotransferase	831	ABG53102.1 *Trichodesmium erythraeum*	57	sulfotransfer
nrX	cephalosporin hydroxylase	774	ABG50679.1 *Trichodesmium erythraeum*	77	N-1 hydroxylation
nrW	ferredoxin	327	ZP_00106179.2 *Nostoc punctiforme*	99	electron carrier
nrV	succinate dehydrogenase	1653	ABA24604.1 *Anabaena variabilis*	92	dioxygenase reductase
nrU	alcohol dehydrogenase	750	ZP_00111652.1 *Nostoc punctiforme*	83	reduction of C-1
nrT	phenylpropionate dioxygenase	1005	ZP_00243439.1 *Rubrivirax gelatinosus*	48	C-12 hydroxylation
nrS	phytanoyl-CoA dioxygenase	726	ABG30370.1 *Roseobacter denitrificans*	41	ring formation
orf24	unknown protein	576	no similarity found		unknown
nrR	acyl transferase	777	AAU26161.1 *Legionella pneumophila*	54	unknown
nrQ	unknown protein	777	EAR64935.1 *Bacillus* sp. NRRL B-14911	46	unknown
nrP	RTX-toxin	1227	ABA20206.1 *Anabaena variabilis*	68	binding of PSTs
nrO	adenylylsulfate kinase	603	ZP_00053494.2 *Magnetospirillum magnetotacticum*	76	PAPS biosynthesis
orf29	transposase, IS4	1350	EAO22567.1 *Symrophobacter fumaroxidans*	61	transposition
nrI	PhoU	666	BAB76200.1 *Nostoc* PCC7120	87	signal transduction
nrZ	histidine kinase	1353	ABA22975.1 *Anabaena variabilis*	78	signal transduction
ompR	OmpR	819	ZP_00108178.2 *Nostoc punctiforme*	91	signal transduction
hisA	PROFAR isomerase	774	ABA22979.1 *Anabaena variabilis*	90	histidine biosynthesis
orf34	unknown protein	396	ZP_00345366.1 *Nostoc punctiforme*	84	unknown

FIGURE 2 (cont)

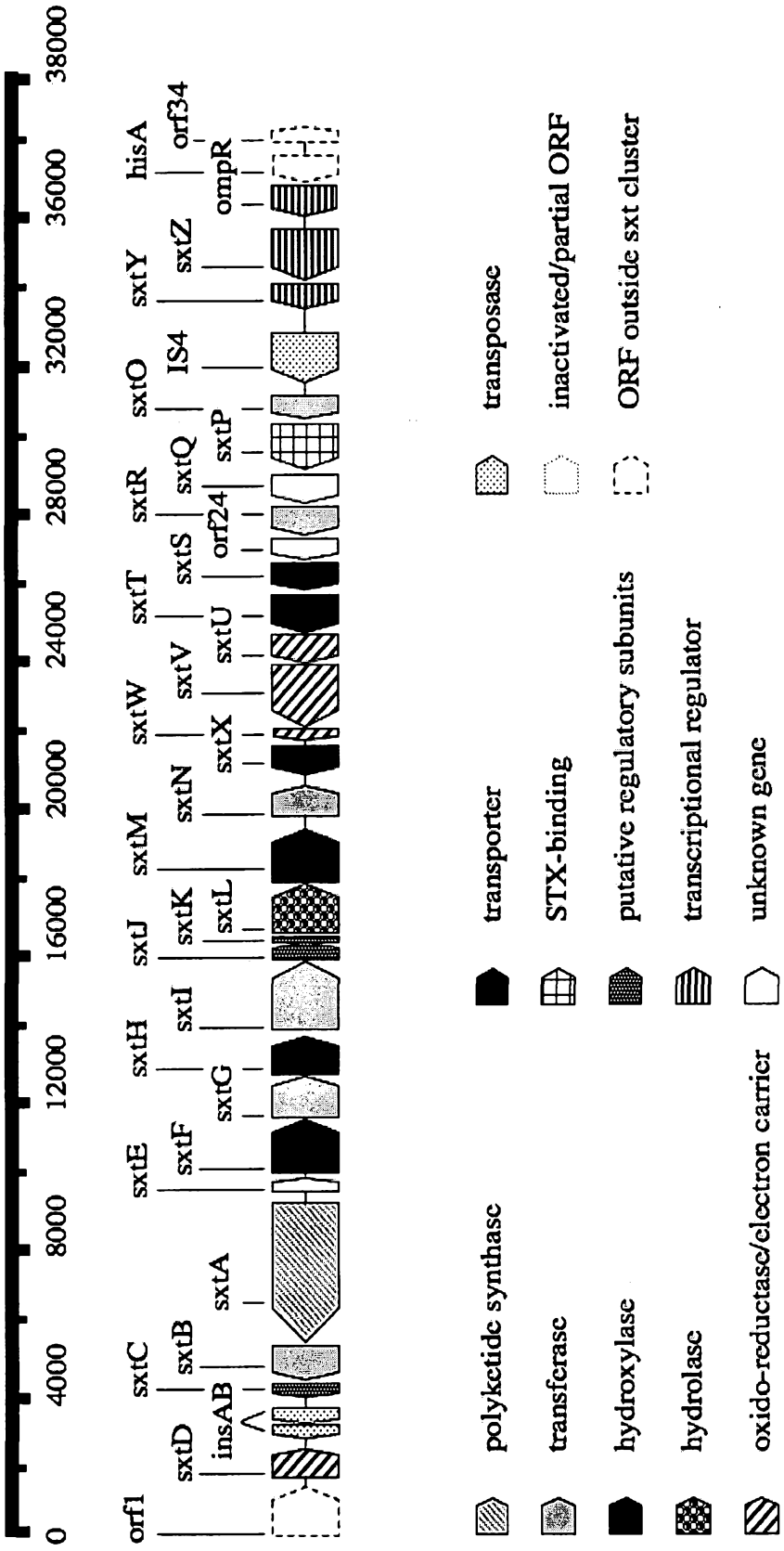

0
4000
8000
12000
16000
20000
24000
28000
32000
36000
38000
orf1
sxtD
insAB
sxtC
sxtB
sxtA
sxtE
sxtF
sxtG
sxtH
sxtI
sxtJ
sxtK
sxtL
sxtM
sxtN
sxtX
sxtW
sxtV
sxtU
sxtT
sxtS
orf24
sxtR
sxtQ
sxtP
sxtO
IS4
sxtY
sxtZ
ompR
orf34
hisA
polyketide synthase
transferase
hydroxylase
hydrolase
oxido-reductase/electron carrier
transporter
STX-binding
putative regulatory subunits
transcriptional regulator
unknown gene
transposase
inactivated/partial ORF
ORF outside sxt cluster

FIGURE 3

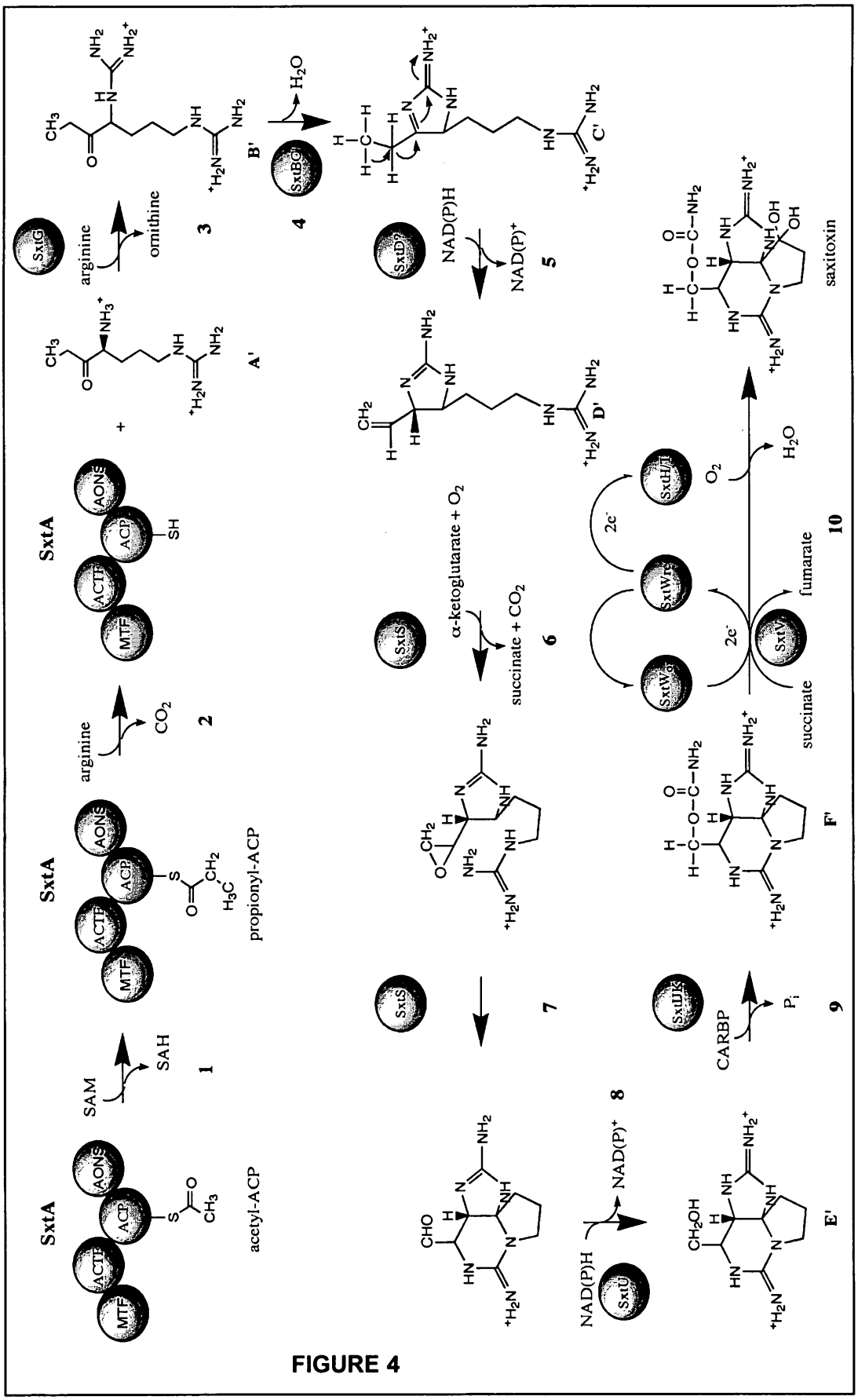

SxtA
MTF
ACTF
ACP
AONS
acetyl-ACP
SAM
SAH
1
propionyl-ACP
arginine
CO2
2
A'
arginine
ornithine
3
B'
SxtBG
H2O
4
SxtD?
NAD(P)H
NAD(P)+
5
D'
SxtS
α-ketoglutarate + O2
succinate + CO2
6
7
SxtU
NAD(P)H
NAD(P)+
8
E'
SxtUK
CARBP
Pi
9
SxtW
SxtWrs
SxtH/I
2e-
O2
H2O
succinate
fumarate
F'
10
saxitoxin

FIGURE 4

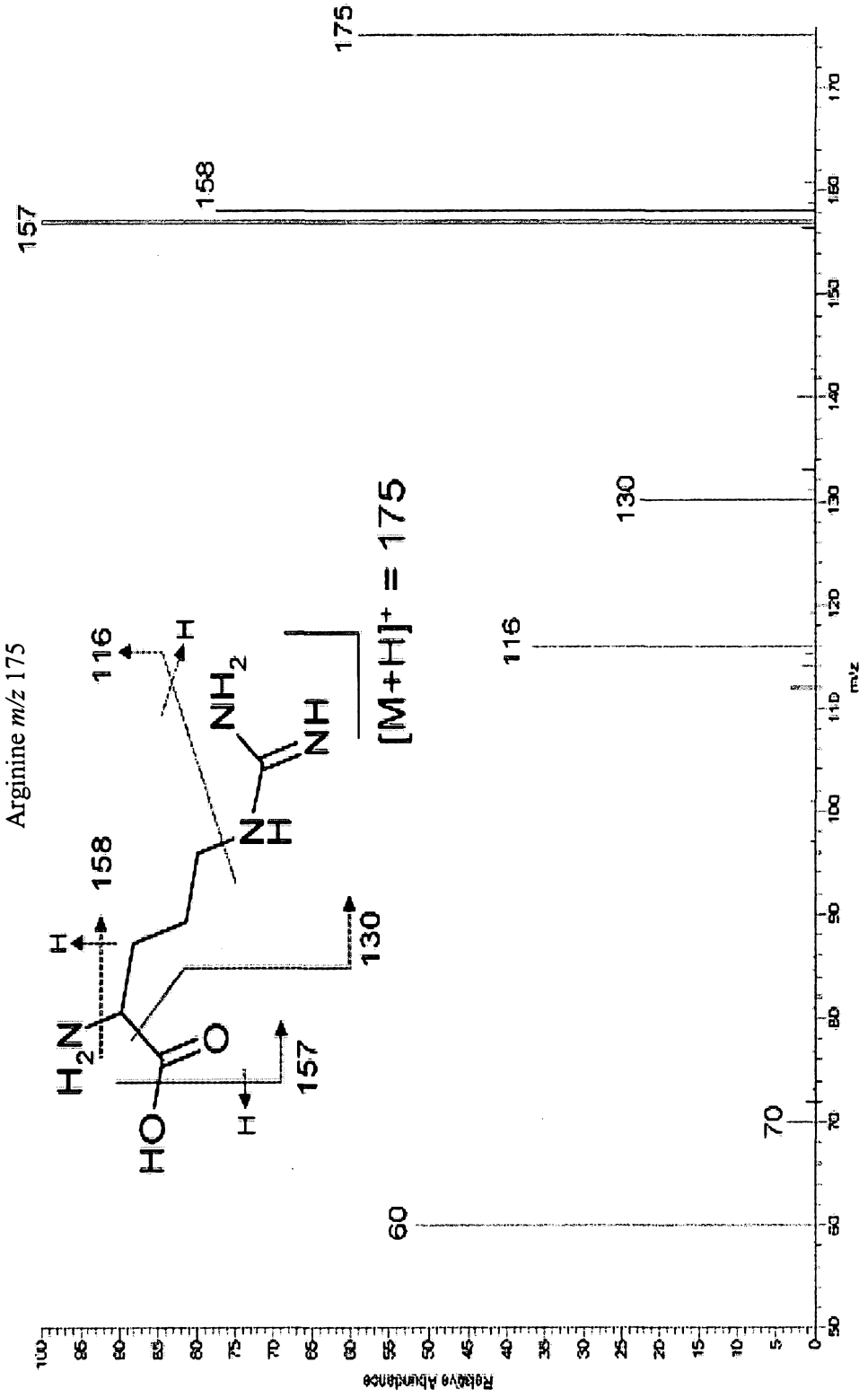

Arginine m/z 175
[M+H]+ = 175
175
158
157
130
116
70
60
m/z
Relative Abundance

FIGURE 5A

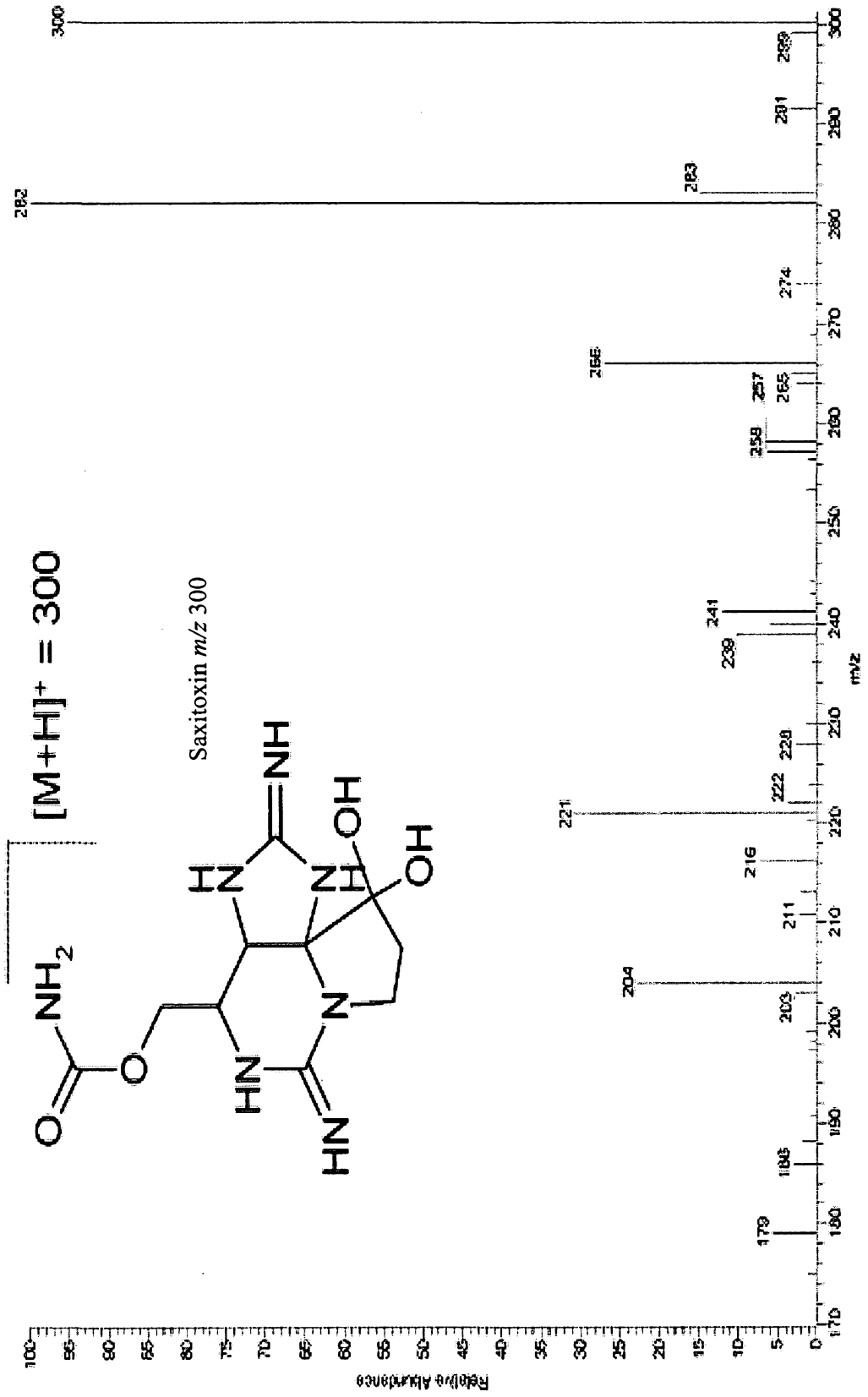

[M+H]+ = 300
Saxitoxin m/z 300
NH2
O
O
HN
NH
HN
NH
OH
OH
N
m/z
Relative Abundance

FIGURE 5B

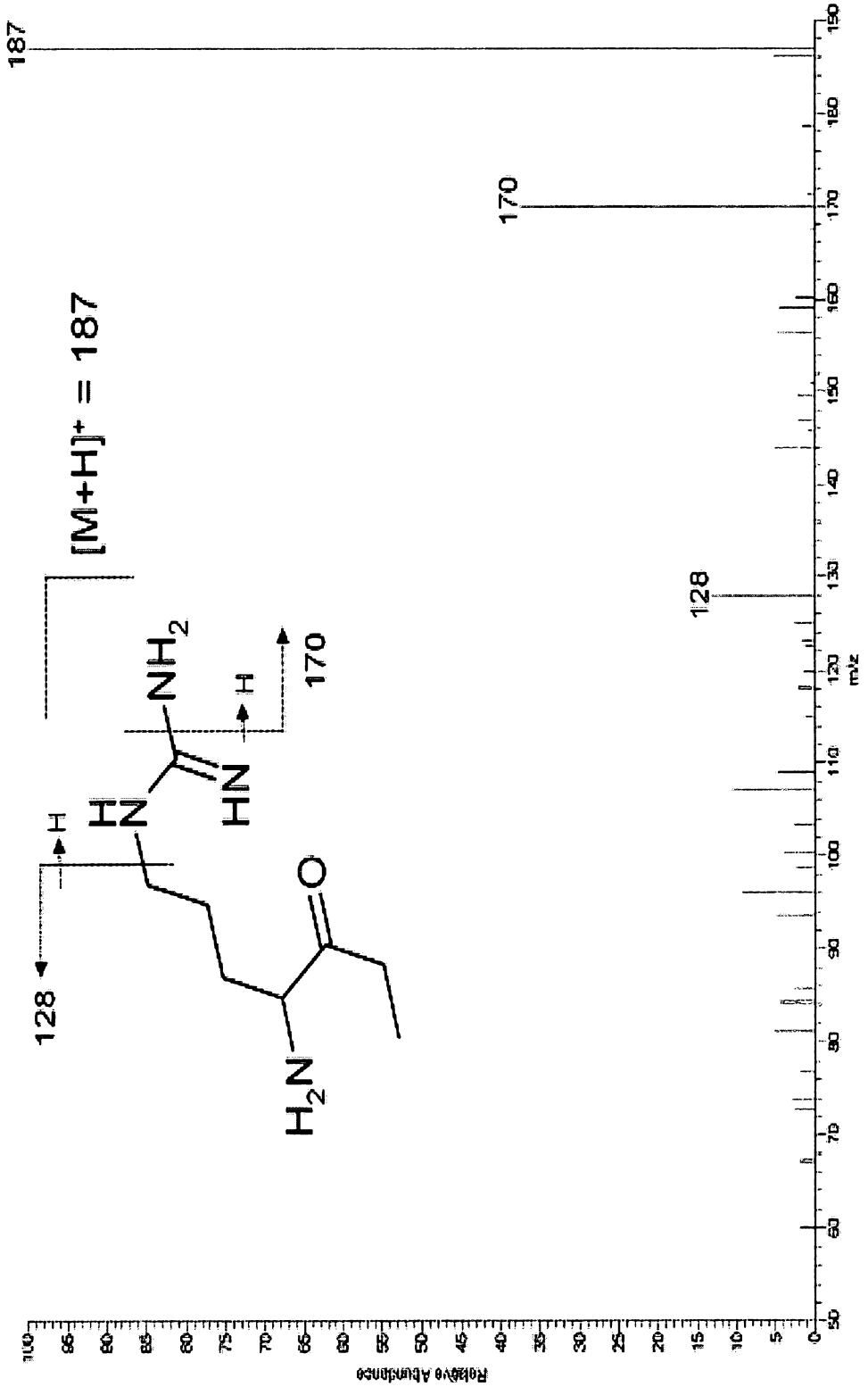

187
170
128
[M+H]+ = 187
NH2
H
170
HN
HN
H
128
O
H2N
m/z
Relative Abundance

FIGURE 5C

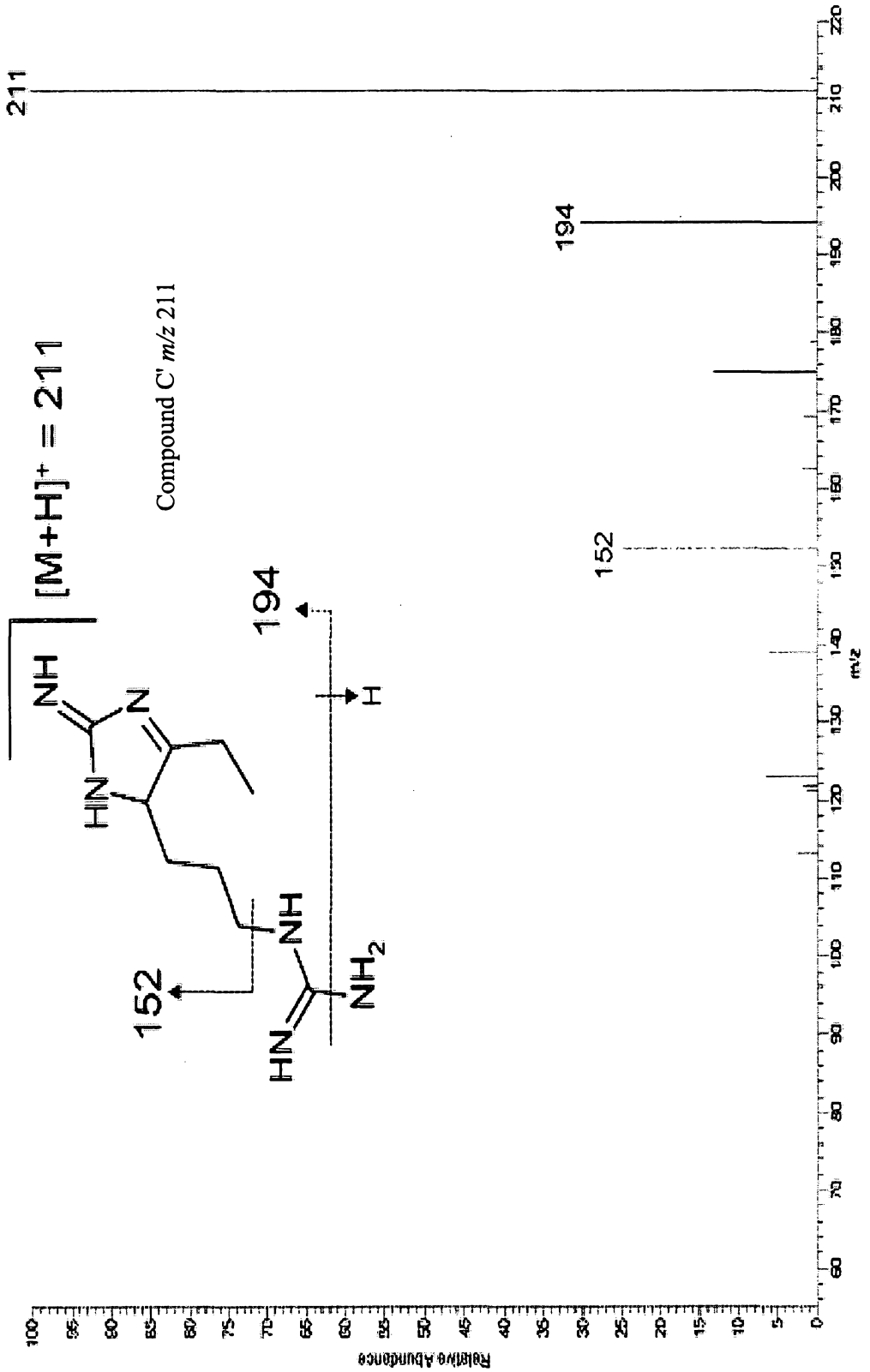

211
194
152
[M+H]+ = 211
Compound C' m/z 211
194
H
152
NH
NH2
HN
Relative Abundance
m/z

FIGURE 5D

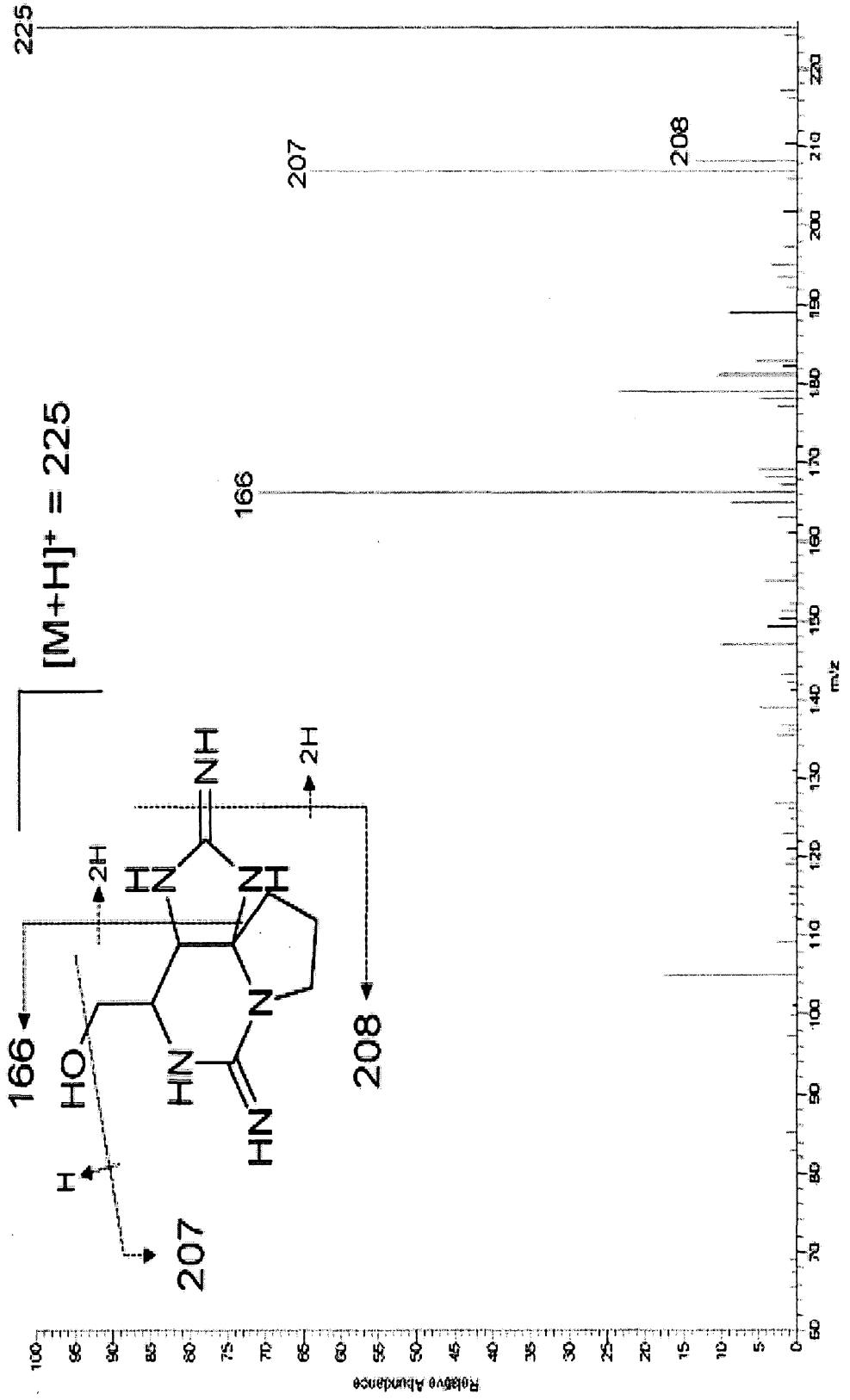

225
207
208
166
[M+H]+ = 225
2H
2H
166
208
207
HO
H
NH
HN
HN
N
Relative Abundance
m/z

FIGURE 5E

Name	Enzyme Family	Size (bp)	Psi-Blast similarity match	% ID	Putative function
cyrD	PKS CrpB	5631	ABM21570.1 *Nostoc sp.* ATCC 53789	58	PKS KS-AT-DH-KR-ACP
cyrF	PKS CrpB	4074	ABM21570.1 *Nostoc sp.* ATCC 53789	68	PKS KS-AT-ACP
cyrG	cytosine deaminase /Aminohydrolase/ Dihydroorotase	1437	BAF59909.1 *Pelotomaculum thermopropionicum* SI	50	Uracil ring formation
cyrI	Prolyl 4-Hydroxylase	831	ABB06365.1 *Burkholderia* sp. 383	43	Hydroxylation of C7
cyrK	MatE Na+-driven multidrug efflux pump	1398	EAW39051.1 *Lyngbya* sp. PCC 8106	65	Exporter
cyrL	Transposase	750	ABG50981.1 *Trichodesmium erythraeum* IMS101	70	Transposase
cyrH	cytosine deaminase /Aminohydrolase/ Dihydroorotase	1431	BAF59909.1 *Pelotomaculum thermopropionicum* SI	50	Uracil ring formation
cyrJ	branched-chain amino acid aminotransferase	780	*Trichodesmium erythraeum* IMS101	53	sulfotransferase
cyrA	Amidinotransferase AoaA	1176	AAX81898.1 *Cylindrospermopsis raciborskii*	100	amidinotransferase
cyrB	NRPS/PKS AoaB	8754	AAM33468.1 *Aphanizomenon ovalisporum*	97	NRPS/PKS A-domain, pp, KS, AT, DH, Met, KR, ACP
cyrE	PKS	5667	ABA23591.1 *Anabaena variabilis* ATCC 29413	62	PKS KS-AT-DH-KR-ACP
cyrC	PKS AoaC	5005	AAM33470.1 *Aphanizomenon ovalisporum*	97	PKS KS-AT-KR-ACP
cyrM	Partial Transposase	318	ABG50981.1 *Trichodesmium erythraeum* IMS101	70	Transposase
cyrN	Adenylylsulfate kinase (PAPS)	600	CAM76460.1 *Magnetospirillum gryphiswaldense* MSR-1	75	Adenylylsulfate kinase (PAPS)
cyrO	hypothetical protein	1548	EAW46978.1 *Nodularia spumigena* CCY9414	74	Regulator

FIGURE 6

Cyanobacterial Strain	16s rRNA	*cyrJ*	Toxicity	Reference
Cylindrospermopsis raciborskii T3	+	-	SXT	Lagos et al. (1999)
Anabaena circinalis 344B	+	-	N.D.	AWQC
Cylindrospermopsis raciborskii Germ1	+	-	N.D.	Neilan et al. (2003)
Anabaena circinalis 310F	+	-	N.D.	AWQC
Cylindrospermopsis raciborskii 44D	+	-	N.D.	NA
Anabaena circinalis 118C	+	-	SXT	Fergusson et al. (2000)
Anabaena circinalis 323A	+	-	N.D.	AWQC
Anabaena circinalis 323H	+	-	N.D.	AWQC
Cylindrospermopsis raciborskii VOLL2	+	-	N.D.	Neilan et al. (2003)
Cylindrospermopsis raciborskii VOLL1	+	-	N.D.	Neilan et al. (2003)
Cylindrospermopsis raciborskii HUNG1	+	-	N.D.	NA
Cylindrospermopsis raciborskii 023B	+	+	CYLN	Wilson et al. (2000)
Cylindrospermopsis raciborskii 05E	+	+	CYLN	Schembri et al. (2001)
Cylindrospermopsis raciborskii 4799	+	+	CYLN	Neilan et al. (2003)
Cylindrospermopsis raciborskii 24C	+	+	CYLN	Schembri et al. (2001)
Cylindrospermopsis raciborskii AWT 205	+	+	CYLN	Hawkins et al. (1997)
Aphanizomenon ovalisporum AO/QH	+	+	CYLN	NA

FIGURE 7

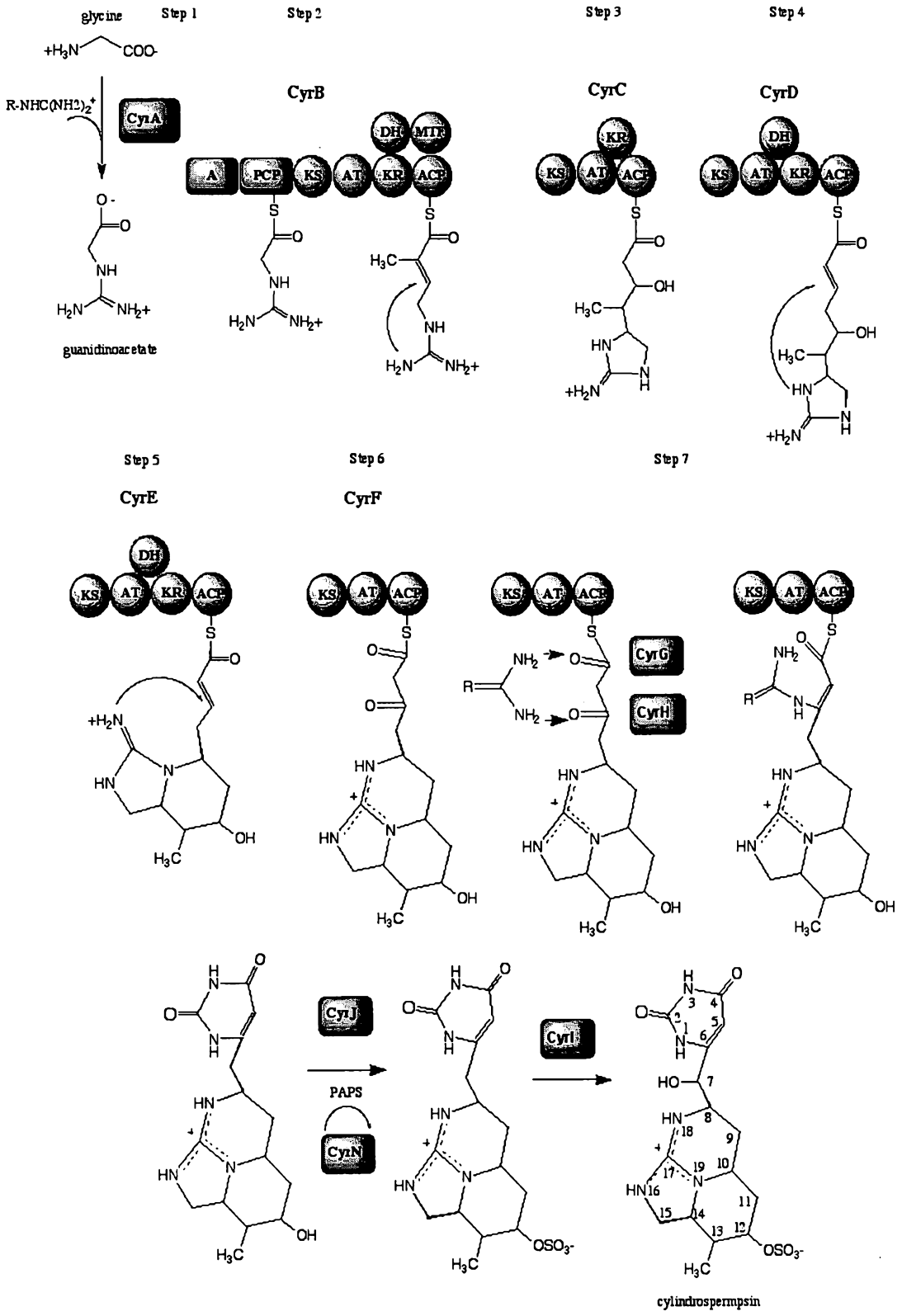

glycine
Step 1
Step 2
Step 3
Step 4
CyrA
CyrB
CyrC
CyrD
guanidinoacetate
Step 5
Step 6
Step 7
CyrE
CyrF
CyrG
CyrH
CyrJ
PAPS
CyrN
CyrI
cylindrospermpsin

FIGURE 8

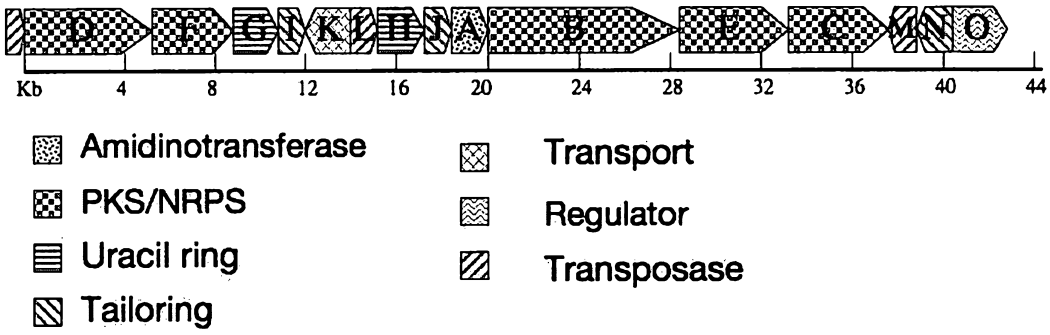

D
F
G
I
K
L
H
J
A
B
E
C
M
N
O
Kb
4
8
12
16
20
24
28
32
36
40
44
Amidinotransferase
PKS/NRPS
Uracil ring
Tailoring
Transport
Regulator
Transposase

FIGURE 9

SEQUENCE LISTING

<110> NewSouth Innovations Pty Ltd.

<120> Detection of Cyantoxic Organisms

<130> 852090

<160> 186

<170> PatentIn version 3.2

<210> 1
<211> 37606
<212> DNA
<213> Cylindrospermopsis raciborskii T3

<400> 1
atgatcccag ctaaaaaagt ttatttttta ttgagtttag caatagttat ttcacccttt 60

ttatccatga ttgtgggtat ttacgaaaat attaaattta gggtattatt tgatttggtg 120

gtcagggcac taatggtggt tgactgcttc aatatcaaaa aacatcgggt caaaattagt 180

cgtcaattac ctctacgttt atctattgga cgtgagaatt tagtaatatt gaaggtagag 240

tctgggaatg tcaatagtgc tattcaaatt cgtgattact atcccacaga atttcccgta 300

tccacatcta acctgatagt taaccttccc cctaatcata ctcaggaagt aaagtacacc 360

attcgaccta atcaacgggg agaattttgg tggggaaata ttcaagttcg acagctggga 420

aattggtctc tagggtggga caattggcaa attccccaaa aaactgtggc taaggtgtat 480

cctgatttgt taggactcag atccctcgct attcgtttaa ccctacaatc ttctggatct 540

atcactaaat tgcgtcaacg gggaatggga acggaatttg ccgaactccg taattactgc 600

atgggggatg atctacggtt aattgattgg aaagctacag ctagacgtgc ttatggaaat 660

ctgagtcccc tagtaagagt tttagagcct caacaggaac aaactctgct tatattatta 720

gatcgtggta gactaatgac agctaatgta caagggttaa aacgatatga ttggggttta 780

aataccacct tgtctttggc attagcagga ttacataggg gcgatcgcgt aggagtaggg 840

gtatttgact cccagctgca tacctggata cctccagagc gaggacaaaa tcatctcaat 900

cggcttatag acagacttac acctattgaa ccagtgttag tggagtctga ttatttaaat 960

gccattacct atgtagtaaa acaacagact cgtagatctc tagtagtgtt aattactgat 1020

ttagtcgatg ttactgcttc ccatgaacta ctagtagcgc tgtgtaaatt agtgcctcga 1080

tatctacctt tttgtgtaac actcagggat cctgggattg ataaaatagc tcataatttt 1140

agtcaagact taacacaggc ttataatcga gcagtttctt tggacttgat atcacaaaga 1200

gaaattgctt ttgctcagtt gaaacaacag ggagttttgg tgttggatgc accagcaaat 1260

caaatttccg agcagttggt agaaaggtac ttacaaatca aagccaaaaa tcagatttga 1320

ctccctgtcg agataattga gaacttctgg aaagaatagc ccaataaact cgacaaagaa 1380

cgtggttaga agttctttaa agagtctatc atgccgaatc atattttaac agaagagcga 1440

tcgctcttcc taagggatag agtctgaaag ccacttcaac ggacgataat gcaactcttg 1500

ttccagctgg agtgcggaga attaccacat ccgaaataga caaaaagaaa taattggagt 1560

taagaagata agtacataaa tagtgataat atacaaaact agtcagcacg gattaaattt 1620

actaatgata gatacaatat cagtactatt aagagagtgg actgtaattt cccttacagg 1680

tttagccttc tggctttggg aaattcgctc tcccttccat caaattgaat acaaagctaa 1740

attcttcaag gaattgggat gggcgggaat atcattcgtc tttagaaatg tttatgcata 1800

tgtttctgtg gcaattataa aactattgag ttctctattt atgggagagt cagcaaattt 1860

tgcaggagta atgtatgtgc ccctctggct gaggatcatc actgcatata tattacagga 1920

cttaactgac tatctattac acaggacaat gcatagtaat cagtttcttt ggttgacgca 1980

caaatggcat cattcaacaa agcaatcatg gtggctgagt ggaaacaaag atagctttac 2040

cggcggactt ttatatactg ttacagcttt gtggtttcca ctgctggaca ttccctcaga 2100

ggttatgtct gtagtggcag tacatcaagt gattcataac aattggatac acctcaatgt 2160

aaagtggaac tcctggttag gaataattga atggatttat gttacgcccc gtattcacac 2220

tttgcatcat cttgatacag ggggaagaaa tttgagttct atgtttactt tcatcgaccg 2280

attatttgga acctatgtgt ttccagaaaa ctttgatata gaaaaatcta aaaatagatt 2340

ggatgatcaa tcagtaacgg tgaagacaat tttgggtttt taatagactt gggttctaag 2400

tggaatggac ggaaaaaatg gcggttaccc gcatctttaa tatatcctct ttttggggtt 2460

gagatttgga taaagcggct tgtactctgt cattattcaa atagccatgg cgttgcatat 2520

ttgcgggatg atttaagatt ttctcctaat ttgaaaaatt tctcttgtag gacgattgcg 2580

aagcactcgc gagattgcat tattaataaa accctgatag tcacccccaa cttattgcag 2640

aaaaactttt ttctcttagg taataaatta gtagtttaat tgaaaagcat agcatctctt 2700

ttgacttgga ataacaaaat gtcttacgat gtagtctagc taaatagtga cgcaaacgac 2760

tgttttctcc ctcaactcta gtcattgatg ttttactaat aatttggtct ccatcgggaa 2820

taaattttgg gtaaacttta tagccatccg taatccaaaa ataggatttc caatgctcta 2880

tctttttcca taatttggca aatgttttgg cacttctatc tcccactaca tattgaataa 2940

ttcccgaacg tttgttatct acaactgtcc agacccatat cttgtttttt tttaccaata 3000

aatgtttcca actcatccag ttgacaaact tcaggtgttt gggaattatt attactatct 3060

gataactgac gacctagctt tttgacccaa cgaatgactg tattgtgatt tactttagtc 3120

attctttcaa ttgccctaaa tccattccca tttacataca tggttaaaca tgcttccttt 3180

acttcttggg aataacctct aggagaataa gattcaataa attgacgacc acaattcttg 3240

cattgataat tttgttttcc ccttctctgg ccatttttc taatattatt ggaatcacag 3300

tttgaacagt tcatcttgat ttcttcctcg cggcgatcgc ctgctaaaaa ttcttcccct 3360

tattatacat catcccgtgc aggtgcaacg cccaaatagc catagtttat gatcggtatc 3420

gaattcgcta ttgtttttc tgccatatcc cttacctaag atgggacgat attcgctcat 3480

aataccactg tcaattagat catcagcaac atggtgagtg tatcctgacg accatcgata 3540

tggccaccaa gatcactagc taccccactg ggcaacaatt cgagtaaaag cgagtagccc 3600

tactgtagca ttgaaaccat ccaagtttga agttaaatac ctaaaattat gacctcattt 3660

tcatttctag acgttcagca acgggcatta actcacgtat cagatcaaag tttcctacgt 3720

tccgtctcat ccagtctaat aagaattttt ctccttcatc tagcttacct ttatcatcaa 3780

caaaaaccat ctgctcgcac caatctacaa atccggaatt agtcatctca tagactaaaa 3840

tgatgggagg aaagtgtgcg aatcccattt tttcaatgac ttccatacaa accagcttaa 3900

atacttgttc gtttgtcaat tcattagaca taaagaattt tcctttaatc aattctgttt 3960

ctaatcctac cacagagtaa taactcttgg tctggaacat aaattattct gtttttatca 4020

atgcgtaagt cataacttat tacttgacgg agttgcaggg gcatacctta acttgacctt 4080

gggagcgata gaagaaagga aggcttcagt gacgggtctt tgactaatcc cagtttccac 4140

ttcaactaaa acagcatcac aaatgtcgaa tagtgattga gaatatctat tcatattcat 4200

gaaagtcaga gcagattcca tcggagacat ggatgaatta aaggcagcgt tttcagcgta 4260

tcgacctgta aatatattcc cgtgggaatc ttttaacgct acccctgcaa aatttttcgt 4320

gtagggagca taactttgat tggcagcgga tagagcagca agcacaacat catcggtaga 4380

ataggtctcc agatcatgaa atactgtttg cattaatcca cctgtgagtc ctagatccgc 4440

tggtccaaat ggctcgggta gaaaatgtgg gagtttattt gaggtataag tttgctcagg 4500

ctgtgattca ttagacttca caagaagaac aaaattttga tttacagttg ccatctcgta 4560

taaaaattgt cggcagtatc cacatggtgc ttcgtggatt gctaatgctt gtaaaccggt 4620

ttctccgtgc aaccacgcat ttatggtggc ggattgttct gcgtgaactg agaaactaag 4680

tgcctgtcct acaaattcca tgtcggcacc aaaataaaga gttccagaac ccagttgatt 4740

cttagattgt ggtttaccaa gagcgatcgc ccctacataa aactgcgata ttggtaccct 4800

agcataagtt gcggctacgg gtagtaattg aatcattaac gtactaatat tagtaccaag 4860

tcgatcaatc caagatgcga caacacttga gtcaattaca gcatgttggg caagaattgt 4920

ccttaactct gattgaatgg aacgtggaac cttggcaatc gcctgttcta atgctacatg 4980

ggtcatttgg gttattcttg gacagagaga taaagatata ttagttttta tgaatcaatt 5040

tcccacttaa tgcttgagta tgttttcctc ctgcttacaa ggcaaagctt tccttttttg 5100

tagcaaatcc caaactgctt tgagagattt aattgcttgg tctatctcct cttcggtatt 5160

ggcggctgta atcgaaaacc ttaaagcact tttatttaaa ggtacgattg gaaaaatagc 5220

aggagtaatt aaaataccat attcccaaag gagttgacac acatcaatca tgtgttgagc 5280

atctcccact aacacgccta cgatgggaac gtaaccatag ttatccactt cgaatccaat 5340

ggctcttgct tgtgtaacca atttgtgagt taggtgataa atttgttttc ttaactgctc 5400

cccctcctga cgattcacct gtaatccggc taaggcactt gccaaactcg caacaggaga 5460

aggaccagaa aatatggcag tccaagcgtt gcggaagttg gttttgatcc ggcgatcgcc 5520

acaagttaag aatgctgcgt aagaagaata ggctttggac aaaccagcta catagatgat 5580

attatcctct gcaaaccgca ggtcaaaata attcaccatc ccgtttcctt tgtaaccgta 5640

aggcatatcg ctgctgggat tttcgcccaa aatgccaaaa ccatgagcat catccatgta 5700

aattaaggca ttgtactctt ttgccagatg cacgtaagct ggcagatcgg gaaaatctgc 5760

cgacatggaa tacacgccat caatgacaat aatctttact tgttcaggcg gatattttgc 5820

tagtttttcg gctaaatcgt tcaaatcatt atgtcgatat tggatgaact gggctccttt 5880

gtgctgagcc agacagcacg cttcataaat acaacgatgt gcagctatgt caccaaagat 5940

gacaccatta ttcccagtta atagtggtaa aattcctatc tgaagcagtg ttacagctgg 6000

aaatactaaa acatcaggta cgcctaaaag tttggacaat tcttcctcca attcctcata 6060

aattgctggg gaagcaacaa gccgagtcca gcttggatgt gtgccccatt tatccaaagc 6120

tggtggaatt gcttccttaa cttttggatg caagtcaaga cctaaatagt tgcaagaagc 6180

aaagtctatc acccaatgtc cgtcaattag caccttgcga ccttgttgtt ctgtgacgac 6240

tcttgtgact tgaggaattt tttgttggtt aactacgttt tccagagtgt tgatttcgtt 6300

ggctgagtca acaggtggag ctagatcaga ttgtttctct tgtaccactt ggttttggaa 6360

ataagtgatg atggcagttg gagtgttctt ttgtaaaaag aacgttccag acagattgat 6420

ccctaaacgt tcctctagga gcgtttgcag ttctaataaa tctaaagaat ctaatcccat 6480

atccagcagt ttttgttgtg gagcgtaggc tgcctgacgt tgggaaccca ttacttttaa 6540

gatgcattct ttaacgagat ccgctacagt tttgttttcc ttagttgcag atgttgcttt 6600

tggtaccaat gaaccaattg ctgagttaat atacggtcct ttgcgatcac caggcgagtg 6660

caaagcactg tcgcgcaggt tatattcaat caaaataccc atgccgagat tatctgtatc 6720

ttccggacga taattagcaa taattcccct aatttcggct cctcccgaca catggaaacc 6780

cacaattgga tccagaagct gtcgttgctc attgtgtagc tttaaatact ccatcatcgg 6840

catttgggaa taattgacat aatttcgaca gcgagttaca cccaccacgc tctcaatgcc 6900

gcctttcagg gtacagtagt aaagcataaa gtcccgcaat tcatttccta acccccgcgc 6960

ctgaaactca ggtagaatat ttagtgcgag cagttgaata actgaccctt ggggagtatg 7020

taacgtcggc acttgcgcat attttacatt ctctaatgcc tcagtgctgg taattgtttg 7080

ggaataaatc gcaccaataa tttgatcttc tataatcagc actaaattac cttgcgggtt 7140

tagctcaagt cttcgccgaa tttcatgagt agatgcccgt aaattttctg gccaacactt 7200

gacctccaag tcaactaagg caggtaaatc tgacaaatag gcatgactaa ttttgtaagg 7260

tcttttctcg aagtaattaa gcgtaatgcg agtaaaagga aatgtttttg ggtatctttt 7320

agaaagctct agttttggaa atagacctac ttgtgcagca gacatgagaa aaacctcagc 7380

ttccacaaga tactgctgag aaaatccctg aaacgcatcg aaatgtaagt tttcgctttt 7440

gtctaaaaac tgatagacta cccttggttc caaacaatgg acctccaaaa tcattaaacc 7500

gtgtttattg accacttgag accatctttc taagtgttcc accaaacttt gcaccataac 7560

atgaggagga ataagctctc cttgatcatc gacacagact gattggtaag gtaagtgagc 7620

acgttctttc aattcgtttc ttttctgagg aggaataaag agacgatcat ggtcgaggaa 7680

cgaacggatg tgcaggatat tttcgggatc atgaatgcca tgagcttcta aagaacgcac 7740

catttgttct gggttcccaa tatctccctg taaaactaag tggggaaggc tagcaagggt 7800

gcgtgtggta gcttttaaag aagcttcgtt ataatctaca cctataagac gcaggggata 7860

ctgttcgagt gcttttcccc tagcagactt aaattgaatg gtttcccaga ctcgtttcag 7920

gagagttcca tcgccacacc ccatgtcagt aatgtatttg ggttgttctt ctaatggcaa 7980

ctgattgaat actgagagga tactttcttc taaatcggca aaatatttct ggtgttgaaa 8040

tccactcccg atcacgttaa gggtgcgatc aatgtgcctt tcgtgaccgg aagcatctct 8100

ttggaatacg gagagacaat tgccaaacaa tacatcatga atgcgggaca acataggagt 8160

gtaggacgcc actatggctg tattcaaggc tcgctctccc ataaatcgac caagttcggt 8220

tatggtcaaa cgacctgctg taaggtcagc ccagccaagg tggagaaata acttacccaa 8280

ctcttcttgc actgttgagc ttaatgagga gagcaaaggt ttgtcctccg aatctgcaag 8340

caagttgtgt ttgtgcagtg ccagcaggag tgggatgacc agtaatccat ctaaaaaatc 8400

tgccattagg ggattgtcca ggttccacaa ttggcaagaa cgctcaatcc atcttcccag 8460

caaatttcct tgtttccctt ctaaataaga ctgaattggt aggttgtaca attgaagaat 8520

gtcttccgaa attttgttgt gaatcgctgc ttctgcggtt agagagtatt taagctcctt 8580

atttcgggaa agccaatgta aagactcgag catcctcaaa gcaacttgaa aatgtccgct 8640

gttagctccc agatgttcca ccatttggtt taaagagaga ggactttcat cggcgagtaa 8700

ttcaaaaaca ccttttctc gacacgcaag aataacggga accgccacaa agccgtgagt 8760

ataacgatta atcttttgta acatttagac gattattgat taatttatga ggaatgcatt 8820

tttagtgcat accacgagat tttgattgtc tcagaagttg tgtgaaaaag caagacaagt 8880

agaccaaaaa aataagctaa ataagtgtag tagcaataaa aagacgaatc gcaattgtac 8940

gtgtcttgac taacaagcca agtctctcta gataataatc gccctctacc agttgcgtaa 9000

gtcccattgt tgttttaaac tttaattgct aattaaacag ttatcaaatc ctgttcataa 9060

cggatattta cagcaatttt cggttatata aaattgcata tactgtaagt aatagcagaa 9120

aattaattta ggtaggaaaa tgttgaaaga tttcaaccag tttttaatca gaacactagc 9180

attcgtattc gcatttggta ttttcttaac cactggagtt ggcattgcta aagctgacta 9240

cctagttaaa ggtggaaaga ttaccaatgt tcaaaatact tcttctaacg gtgataatta 9300

tgccgttagt atcagcggtg ggtttggtcc ttgcgcagat agagtgatta tcctaccaac 9360

ttcaggagtg ataaatcgag acattcatat gcgtggctat gaagccgcat taactgcact 9420

atccaatggc tttttagtag atatttacga ctatactggc tcttcttgca gcaatggtgg 9480

ccaactaact attaccaacc aattaggtaa gctaatcagc aattaggttg tatcatgata 9540

agatgaagta gtttaaccat ggcaccacca gccaaaaact ttttaacgct agggtgtaac 9600

agttatgggt gtggaatgta ggttgtatcc agtgcatgaa acagccataa ttttagtata 9660

agcaaacact aagattggag aattcatgga aacaacctca aaaaaattta agtcagatct 9720

gatattagaa gcacgagcaa gcctaaagtt gggaatcccc ttagtcattt cacaaatgtg 9780

cgaaacgggt atttatacag cgaatgcagt catgatgggt ttacttggta cgcaagtttt 9840

ggccgccggt gctttgggcg cgctcgcttt tttgacctta ttatttgcct gccatggtat 9900

tctctcagta ggaggatcac tagcagccga agcttttggg gcaaataaaa tagatgaagt 9960

tagtcgtatt gcttccgggc aaatatggct agcagttacc ttgtctttac ctgcaatgct 10020

tctgctttgg catggcgata ctatcttgct gctattcggt caagaggaaa gcaatgtgtt 10080

attgacaaaa acgtatttac actcaatttt atggggcttt cccgctgcgc ttagtatttt 10140

gacattaaga ggcattgcct ctgctctcaa cgttccccga ttgataacta ttactatgct 10200

cactcagctg atattgaata ccgccgccga ttatgtgtta atattcggta aatttggtct 10260

tcctcaactt ggtttggctg gaataggctg ggcaactgct ctgggttttt gggttagttt 10320

tacattgggg cttatcttgc tgattttctc cctgaaagtt agagattata aacttttccg 10380

ctacttgcat cagtttgata aacagatctt tgtcaaaatt tttcaaactg gatggcccat 10440

ggggtttcaa tgggggggcgg aaacggcact atttaacgtc accgcttggg tagcagggta 10500

tttaggaacg gtaacattag cagcccatga tattggcttc caaacggcag aactggcgat 10560

ggttatacca ctcggagtcg gcaatgtcgc tatgacaaga gtaggtcaga gtataggaga 10620

aaaaaaccct ttgggtgcaa gaagggtagc atcgattgga attacaatag ttggcattta 10680

tgccagtatt gtagcacttg ttttctggtt gtttccatat caaattgccg gaatttattt 10740

aaatataaac aatcccgaga atatcgaagc aattaagaaa gcaactactt ttatcccctt 10800

ggcgggacta ttccaaatgt tttacagtat tcaaataatt attgttgggg ctttggtcgg 10860

tctgcgggat acatttgttc cagtatcaat gaacttaatt gtctggggtc ttggattggc 10920

aggaagctat ttcatggcaa tcattttagg atgggggggg atcgggattt ggttggctat 10980

ggttttgagt ccactcctct cggcagttat tttaactgtt cgtttttatc gagtgattga 11040

caatcttctt gccaacagtg atgatatgtt acagaatgcg tctgttacta ctctaggctg 11100

agaaaagcta tatgaccaat caaaataacc aagaattaga gaacgattta ccaatcgcca 11160

agcagccttg tccggtcaat tcttataatg agtgggacac acttgaggag gtcattgttg 11220

gtagtgttga aggtgcaatg ttaccggccc tagaaccaat caacaaatgg acattccctt 11280

ttgaagaatt ggaatctgcc caaaagatac tctctgagag gggaggagtt ccttatccac 11340

cagagatgat tacattagca cacaaagaac taaatgaatt tattcacatt cttgaagcag 11400

aaggggtcaa agttcgtcga gttaaacctg tagatttctc tgtccccttc tccacaccag 11460

cttggcaagt aggaagtggt ttttgtgccg ccaatcctcg cgatgttttt ttggtgattg 11520

ggaatgagat tattgaagca ccaatggcag atcgcaaccg ctattttgaa acttgggcgt 11580

atcgagagat gctcaaggaa tattttcagg caggagctaa gtggactgca gcgccgaagc 11640

cacaattatt cgacgcacag tatgacttca atttccagtt tcctcaactg ggggagccgc 11700

cgcgtttcgt cgttacagag tttgaaccga cttttgatgc ggcagatttt gtgcgctgtg 11760

gacgagatat ttttggtcaa aaaagtcatg tgactaatgg tttgggcata gaatggttac 11820

aacgtcactt ggaagacgaa taccgtattc atattattga atcgcattgt ccggaagcac 11880

tgcacatcga taccacctta atgcctcttg cacctggcaa aatactagta aatccagaat 11940

ttgtagatgt taataaattg ccaaaaatcc tgaaaagctg ggacattttg gttgcacctt 12000

accccaacca tatacctcaa aaccagctga gactggtcag tgaatgggca ggtttgaatg 12060

tactgatgtt agatgaagag cgagtcattg tagaaaaaaa ccaggagcag atgattaaag 12120

cactgaaaga ttggggattt aagcctattg tttgccattt tgaaagctac tatccatttt 12180

taggatcatt tcactgtgca acattagacg ttcgccgacg cggaactctt cagtcctatt 12240

tttaagattt atttcgatta tcctttatcc tgatcatcca gagtgataag agcattacaa 12300

ctaggagaca attatgacaa ctgctgacct aatcttaatt aacaactggt acgtagtcgc 12360

aaaggtggaa gattgtaaac caggaagtat caccacggct cttttattgg gagttaagtt 12420

ggtactatgg cgcagtcgtg aacagaattc ccccatacag atatggcaag actactgccc 12480

tcaccgaggt gtggctctgt ctatgggaga aattgttaat aatactttgg tttgtccgta 12540

tcacggatgg agatataatc aagcaggtaa atgcgtacat atcccggctc accctgacat 12600

gacaccccca gcaagtgccc aagccaagat ctatcattgc caggagcgat acggattagt 12660

atgggtgtgc ttaggtgatc ctgtcaatga tataccttca ttacccgaat gggacgatcc 12720

gaattatcat aatacttgta ctaaatctta ttttattcaa gctagtgcgt ttcgtgtaat 12780

ggataatttc atagatgtat ctcattttcc ttttgtccac gacggtgggt taggtgatcg 12840

caaccacgca caaattgaag aatttgaggt aaaagtagac aaagatggca ttagcatagg 12900

taaccttaaa ctccagatgc caaggtttaa cagcagtaac gaagatgact catggactct 12960

ttaccaaagg attagtcatc ccttgtgtca atactatatt actgaatcct ctgaaattcg 13020

gactgcggat ttgatgctgg taacaccgat tgatgaagac aacagcttag tgcgaatgtt 13080

agtaacgtgg aaccgctccg aaatattaga gtcaacggta ctagaggaat ttgacgaaac 13140

aatagaacaa gatattccga ttatacactc tcaacagcca gcgcgtttac cactgttacc 13200

ttcaaagcag ataaacatgc aatggttgtc acaggaaata catgtaccgt cagatcgatg 13260

cacagttgcc tatcgtcgat ggctaaagga actgggcgtt acctatggtg tttgttaatt 13320

tcagggttgt tggtatctgg ataggtatgg ttttgagtcc actgctatct ggagggattt 13380

taatggttgg tttttatcaa cagcttgcca ataagtatta ctaatagtga tgatggggaa 13440

gagaatcaaa ctatactcac caacaaggtg ttaaaatgca gatcttagga atttcagctt 13500

actaccacga tagtgctgcc gcgatggtta tcgatggcga aattgttgct gcagctcagg 13560

aagaacgttt ctcaagacga aagcacgatg ctgggtttcc gactggagcg attacttact 13620

gtctaaaaca agtaggaacc aagttacaat atatcgatca aattgttttt tacgacaagc 13680

cattagtcaa atttgagcgg ttgctagaaa catatttagc atatgcccca aagggatttg 13740

gctcgtttat tactgctatg cccgtttggc tcaaagaaaa gctttaccta aaaacacttt 13800

taaaaaaaga attggcgctt ttgggggagt gcaaagcttc tcaattgcct cctctactgt 13860

ttacctcaca tcaccaagcc catgcggccg ctgcttttt tcccagtcct tttcagcgtg 13920

ctgccgttct gtgcttagat ggtgtaggag agtgggcaac tacttctgtc tggttgggag 13980

aaggaaataa actcacacca caatgggaaa ttgattttcc ccattccctc ggtttgcttt 14040

actcagcgtt tacctactac actgggttca aagttaactc aggtgagtac aaactcatgg 14100

gtttagcacc ctacggggaa cccaaatatg tggaccaaat tctcaagcat ttgttggatc 14160

tcaaagaaga tggtactttt aggttgaata tggactactt caactacacg gtggggctaa 14220

ccatgaccaa tcataagttc catagtatgt ttggaggacc accacgccag gcggaaggaa 14280

aaatctccca aagagacatg gatctggcaa gttcgatcca aaaggtgact gaagaagtca 14340

tactgcgtct ggctagaact atcaaaaaag aactgggtgt agagtatcta tgtttagcag 14400

gtggtgtcgg tctcaattgc gtggctaacg gacgaattct ccgagaaagt gatttcaaag 14460

atatttggat tcaacccgca gcaggagatg ccggtagtgc agtgggagca gctttagcga 14520

tttggcatga ataccataag aaacctcgca cttcaacagc aggcgatcgc atgaaaggtt 14580

cttatctggg acctagcttt agcgaggcgg agattctcca gtttcttaat tctgttaaca 14640

taccctacca tcgatgcgtt gataacgaac ttatggctcg tcttgcagaa attttagacc 14700

agggaaatgt tgtaggctgg ttttctggac gaatggagtt tggtccgcgt gctttgggtg 14760

gccgttcgat tattggcgat tcacgcagtc caaaaatgca atcggtcatg aacctgaaaa 14820

ttaaatatcg tgagtccttc cgtccatttg ctccttcagt cttggctgaa cgagtctccg 14880

actacttcga tcttgatcgt cctagtcctt atatgctttt ggtagcacaa gtcaaagaga 14940

atctgcacat tcctatgaca caagagcaac acgagctatt tgggatcgag aagctgaatg 15000

ttcctcgttc ccaaattccc gcagtcactc acgttgatta ctcagctcgt attcagacag 15060

ttcacaaaga aacgaatcct cgttactacg agttaattcg tcattttgag gcacgaactg 15120

gttgtgctgt cttggtcaat acttcgttta atgtccgcgg cgaaccaatt gtttgtactc 15180

ccgaagacgc ttatcgatgc tttatgagaa ctgaaatgga ctatttggtt atggagaatt 15240

tcttgttggt caaatctgaa cagccacggg gaaatagtga tgagtcatgg caaaaagaat 15300

tcgagttaga ttaacttatg agtgaatttt tcccacaaaa aagtggtaaa ttaaagatgg 15360

aacagataaa agaacttgac aaaaaaggat tgcgtgagtt tggactgatt ggcggttcta 15420

tagtggcggt tttattcggc tttttactgc cagttatacg ccatcattcc ttatcagtta 15480

tcccttgggt tgttgctgga tttctctgga tttgggcaat aatcgcacct acgactttaa 15540

gttttattta ccaaatatgg atgaggattg gacttgtttt aggatggata caaacacgaa 15600

ttattttggg agttttattt tatataatga tcacaccaat aggattcata agacggctgt 15660

tgaatcaaga tccaatgacg cgaatcttcg agccagagtt gccaacttat cgccaattga 15720

gtaagtcaag aactacacaa agtatggaga aaccattcta atgctaaaag acacttggga 15780

ttttattaaa gacattgccg gatttattaa agaacaaaaa aactatttgt tgattcccct 15840

aattatcacc ctggtatcct tgggggcgct gattgtcttt gctcaatctt ctgcgatcgc 15900

acctttcatt tacactcttt tttaaattgc catattatga gtaacttcaa gggttcggta 15960

aagatagcat tgatgggaat attgattttt tgtgggctaa tctttggcgt agcatttgtt 16020

gaaattgggt tacgtattgc cgggatcgaa cacatagcat tccatagcat tgatgaacac 16080

agggggtggg tagggcgacc tcatgtttcc gggtggtata gaaccgaagg tgaagctcac 16140

atccaaatga atagtgatgg ctttcgagat cgagaacaca tcaaggtcaa accagaaaat 16200

accttcagga tagcgctgtt gggagattcc tttgtagagt ccatgcaagt accgttggag 16260

caaaatttgg cagcagttat agaaggagaa atcagtagtt gtatagcttt agctggacga 16320

aaggcggaag tgattaattt tggagtgact ggttatggaa cagaccaaga actaattact 16380

ctacgggaga aagtttggga ctattcacct gatatagtag tgctagattt ttatactggc 16440

aacgacattg ttgataactc ccgtgcgctg agtcagaaat tctatcctaa tgaactaggt 16500

tcactaaagc cgtttttat acttagagat ggtaatctgg tggttgatgc ttcgtttatc 16560

aatacggata attatcgctc aaagctgaca tggtggggca aaacttatat gaaaataaaa 16620

gaccactcac ggattttaca ggttttaaac atggtacggg atgctcttaa caactctagt 16680

agagggtttt cttctcaagc tatagaggaa ccgttattta gtgatggaaa acaggataca 16740

aaattgagcg ggtttttga tatctacaaa ccacctactg accctgaatg gcaacaggca 16800

tggcaagtca cagagaaact gattagctca atgcaacacg aggtgactgc gaagaaagca 16860

gatttttag ttgttacttt tggcggtccc tttcaacgag aacctttagt gcgtcaaaaa 16920

gaaatgcaag aattgggtct gactgattgg ttttacccag agaagcgaat tacacgtttg 16980

ggtgaggatg aggggttcag tgtactcaat ctcagcccaa atttgcaggt ttattctgag 17040

cagaacaatg cttgcctata tgggtttgat gatactcaag gctgtgtagg gcattggaat 17100

gctttaggac atcaggtagc aggaaaaatg attgcatcga agatttgtca acagcagatg 17160

agagaaagta tattgcctca taagcacgac ccttcaagcc aaagctcacc tattacccaa 17220

tcagtgatcc aataaagaac tgggcatcac ttatgatgtt tactaatttc agttccgttg 17280

atgttaatgc gtaacttta ttactagttg taaagctgag atatgacaaa taccgaaaga 17340

ggattagcag aaataacatc aacaggatat aagtcagagc ttagatcgga ggcacgagtt 17400

agcctccaac tggcaattcc cttagtcctt gtcgaaatat gcggaacgag tattaatgtg 17460

gtggatgtag tcatgatggg cttacttggt actcaagttt tggctgctgg tgccttgggt 17520

gcgatcgctt ttttatctgt atcgaatact tgttataata tgcttttgtc gggggtagca 17580

aaggcatctg aggcttttgg ggcaaacaaa atagatcagg ttagtcgtat tgcttctggg 17640

caaatatggc tggcactcac cttgtctttg cctgcaatgc ttttgctttg gtatatggat 17700

actatattgg tgctatttgg tcaagttgaa agcaacacat taattgcaaa aacgtattta 17760

cactcaattg tgtggggatt tccggcggca gttggtattt tgatattaag aggcattgcc 17820

tctgctgtga acgtccccca attggtaact gtgacgatgc tagtagggct ggtcttgaat 17880

gccccggcca attatgtatt aatgttcggt aaatttggtc ttcctgaact tggtttagct 17940

ggaataggct gggcaagtac tttggttttt tggattagtt ttctagtggg ggttgtcttg 18000

ctgattttct ccccaaaagt tagagattat aaacttttcc gctacttgca tcagtttgat 18060

cgacagacgg ttgtggaaat ttttcaaact ggatggccta tgggttttct actgggagtg 18120

gaatcagtag tattgagcct caccgcttgg ttaacaggct atttgggaac agtaacatta 18180

gcagctcatg agatcgcgat ccaaacagca gaactggcga tagtgatacc actcggaatc 18240

gggaatgttg ccgtcacgag agtaggtcag actataggag aaaaaaaccc tttgggtgct 18300

agaagggcag cattgattgg gattatgatt ggtggcattt atgccagtct tgtggcagtc 18360

attttctggt tgtttccata tcagattgcg ggactttatt taaaaataaa cgatccagag 18420

agtatggaag cagttaagac agcaactaat tttctcttct tggcgggatt attccaattt 18480

tttcatagcg ttcaaataat tgttgttggg gttttaatag ggttgcagga tacgtttatc 18540

ccattgttaa tgaatttggt aggctggggt cttggcttgg cagtaagcta ttacatggga 18600

atcattttat gttggggagg tatgggtatc tggttaggtc tggttttgag tccactcctg 18660

tccggactta ttttaatggt tcgtttttat caagagattg ccaataggat tgccaatagt 18720

gatgatgggc aagagagtat atctattgac aacgttgaag aactctcctg acgaacagat 18780

tgaattgcct tggtcttgac acttcgttaa cctaagcatg agagtatagg ctatactctg 18840

ccgtggttaa ctgagtgttg tcctggatcg aggacgcagc ctggctgagc aacaaaaaag 18900

actggaatct tgacctgtca atggttttaa ctgctagttt gcggctggtg tcagcagctt 18960

cgccatttct gcgcctaaga cttgacctag ccataatatt ttagtattat gatgagcgat 19020

cttaatcaaa ggcaaaaaat ttacaattaa tctattgtta cattaatttt gctcctcatt 19080

ctgtttaaat tttcagtgac attgtaatct aactcaaaat gaaaacaaac aaacatatag 19140

ctatgtgggc ttgtcctaga agtcgttcta ctgtaattac ccgtgctttt gagaacttag 19200

atgggtgtgt tgtttatgat gagcctctag aggctccgaa tgtcttgatg acaacttaca 19260

cgatgagtaa cagtcgtacg ttagcagaag aagacttaaa gcaattaata ctgcaaaata 19320

atgtagaaac agacctcaag aaagttatag aacaattgac tggagattta ccggacggaa 19380

aattattctc atttcaaaaa atgataacag gtgactatag atctgaattt ggaatagatt 19440

gggcaaaaaa gctaactaac ttctttttaa taaggcatcc ccaagatatt atttttctt 19500

tcgatatagc ggagagaaag acaggtatca cagaaccatt cacacaacaa aatcttggca 19560

tgaaaacact ttatgaagtt ttccaacaaa ttgaagttat tacagggcaa acacctttag 19620

ttattcactc agatgatata attaaaaacc ctccttctgc tttgaaatgg ctgtgtaaaa 19680

acttagggct tgcatttgat gaaaagatgc tgacatggaa agcaaatcta gaagactcca 19740

atttaaagta tacaaaatta tatgctaatt ctgcgtctgg cagttcagaa ccttggtttg 19800

aaactttaag atcgaccaaa acatttctcg cctatgaaaa gaaggagaaa aaattaccag 19860

ctcggttaat acctctacta gatgaatcta ttccttacta tgaaaaactc ttacagcatt 19920

gtcatatttt tgaatggtca gaacactgag tttgatcgta accgttcaga ggggggatag 19980

aagcgcgatt agggagatcc aaaaaataaa atatctagcc gtctaacctc tttattttca 20040

tcgattcttc ttaccgttcc ctattccctc ccttcaccag ttcgtttttg ggtaggtgca 20100

agatctgagc ctcccaccta gggccgatct ggcagtgcgc gatcgccact agcccatgga 20160

aaactagcac tttttgggga acagccaaaa cctttattga gtaagaattt gaaaaagtgc 20220

aagttaagag gcaatgacta aaaatttttt tctactcttt tcaggataga attccagttt 20280

ctagagccgt tgtaaccgta catatcttga tagtacgtat cgatgaggta ctcattttcg 20340

tggagcatta accagctttt taactccgct aatttctgct ctccttttc tattaattct 20400

tgctcatcca aatcatccct gtccaactcc tccctgtcca actcccacat agttttgttg 20460

gtatcttcga caatcaagta gtctccactt tttagaccgt tttcgtgaaa atattcaact 20520

actcccaccg cattagcatg ggcatcttct acgatcaacc agggatgagc aagcccagaa 20580

agcagttccg acgacattat tgcacccata ttgttacaat ccccctctaa aaaatgaacg 20640

cgagagtcag tttttgcttt ctcgtcgagt agggaaagat cgatatcgat acagtagaca 20700

caaccttcta tttggaacag ttctaagtga tcggctagcc aaatcgcgct gccaccgctt 20760

aatgctccta tttcgattat tgttttcggg cgaagctcat acaggagcat tgaataaaga 20820

gctatttcgg tgcacccttt caggaagggt atccctttcc aagtgaacaa atcgcggttt 20880

gccaagagcg ctctccaagc tggcactgga atagcacatt tatcttctct ttcagaaatt 20940

ttggcaaacc gattaggttt gaaaggtgca actttatagg cggcttcttg aacaaatttt 21000

tggaagctca tctaattttc ctcttaggtg ttagaacatt tgtaaaatct tggcgatttt 21060

ttgttttctt tcttgaatat agcaaccgcc aaggcggttt gagcataaac tggatgtagt 21120

ccccgtgttt tacggttgag acttaggtaa agcggctttg tttgtactct cccattattc 21180

aaatagccgt agtttatgat cggtatccaa ttcgctattg ttttttctgc catatcccca 21240

acctaagatg cgacgatatt cacccataat gccactgtca attaaatcat cctcgttgac 21300

tgcaacattg gtatgagatt gcggcgcaac atagagcgca tccgcaggac aatatgcttc 21360

acagatgaaa caagtttgac agtcttcctg tcgggcgatc gcaggcggtt ggttgggaac 21420

tgcatcaaag acattggtag ggcatacttg gacgcaaaca ttacaattaa tacagagttt 21480

atggctgaca agctcgatca tcatactgct cctgctacaa ctttaatact ggggctgtgg 21540

tttaagtggt taatactggt ggtgtagcgc tcgcatcctt cacccaatcc cgtctcaccc 21600

aaagcctttc taagccgccc gtggcttggt aataaagctg atttggatcg gtttcaggat 21660

agtctatgcg aatatgttcg ctacgcgttt ccttgcgatg taaagcgcta aaatatgccc 21720

atcgtgctac agacacaaga gcagccgctc gacgagaaaa ttccagatcg cgcactgtat 21780

cttgtttcgg gttcccttgt acttgctgcc acagcatttc taatttggcg agggaatcca 21840

aaagtccctg ctcacagcgc aagtaattct tctctaatgg gaacatctcg gcttgtacac 21900

cgcggacaac tgcctcgcta tcgaatgttt cggaaccagg gtactgggaa cgtaatccgg 21960

cttgacctgc tggacgcaca acccgttcat ggacatgagc gcccaaactc ttggcaaagg 22020

cggctgcacc ttcccctgcc cattgtcctg tagagattgc ccaagcagca ttaggaccat 22080

caccccaga agctatccca gctaaaaact cccgcgatgc tgcatctccg gcggcataca 22140

gtccaggaac ttttgtacca caactatcat tcacaatccg aattccacct gtaccacgga 22200

ctgtaccttc taaaaccagt gttacaggta ctcgttctgt ataagggtca atgccagctt 22260

ttttataggg tagaaaggcg atgaagtgag acttttcaac caatgcttgg atttcaggtg 22320

tggctcgatc caaacgagca taaacgggac ctttcaggag ggcattgggc aggaacgatg 22380

gatcgcgacg accattgata tagccaccaa gatcgttacc tgcctcatcg gtgtaactag 22440

cccagtaaaa gggagcagcc cttgtcactg tggcattgaa agcggtcgag atggtatagt 22500

gactggaagc ttccatactg gagagttcgc cgccagcttc caccgccatc agcagtccat 22560

cgcctgtatt ggtattgcaa cctaaagctt tacttaggaa tgcacaaccg ccattcgcta 22620

gaactactgc accagcgcga acggtatagg tgcgatgatt ttgcctctgt acacctctag 22680

ctccagccac ggagccgtcc tgggctaata acagttctag agccggactt tggtcgaaaa 22740

tttgcacacc cacacgcaac aggttcttgc gaagtacccg catatattcc ggaccataat 22800

aactctggcg cacggattcc ccattttctt tggggaaacg atagccccaa tcttccacta 22860

agggcaaact cagccaagct ttttcaatta cacgttcaat ccaacgtaag ttagcgaggt 22920

tatttccttt gctgtaacat tcggatacat ctttctccca attctctgga gaaggtgcca 22980

tgacgctatt gccactggca gcagctgcac cgctcgtacc tagaaaacct ttatcaacaa 23040

tgatgacttt gacaccttgg gctccagccg cccatgctgc ccatgcggcg gcaggaccac 23100

caccaattac cagcacgtca gcagttaatt gtagttcagt gccgctatag gctgtaagca 23160

attgcttttc ctccttgttt aaagtcaagt tcatactttt aattatcttc tgcagtcggt 23220

cgaatcaaaa tttcatttac atttacatga tcgggttgtg tcactgcata aattatagct 23280

cttgcaatat cctcactttg taaaggtgtt attgtactaa gttgttcttt actaagctgt 23340

ttcgtgatcg ggtcagaaat taagtcatta aatggcgtat cgactaaacc tggctcaatg 23400

atggtaacgc gaatgttgtc taaagatacc tcctggcgta atgcttctga aagagcattg 23460

acgcctgatt tggcagcact ataaacgacc gcaccggact gcgctatcct gccatcgaca 23520

gaagatatat tgactatatg accggatttt tgggccttca gaagaggcaa aactgcgtgg 23580

atagcatata aaactcccag aacattcaca tcgaatgctc gcctccagtc tgcgggattt 23640

ccagtatcaa ttgcaccaaa cacaccaatt cctgcattat tcaccaaaat atctacatgt 23700

cctagctcaa ccttggtctt ttggactaga tgatttactt gagattcgtc tgtaatatct 23760

gtaacaatag gcaatgcttg accaccactg gcttcaatcc gttttgctag tgcatgcaaa 23820

agctcagcac gtcttgcggc gatcgcaact tttgcccccc ccgcagctaa agcaaatgct 23880

gtagcctctc caatcccaga ggaagctcca gtaataatcg ccacttttcc atccaattta 23940

cctgccatca gtcactcctt agttttcgtt ttgctggtgc aatatgtaat aagtgcgttt 24000

tgtacttgat tttgttcttt ggtgattttt atataggagc gcataaagtg cttagtgatc 24060

actttatttt ttagtgccat tcaacttaaa ttaacaaacc ccataagtaa cacctagttg 24120

ctttagccat cgacgatagg caagtgtgca tctatctgat ggtacgtgga tttcgtgtga 24180

aaacaattgt gtatttatct gctttggagt taacagtggt aaacgtaccg gctgttgtgc 24240

atgtaagatc cgaatatctt gttctattgt ttcgtcatat tcagttagca tctttgactc 24300

taacgtttca tacccgttcc acattatcaa catacgcaat acactatttt cctcatcaat 24360

cggtgtgatc gtcattaaat ccacaatcct catttcaggg gattctgaaa cgcagtattg 24420

acataaagga tgactaagcc tgaaccaatt aacccaagag tcatcttcga tatggctgac 24480

aatccttgat gtctggaatt gatacttacc catagtaagg ccatctttat ctaatttcac 24540

ctcaaattct tccacttttg tataattgcg atcacctaac caaccgtcat ggataaaagg 24600

aaaatgagac acgtctaagg aattatccat cacacgaaac gcactagctt taatcaagta 24660

agacttggta taagtcttgt gataattcgg atcatcccat tcaggaaatg aaggtatatc 24720

attaacagga tcgcccaagc acacccacac taagccatag cgctcctggg agtgatatgt 24780

cctggcttca gcacttgccg gtggtaccat gccagggtga gctgggatct gtatgcattt 24840

accagcctca ttgtatctcc atccgtgata cggacaaact aaagtattat tcgtaatttc 24900

tcccatagac agaggaacac ctcggtgggg gcagtagtca agccatacct gtatgggtga 24960

attttgttca taactgcgcc ataataccaa cttcactccc aacaaacgag atctggtgat 25020

acttccaggt ttacagtctt ctacattggc gactacgtgc cagttattga ttaagattgg 25080

gtcggtagtt gtcataattg tctcctagtt ttgccagcca gcgaggcgta agtcagaatt 25140

taagtttatg cttgtgtttg agcctgcgat cgctaaatta tccttttcaa ggcatccacc 25200

aacagtggtt tgatgttgtt ttttgtaaaa atcagagtta gcatcctgta atcggtaatt 25260

gaagtgttgg cagctgcggt atgccataca gttggtgtat aaaacattgc tgcccctcct 25320

ggaagtgaaa gacatatttc tgcatttagt gaattggcag aagatgaatc taatgagtgt 25380

tcccattggt ggctacttgg tataactcgc attgtaccca tagtattatc tgtatcctgt 25440

aagtatatag ttatgaatac catggcttga ttggctactg gaaccaacaa ccgaagcgcg 25500

tcgtcattta actcgttttt tgacatggat gcaagtgcgt tcaatacttc aactacatat 25560

ccatggtctt gatgccaagc aatgtatcct gtacctgcac gaattatggc tagatcggtg 25620

atcaatagga agatatcaga cccaattaga gcctgtactg gtcccatcac agttggaagc 25680

tctaaaagcc tctgaattat cttttgatac ctaactggat ctgggatagt atgctcagac 25740

caccactcat agtcacccgc caatactccc ccacgttttt gttcggtaat aagttctact 25800

tcatgccgta tttcttcaat taacgctttt ggtacagctt cttcaactgt gaaataacca 25860

tcatttgtgt aagcttgttt ttgttccgct gtgagcatct ctcttattct cttgcaattc 25920

aaaggattta gtggatcgtc tggacataat taaggtcaat actgctgtaa ctatcaatgg 25980

ttagtaggaa ttatcctata gctgttcttt ctctggatag aagaaaggtt gtgagaagct 26040

cgctccgact tcatttcagc caatttttct gcagaccaat actgaaaata tcccaatctt 26100

aataattcat cactagcctc ttgtaactgg ctgaatgact gtactgatgc taaaacatac 26160

ttagggtgag ttatgattac gttattcaca ttctccgcgt catcaccaac atattgtttg 26220

tctggatgcg atcctaaagc taccaaatcg tattctggta atacataatt cgccttggta 26280

atgtaccttt ccaacctctg tgcatctagg ttttgagggt cgcagccaaa aatcaccatt 26340

tcaaagtcat tattccatgt tcttatctgt tccattagaa gctctggcag ttcaggtcca 26400

tgaaaccaac gaacactaac acggttattt aaccaagctg ccttcgcgta aggacagggt 26460

ggaaaatttc ctgttagagg attgggaatg ctgacaacat tgataatcca atcctctatt 26520

tcttggcgaa attgttcgat atttatcata actgttgatt tttcctcctt tgtagtaatt 26580

agtagttaaa ggatttagtg gatattaatc taggtcatag tataaccata tattaggctc 26640

gatgtatatt cccatattgt tgggatagtc aattttgaca ggtactaagc ctttgggaat 26700

aatatagtca ccagtttctg gaaaacgcat cccaactcta tcttcccaac cgtcaatagt 26760

atcattaatt gttgtggatt taaaacagat ccctgcaatt ttagccccat gtttgacatt 26820

aactcgtaac caagggtcaa atataagacc atttttatct cgccaggtaa tataccgctc 26880

tatgggtata agtgggtaaa gatattttag gcttggacgt gcagccatga tcaaagaatt 26940

aagaccgtgg tattgagcaa gttctttcat gtatccaatc agatactgac tcaagttttt 27000

gccttgatac tctggtagga ttgaaatcga tactacacat aacgcattag gcaggcggtt 27060

ctgttctcgg tcttcaagcc acttggctaa agcccagtca caaccttcgt ccggtaactc 27120

atcaaaacgg ctttcataag ttaaagggat acagtttcct tgcgctatca taagctgtgt 27180

ggtagcttct actaacccaa actggaattc tggataaatt tcaaatagag ctaaggaagc 27240

tggatctgcc cagacatcat gtatcaaaaa ttttgggtat gcttgatcaa agacactcat 27300

cgtcctttcc acaaaatcag aagtttcttt tggggttaca aagctatact ctaaattatg 27360

ctgtacaatt tgaatggtca ttggttattg gctaatcctt aaatttatac tggaagtcaa 27420

atgagatctc actatcgtta ttatctggaa gtacttgcac tgtcaattca ttaccgactt 27480

tcccattccc aggcataatt aataagttag ggtgaggtgg aatgccgtcg tactgtcgga 27540

cgcggcgaaa aatgctcgaa ttctcgccac catgtttatt caagaggact tcaactggtg 27600

tgatgacaaa agtcattcct gacccaaggt ggcgcgatcg ccgcttttga tttgctggag 27660

tggaaacact aacaaataag gcacaccctc ctagagaata agaccagtta gcagactgcg 27720

gatcggcaga ccaatggcag ggacaagaca ccgcatcaag gctatgtaac gcattcaaaa 27780

aatcaaatgc ttgacctgca tattcctcta ctgtaagaac tgttggttca ggtgggaaaa 27840

agatgacaag tgtcagaaga tccgcatttt cgtgctgaag caattcgttt tcattaactt 27900

catcaatgta tttgtagata ccctcaagcg tatgctcaac caagatcggg tcagttaaag 27960

atgagactat caggtatcta atcattccct tctgttcccc gatagttccc cagaagcaag 28020

ggaaggcaga atcgctgatt gtttcaacaa atgttgagta gctagtgcgt acccaagcag 28080

gaaggcactc ctctagaaga gaggattcca tctggctttt gttccagatt ggtgtaactc 28140

cgtcaggaca taaattcttg attaccatag ctgagttgaa aagtgagctt atttatacaa 28200

aaacgatgga agtgacacct gatggatggg acttcaaccc cctacacata attattatca 28260

ttactatgtg gcaggtcctt ctatatctta ttttttggaa gtccctgaaa attattcaac 28320

aagatcgaga cgttgttgtt gccagaattt gtgacagcca ggtcaagctt gctgtcgccg 28380

ttgaaatccg caattgctat agattcagga ttagtaccga ctggaaagtt agtagctatg 28440

ccaaaagacc cattaccatt tcctggtaag accgagacgt tattgctact ataatttgta 28500

acagccaggt caagtttact gtcgccattc acatctctaa tcgctacaga gtagggatta 28560

gtaccggctg gaaagttagt ggctgcgcca aaagacccat taccatttcc cagtaagacc 28620

gagacgttat tgctgctagt atttgcaaca gccaggtcaa gcttgctgtc gccatttaca 28680

tccccagttg ctacaaatat gggattagta ccgactggaa agttagtggc tgcgccaaaa 28740

gacccattac catttcccag taagaccgag acgttattgc tgacccaatt tgtaatagca 28800

aggtcgagct tactgtcgct attaaaatcc gcaatcgcta cggaaatcga ataagtatcg 28860

acagggaagc tgctggctgc gccaaaagac ccattaccat ttcccagtaa aaccaagacc 28920

ttattgtcga accaatttgt aaaagcaagg tcaagctcac tatcgttatt cacatctcca 28980

atggctacag aataagggtt agtaccaact gaaaagttag tggctgcgcc aaaagaccca 29040

ttaccatttc ctagtaagac cgagacgtta ttgctactaa aatttgcaac agccaggtca 29100

agcttgctgt cgccatttac atccccagtc actacaaaga cgggattagt accgactgga 29160

aagttagtgg ctgcgccaaa agacccatta ccatttccca gtaagaccga gacgttattg 29220

tcgaaccaat ttgtaacagc caggtcgagc ttactatcgc tattgaaatc cccaactgct 29280

acagagtcag catcaagacc agttgggaag ttaatagcag tagcataact actcctgtgg 29340

gcaaatctca ctcctacgga caaattaacc ggaacactaa attgcccaga aagcttttca 29400

ttcttcagat aatagtcagt tatatttgct aatgcaacag gagttataca taaaaatgta 29460

ctaacagata atatccccgc tataattagt aaagtgagcc ttttcacgag ttgtatagtt 29520

caaatgtatt aacaatgttt gtagccatac accatcgtgt atgaagaaag gtattgatcg 29580

caaaatatct atccttgatc tagcctatca cctaagttaa gccatattga gttctattta 29640

gattttcttt ataaatcagc tataatctat tgtttgaaaa ttgtgaattt gttttccacg 29700

tatttgagta gttgttctag gctttcctcg acggtgagtt cggatgtttc cacccataaa 29760

tctgggctat tgggtggttc ataaggggcg ctgattcccg taaatccatc tatttcccca 29820

ctgcgtgctt ttagataaag acctttcgga tcacgctgct cacaaagttc cagtggagtt 29880

gcaatgtata cttcatgaaa tagatctcca gctagtctac gcacctgttc tcggtcattc 29940

ctgtagggtg agatgaaggc agtgatcact aggcatcctg actccgcaaa gagtttggca 30000

acctcaccca aacgacggat attttctgag cgatcactag cagaaaatcc taaatcggaa 30060

cacagtccat gacgaacact atcaccatct aaaacaaagg tagaccatcc tttctcgaac 30120

aaagtctgct ctaattttaa agccaatgtt gttttaccag ccccggacag tccagtaaac 30180

catagaatcc cgcttttatg accattcttt agataacgat catatggaga tataagatgt 30240

tttgtatagt gaatattagt tgatttcata ttgctggagt ttagactaaa cagaagagcg 30300

atcgctccat gcctgagatt ttagtcagta tttccactcc tgtcaaacca ccaaaaacac 30360

ggggtaacct ggaaaattcc cctggggatc agctgaaaac tgctgtttaa cctgcattat 30420

tcatgaaggc aaaaacagga aaaacaaaac ctaacattta taccccaatt tatggcggaa 30480

ctaacttaat aagtaaaaag taaattaaac ctaattaaaa tccctgattt taaccccaaa 30540

atcaatattt taaacctcaa aacttctctt aatcccccat ttagacacac ctatcctatc 30600

aaggcttaat tttaagaaaa aattatttca aactcgctcg ccaaacgctc cataatcaaa 30660

ttaatttcag acgaaaaagg acagtaatat ggtagctcta ccaacaccct tcttgcggaa 30720

actgtcacct tcgctgctat tttgataatc gtttccctta acctaggaac ctgggcttta 30780

gccagttttg ttccctgtgc tgcttgccga attcccaaca ttaaaatgta agctgcttga 30840

gataaaaata accgaaactg attgacaata aatttctcac agctgagtct atctgatttt 30900

atccccagtt ttaattcctt aattctatgc tctgaagtag ctcctctttg aacataaaat 30960

ttatcgtata aatcctgagc ttctgtttcc aagctagtaa ttataaatct aggattgggt 31020

ccttttcta gccattctgc tttcataatt actcgccgag gttctgacca actccgagct 31080

gcgtaataca catcatcaaa taaacgaact ttttctcctg tgcgacaata ttccagtctg 31140

gctcggtcaa gaaggtaatt aatttttcgt tttaagacat cattattgct gaatccaaaa 31200

acatatccaa ccccgctttt ttcacaaacc tcaatgattt ctggtaacga gaaacccccg 31260

tctcccctca gaacaattct aatttcaggt aaggctcttt tgattcgcaa aaataaccat 31320

tttagaatgc cagctactcc tttaccagag tgagaatttc ccgcccttag ttgtagaact 31380

aatggataac cactggaagc ttcattaatc agaactggaa agtagatatc atgcctatgg 31440

taaccattaa ataagctcag ttgttgatga ccatgagtta gagcatccca cgcatctatg 31500

tccaggacaa tctcttttga ttcccgagga taggattcta ggaatttatc aacaaataac 31560

cgacgaattt gtttgatatc tttttgagtc acctgatttt ctaaacgact catagttggt 31620

tgactagcta ataagttttc tcctactgtg ggaacttgat tacaaactag cttaaaaatt 31680

ggatcttggc gcaatttatt actatcgttg ctatcttcat agccagcaat tatttgataa 31740

attcgttggc taattaattg agaaagagaa tgtttgactt tagtttggtc ccgattatcc 31800

gtcaaacaat ctgccatatc ttgacaaatt tttacctttt cttctacttg tcgtgccaga 31860

ataattccgc catcactact taaactcata tcagaaaaag tcagatctaa agtttttta 31920

tcgaagaaat ttaaagataa tcttgaggaa gatttagtca tatatagtgg ataggtttaa 31980

tttttaaaat cctgatttat tatagctgtt tttattcctt tttttcagtt tataactaaa 32040

gttagttatt atttaatttg gtgacggata ggaattacag agtgttggga tgacaaaatt 32100

gccgtagctg ttgcagtata acccttttcag cgatttttat tctactctga tgaataatcc 32160

aggataggct tgccatcact ttctgggtag acaatgtcag gcgcgattgt ctccccaccc 32220

tgattaacgt tagattttat caccccccagt tgagtttttg gtgcaatttc cctcaccata 32280

tctatacctc ccattcactt tggtattgac tcaatcggtt caatttacta taacatgact 32340

tatgtggggg tgtgtgcata ccctcactta aaattaatgg atttgaatct cctcgcactg 32400

ctgcaacttg aaaaactctg agagtcagtt gagagctaac tctaccagga ggagagtttt 32460

taaaaacccc cttcccgagc gatcgcataa tttatggtat acaagaatag tgggtgaaaa 32520

actaactggc gatcgctctt ttcatttaag agacacccct tagttttttt tgcagtctca 32580

tgaatttaaa cgatatctaa ttattttcaa cctatctttg ccctgtaaca atgtatgcta 32640

ccctttgacc aatattagta gcatgatctg ccattctctc taaacactga attgctaatg 32700

ttaatagtaa aatgggctcc actaccccgg gaacatcttt ctgctgcgcc aaattacgat 32760

ataacttttt gtaagcatca tctactgtat catctaataa tttaatcctt ctaccactaa 32820

tctcgtctaa atccgctaaa gctactaggc tggtagccaa catagattgg gcatgatcgg 32880

acataatggc aacctccccc aaagtaggat gggggggata gggaaatatt ttcattgcta 32940

tttctgccaa atctttggca tagtccccaa tacgttccaa gtctctaact aattgcatga 33000

atgagcttaa acaccgagat tcttggtctg tgggagcttg actgctcata attgtggcac 33060

aatcgacttc tatttgtctg tagaagcgat caatttttt gtctaatctc cgtatttgct 33120

cagctgctgt taaatcccga ttgaatagag cttggtgact cagacggaat gactgctcta 33180

ctaaagcacc catacgcaaa acatctcgtt ccagtctttt aatggcacgt ataggttgag 33240

gtttttcaaa aattgtatat ttcacaacag ctttcatatt tttaatctcg ggtttaatat 33300

atttctagct attatagtct tgattcagaa atatccgcca tcatgttgaa ccacctgggg 33360

aagatgaatt tgtatccaag caccaccggt atcaggatgg ttcatggccc tgattttgcc 33420

accatgagct ataattattt ggcggacaat ggataaccct aaaccactac cagtaatttc 33480

tactgtttca ttctcagagc gggactcgcg gtgtctagct ttgtcccccc gataaaatct 33540

ttgaaagaca tggggtagat ccatgggagc aaatccaacc ccggaatcaa taatgttaat 33600

ttctaaaatc tgatttgata cttggtttaa tattgtatct gcttctggat caaccccatt 33660

aatagacttc tccccacaaa ctggattcat ttcaatgaaa atagtaccgt tcaggttgct 33720

gtatttaata cagttatcta acagattaag aaacacttga taaattctgg acttatcagc 33780

acatatatag acctttttccg ggccggagta agaaatacta agatgctgat tagcggctag 33840

gggctctaaa ttctcccaga ctgaaaaaat tagggagcgg acttctagca tttccaaatt 33900

cagttgtatg gaggaggtta tttccatctg ggtcaggtct aaccaatttt ggactaaatt 33960

aattagtctg tcaacctcct gcatcaagcg gatgacccaa cggtttagag ggggatctaa 34020

gcgagtttgc agggtttctg cgaccagacg aatggaagtc agaggtgttc tcagttcatg 34080

ggccaggtct gaaaaagagc ggtcacgttg ctgatgaatg tctacaaatt gttggtgact 34140

ttctagaaac acacccactt gtccccccgg taggggaaaa ctgttagctg ctaaagacaa 34200

tggctttaat cctaaaatac cctgaccatg atctcgggaa gggtgaaaaa tccactcttg 34260

catttgcggt ttttgccaat cccgggtttg ctcaattaac tgatccagct cataggatct 34320

cactaattcc agtagcaggc gcacttgacc cggttgccat ctttgtaaat acagcatttc 34380

ccgcgcgcac tgattacacc atagtagttg gttttcttca tctacttgta aatatcccaa 34440

aggcgcagca tccagcaact gttcataagc tttgagtgac aagcgtaagt tttgttgctc 34500

atctctaacg gtagatattt tacgatgtaa tccagctaat aggggtaata atatcttttc 34560

agcgtgaggg tttaagggtt gggttaactg ctccaaatga ctgttaagtt gaaattgttg 34620

ccaaagccaa aaaccaaaac cgactgccaa acccagaaga aatcccaata agaacatttg 34680

atcgtaagtg tgctatttga ccggaattaa agggggagga tccaagcacg gtctttacag 34740

gacggctttt tctaattgtt aaattataat tataatcggt agggactgct ttgggaaaat 34800

gcgatcgccc aggtatctgt aaccatttct gtaccacagg ttagactgga tcaggtaact 34860

gatacacttc ttgctgaatt ttatgtccaa tcaaaatgac aactcccaaa atgataactc 34920

ccgtgacaag agccaaaaac ccgaatccag cagatggttt aaaataaaaa gaccacgacc 34980

acctaaagga ataggaaaac caaaaacaga atagcccaca tatagaaatc aaccaaatct 35040

atagccaaaa cccctaactg tgacaatata ttctggatgg ctagggtcta actctaattt 35100

ttccctcagc catcgaatgt gaacatccac cgttttactg tcaccaacaa aatcaggacc 35160

ccaaacctgg tctaataact gttcccgtga ccacaccctg cgagcataac tcataaatag 35220

ttctagtaac cggaattctt tcggtgacaa gctcacctcc ctccctctca ctaacacccg 35280

acattcctga ggatttaaac tgatatcctt atattttaaa gtgggtatca agggcaaatt 35340

agaaaaccgc tgacgacgta acagggcgcg acacctagcc accatttccc gtacgctaaa 35400

aggcttagtt aggtaatcat ccgcccctac ctctaaaccc agcacccggt cagtttcact 35460

acctttcgca ctcagaatta aaatcggtat ggaattaccc tggtgacgta acaaacgaca 35520

aatatctaat ccgttgattt gtggcaacat caagtctagc acaagcaggt cgaaggataa 35580

ctcaccaggt tgggtctcta aattcctgat taattccaca gcacaacgac catccttagc 35640

agtcacaact tcataacctt caccctctaa ggctactaca agcatctctc ggatcagttc 35700

ttcgtcttcc actattaaaa cgcgactaac tggttcaata tccgatttag tgaagtatct 35760

agggtaattc agtagtatac attgataaca aaaatttgta agaatgtact ggtctgggtt 35820

tcccactagt atatgatcct cactcattga tgccacatat tggggaacac ggaattcttg 35880

tattcaatac aacaatttgc ttaaatttat aattcaaata ggtgttttat agaaaatttt 35940

gtcgaatatt tccacatttg tggcttttag ttcaggcaaa acgagagaag tctaaagtgg 36000

gtggaatatc ctgaattctt ccaggaccta tagcccgtag tgcttctggt aaactaatat 36060

ccccagtata tagggcttta cccacaatta ctcctgtaac cccctgatgt tctaaagata 36120

ataaggttaa taggtcagta acagaaccca cacccccaga ggcaatcacg ggtatggaaa 36180

tagcagatac caagtctctt aatgctcgca agtttggtcc ctgaagcgta ccatcacggt 36240

ttatatccgt ataaataata gctgccgcac ccaattcctg catttgggtt gctagttggg 36300

gggccaaaat ttgagaagtt tctaaccaac ccctggtagc aactagacca ttccgcgcat 36360

caatcccaat tataatttgc tgggggaatt gttcacacag tccttgaacc agatctggtt 36420

gctctactgc tacagttccc agaattgccc actgtacccc aagattaaat aactgtataa 36480

cgctggagct atcacgtatt cctccgccaa cttcaatagg tatggaaata gcattggtaa 36540

tagcttctat agtagataaa ttaactattt taccagtttt tgctccatct aaatctacta 36600

aatgtagtct tgttgctcct tggtctgccc acattttagc ggtttccaca gggttatggc 36660

tgtaaacctg ggattgtgca tagtcacctt tgtagagtct tacacaacgc ccctctaata 36720

gatctattgc tgggataact tccatgacta attagtgaat aggttaattt cagttgagct 36780

aaatggagaa ggagggattc gaaccctcgg atggacctta cgattccatc aacagattag 36840

caatctgccg ctttcgacca ctcagccacc tctccaggtt tgttataaat tatgatgggt 36900

caatcctaac agacaatttt tggcttgtca agagattttt tgcaagtgga ggaggaaatc 36960

cgtcagggat ttcaatcctg gtcaactttt ttttgatttt gaatataaag ttaagtttaa 37020

caatttctag tggcgctcct ccaacagtag atataaaata tgagttggtc cacaatgaag 37080

gacgtcttga ttttaatagt caaatccctc caaatccatt ataatcccat gaatgctctt 37140

tcaattccta cctggattat ccatatttct agtgtcattg aatgggtagt tgccatttcc 37200

ctcatctgga aatatggcga actgacccaa aaccatagtt ggaggggatt tgccttaggt 37260

atgatacccg ccttaattag cgccctatcc gcttgtacct ggcattattt cgataatccc 37320

cagtccctag aatggttagt caccctccag gctactacta cgttaatagg taattttact 37380

ctttgggcag cagcagtctg ggtttggcgt tctactcgac cgaatgaggt tctcagtatc 37440

tcaaataagg agtagaccgt tatgatgtca aaagaaactc tctttgctct ctccctgttc 37500

ccctatttgg gaatgttgtg gtttctcagt cgcagtcccc aaatgccccc ttaagggctc 37560

tatggattct atggcacttt agtatttgtt ggtgttacca ttccag 37606

<210> 2
<211> 1320
<212> DNA
<213> Cylindrospermopsis raciborskii T3

<400> 2
atgatcccag ctaaaaaagt ttatttttta ttgagtttag caatagttat ttcacccttt 60

ttatccatga ttgtgggtat ttacgaaaat attaaattta gggtattatt tgatttggtg 120

gtcagggcac taatggtggt tgactgcttc aatatcaaaa aacatcgggt caaaattagt 180

cgtcaattac ctctacgttt atctattgga cgtgagaatt tagtaatatt gaaggtagag 240

tctgggaatg tcaatagtgc tattcaaatt cgtgattact atcccacaga atttcccgta 300

tccacatcta acctgatagt taaccttccc cctaatcata ctcaggaagt aaagtacacc 360

attcgaccta atcaacgggg agaattttgg tggggaaata ttcaagttcg acagctggga 420

aattggtctc tagggtggga caattggcaa attccccaaa aaactgtggc taaggtgtat 480

cctgatttgt taggactcag atccctcgct attcgtttaa ccctacaatc ttctggatct 540

atcactaaat tgcgtcaacg gggaatggga acggaatttg ccgaactccg taattactgc 600

atgggggatg atctacggtt aattgattgg aaagctacag ctagacgtgc ttatggaaat 660

ctgagtcccc tagtaagagt tttagagcct caacaggaac aaactctgct tatattatta 720

gatcgtggta gactaatgac agctaatgta caagggttaa aacgatatga ttggggttta 780

aataccacct tgtctttggc attagcagga ttacataggg gcgatcgcgt aggagtaggg 840

gtatttgact cccagctgca tacctggata cctccagagc gaggacaaaa tcatctcaat 900

cggcttatag acagacttac acctattgaa ccagtgttag tggagtctga ttatttaaat 960

gccattacct atgtagtaaa acaacagact cgtagatctc tagtagtgtt aattactgat 1020

ttagtcgatg ttactgcttc ccatgaacta ctagtagcgc tgtgtaaatt agtgcctcga 1080

tatctacctt tttgtgtaac actcagggat cctgggattg ataaaatagc tcataatttt 1140

agtcaagact taacacaggc ttataatcga gcagtttctt tggacttgat atcacaaaga 1200

gaaattgctt ttgctcagtt gaaacaacag ggagttttgg tgttggatgc accagcaaat 1260

caaatttccg agcagttggt agaaaggtac ttacaaatca aagccaaaaa tcagatttga 1320

<210> 3
<211> 439
<212> PRT
<213> Cylindrospermopsis raciborskii T3

<400> 3

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

Ile Ser Pro Phe Leu Ser Met Ile Val Gly Ile Tyr Glu Asn Ile Lys
20 25 30

Phe Arg Val Leu Phe Asp Leu Val Val Arg Ala Leu Met Val Val Asp
35 40 45

Cys Phe Asn Ile Lys Lys His Arg Val Lys Ile Ser Arg Gln Leu Pro
50 55 60

Leu Arg Leu Ser Ile Gly Arg Glu Asn Leu Val Ile Leu Lys Val Glu
65 70 75 80

Ser Gly Asn Val Asn Ser Ala Ile Gln Ile Arg Asp Tyr Tyr Pro Thr
85 90 95

Glu Phe Pro Val Ser Thr Ser Asn Leu Ile Val Asn Leu Pro Pro Asn
100 105 110

His Thr Gln Glu Val Lys Tyr Thr Ile Arg Pro Asn Gln Arg Gly Glu
115 120 125

Phe Trp Trp Gly Asn Ile Gln Val Arg Gln Leu Gly Asn Trp Ser Leu
130 135 140

Gly Trp Asp Asn Trp Gln Ile Pro Gln Lys Thr Val Ala Lys Val Tyr
145 150 155 160

Pro Asp Leu Leu Gly Leu Arg Ser Leu Ala Ile Arg Leu Thr Leu Gln
165 170 175

Ser Ser Gly Ser Ile Thr Lys Leu Arg Gln Arg Gly Met Gly Thr Glu
180 185 190

Phe Ala Glu Leu Arg Asn Tyr Cys Met Gly Asp Asp Leu Arg Leu Ile
195 200 205

Asp Trp Lys Ala Thr Ala Arg Arg Ala Tyr Gly Asn Leu Ser Pro Leu
210 215 220

Val Arg Val Leu Glu Pro Gln Gln Glu Gln Thr Leu Leu Ile Leu Leu
225 230 235 240

Asp Arg Gly Arg Leu Met Thr Ala Asn Val Gln Gly Leu Lys Arg Tyr
245 250 255

Asp Trp Gly Leu Asn Thr Thr Leu Ser Leu Ala Leu Ala Gly Leu His
260 265 270

Arg Gly Asp Arg Val Gly Val Gly Val Phe Asp Ser Gln Leu His Thr

275 280 285

Trp Ile Pro Pro Glu Arg Gly Gln Asn His Leu Asn Arg Leu Ile Asp
290 295 300

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

Ala Ile Thr Tyr Val Val Lys Gln Gln Thr Arg Arg Ser Leu Val Val
325 330 335

Leu Ile Thr Asp Leu Val Asp Val Thr Ala Ser His Glu Leu Leu Val
340 345 350

Ala Leu Cys Lys Leu Val Pro Arg Tyr Leu Pro Phe Cys Val Thr Leu
355 360 365

Arg Asp Pro Gly Ile Asp Lys Ile Ala His Asn Phe Ser Gln Asp Leu
370 375 380

Thr Gln Ala Tyr Asn Arg Ala Val Ser Leu Asp Leu Ile Ser Gln Arg
385 390 395 400

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

Ala Pro Ala Asn Gln Ile Ser Glu Gln Leu Val Glu Arg Tyr Leu Gln
420 425 430

Ile Lys Ala Lys Asn Gln Ile
435

<210> 4
<211> 759
<212> DNA
<213> Cylindrospermopsis raciborskii T3

<400> 4
atgatagata caatatcagt actattaaga gagtggactg taatttccct tacaggttta 60

gccttctggc tttgggaaat tcgctctccc ttccatcaaa ttgaatacaa agctaaattc 120

ttcaaggaat tgggatgggc gggaatatca ttcgtcttta gaaatgttta tgcatatgtt 180

tctgtggcaa ttataaaact attgagttct ctatttatgg gagagtcagc aaattttgca 240

ggagtaatgt atgtgcccct ctggctgagg atcatcactg catatatatt acaggactta 300

actgactatc tattacacag gacaatgcat agtaatcagt ttctttggtt gacgcacaaa 360

tggcatcatt caacaaagca atcatggtgg ctgagtggaa acaaagatag ctttaccggc 420

ggacttttat atactgttac agctttgtgg tttccactgc tggacattcc ctcagaggtt 480

atgtctgtag tggcagtaca tcaagtgatt cataacaatt ggatacacct caatgtaaag 540

tggaactcct ggttaggaat aattgaatgg atttatgtta cgccccgtat tcacactttg 600

catcatcttg atacaggggg aagaaatttg agttctatgt ttactttcat cgaccgatta 660

tttggaacct atgtgtttcc agaaaacttt gatatagaaa aatctaaaaa tagattggat 720

gatcaatcag taacggtgaa gacaattttg ggtttttaa 759

<210> 5
<211> 252
<212> PRT
<213> Cylindrospermopsis raciborskii T3

<400> 5

Met Ile Asp Thr Ile Ser Val Leu Leu Arg Glu Trp Thr Val Ile Ser
1 5 10 15

Leu Thr Gly Leu Ala Phe Trp Leu Trp Glu Ile Arg Ser Pro Phe His
20 25 30

Gln Ile Glu Tyr Lys Ala Lys Phe Phe Lys Glu Leu Gly Trp Ala Gly
35 40 45

Ile Ser Phe Val Phe Arg Asn Val Tyr Ala Tyr Val Ser Val Ala Ile
50 55 60

Ile Lys Leu Leu Ser Ser Leu Phe Met Gly Glu Ser Ala Asn Phe Ala

65 70 75 80

Gly Val Met Tyr Val Pro Leu Trp Leu Arg Ile Ile Thr Ala Tyr Ile
85 90 95

Leu Gln Asp Leu Thr Asp Tyr Leu Leu His Arg Thr Met His Ser Asn
100 105 110

Gln Phe Leu Trp Leu Thr His Lys Trp His His Ser Thr Lys Gln Ser
115 120 125

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

Thr Val Thr Ala Leu Trp Phe Pro Leu Leu Asp Ile Pro Ser Glu Val
145 150 155 160

Met Ser Val Val Ala Val His Gln Val Ile His Asn Asn Trp Ile His
165 170 175

Leu Asn Val Lys Trp Asn Ser Trp Leu Gly Ile Ile Glu Trp Ile Tyr
180 185 190

Val Thr Pro Arg Ile His Thr Leu His His Leu Asp Thr Gly Gly Arg
195 200 205

Asn Leu Ser Ser Met Phe Thr Phe Ile Asp Arg Leu Phe Gly Thr Tyr
210 215 220

Val Phe Pro Glu Asn Phe Asp Ile Glu Lys Ser Lys Asn Arg Leu Asp
225 230 235 240

Asp Gln Ser Val Thr Val Lys Thr Ile Leu Gly Phe
245 250

<210> 6
<211> 396
<212> DNA

<213> Cylindrospermopsis raciborskii T3

<400> 6
tcacccccaa cttattgcag aaaaactttt ttctcttagg taataaatta gtagtttaat 60

tgaaaagcat agcatctctt ttgacttgga ataacaaaat gtcttacgat gtagtctagc 120

taaatagtga cgcaaacgac tgttttctcc ctcaactcta gtcattgatg ttttactaat 180

aatttggtct ccatcgggaa taaattttgg gtaaacttta tagccatccg taatccaaaa 240

ataggatttc caatgctcta tctttttcca taatttggca aatgttttgg cacttctatc 300

tcccactaca tattgaataa ttcccgaacg tttgttatct acaactgtcc agacccatat 360

cttgtttttt tttaccaata aatgtttcca actcat 396

<210> 7
<211> 131
<212> PRT
<213> Cylindrospermopsis raciborskii T3

<400> 7

Met Ser Trp Lys His Leu Leu Val Lys Lys Asn Lys Ile Trp Val Trp
1 5 10 15

Thr Val Val Asp Asn Lys Arg Ser Gly Ile Ile Gln Tyr Val Val Gly
20 25 30

Asp Arg Ser Ala Lys Thr Phe Ala Lys Leu Trp Lys Lys Ile Glu His
35 40 45

Trp Lys Ser Tyr Phe Trp Ile Thr Asp Gly Tyr Lys Val Tyr Pro Lys
50 55 60

Phe Ile Pro Asp Gly Asp Gln Ile Ile Ser Lys Thr Ser Met Thr Arg
65 70 75 80

Val Glu Gly Glu Asn Ser Arg Leu Arg His Tyr Leu Ala Arg Leu His
85 90 95

Arg Lys Thr Phe Cys Tyr Ser Lys Ser Lys Glu Met Leu Cys Phe Ser

100 105 110

Ile Lys Leu Leu Ile Tyr Tyr Leu Arg Glu Lys Ser Phe Ser Ala Ile
115 120 125

Ser Trp Gly
130

<210> 8
<211> 360
<212> DNA
<213> Cylindrospermopsis raciborskii T3

<400> 8
ttatctacaa ctgtccagac ccatatcttg ttttttttta ccaataaatg tttccaactc 60

atccagttga caaacttcag gtgtttggga attattatta ctatctgata actgacgacc 120

tagctttttg acccaacgaa tgactgtatt gtgatttact ttagtcattc tttcaattgc 180

cctaaatcca ttcccattta catacatggt taaacatgct tcctttactt cttgggaata 240

acctctagga gaataagatt caataaattg acgaccacaa ttcttgcatt gataattttg 300

ttttcccctt ctctggccat tttttctaat attattggaa tcacagtttg aacagttcat 360

<210> 9
<211> 119
<212> PRT
<213> Cylindrospermopsis raciborskii T3

<400> 9

Met Asn Cys Ser Asn Cys Asp Ser Asn Asn Ile Arg Lys Asn Gly Gln
1 5 10 15

Arg Arg Gly Lys Gln Asn Tyr Gln Cys Lys Asn Cys Gly Arg Gln Phe
20 25 30

Ile Glu Ser Tyr Ser Pro Arg Gly Tyr Ser Gln Glu Val Lys Glu Ala
35 40 45

Cys Leu Thr Met Tyr Val Asn Gly Asn Gly Phe Arg Ala Ile Glu Arg

50 55 60

Met Thr Lys Val Asn His Asn Thr Val Ile Arg Trp Val Lys Lys Leu
65 70 75 80

Gly Arg Gln Leu Ser Asp Ser Asn Asn Asn Ser Gln Thr Pro Glu Val
85 90 95

Cys Gln Leu Asp Glu Leu Glu Thr Phe Ile Gly Lys Lys Lys Gln Asp
100 105 110

Met Gly Leu Asp Ser Cys Arg
115

<210> 10
<211> 354
<212> DNA
<213> Cylindrospermopsis raciborskii T3

<400> 10
ttatgacctc attttcattt ctagacgttc agcaacgggc attaactcac gtatcagatc 60

aaagtttcct acgttccgtc tcatccagtc taataagaat ttttctcctt catctagctt 120

acctttatca tcaacaaaaa ccatctgctc gcaccaatct acaaatccgg aattagtcat 180

ctcatagact aaaatgatgg gaggaaagtg tgcgaatccc atttttttcaa tgacttccat 240

acaaaccagc ttaaatactt gttcgtttgt caattcatta gacataaaga attttccttt 300

aatcaattct gtttctaatc ctaccacaga gtaataactc ttggtctgga acat 354

<210> 11
<211> 117
<212> PRT
<213> Cylindrospermopsis raciborskii T3

<400> 11

Met Phe Gln Thr Lys Ser Tyr Tyr Ser Val Val Gly Leu Glu Thr Glu
1 5 10 15

Leu Ile Lys Gly Lys Phe Phe Met Ser Asn Glu Leu Thr Asn Glu Gln

20 25 30

Val Phe Lys Leu Val Cys Met Glu Val Ile Glu Lys Met Gly Phe Ala
35 40 45

His Phe Pro Pro Ile Ile Leu Val Tyr Glu Met Thr Asn Ser Gly Phe
50 55 60

Val Asp Trp Cys Glu Gln Met Val Phe Val Asp Asp Lys Gly Lys Leu
65 70 75 80

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

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

Met Lys Met Arg Ser
115

<210> 12
<211> 957
<212> DNA
<213> Cylindrospermopsis raciborskii T3

<400> 12
tcataactta ttacttgacg gagttgcagg ggcatacctt aacttgacct tgggagcgat 60

agaagaaagg aaggcttcag tgacgggtct ttgactaatc ccagtttcca cttcaactaa 120

aacagcatca caaatgtcga atagtgattg agaatatcta ttcatattca tgaaagtcag 180

agcagattcc atcggagaca tggatgaatt aaaggcagcg ttttcagcgt atcgacctgt 240

aaatatattc ccgtgggaat cttttaacgc taccctgca aaatttttcg tgtagggagc 300

ataactttga ttggcagcgg atagagcagc aagcacaaca tcatcggtag aataggtctc 360

cagatcatga aatactgttt gcattaatcc acctgtgagt cctagatccg ctggtccaaa 420

tggctcgggt agaaaatgtg ggagtttatt tgaggtataa gtttgctcag gctgtgattc 480

attagacttc acaagaagaa caaaattttg atttacagtt gccatctcgt ataaaaattg 540

tcggcagtat ccacatggtg cttcgtggat tgctaatgct tgtaaaccgg tttctccgtg 600

caaccacgca tttatggtgg cggattgttc tgcgtgaact gagaaactaa gtgcctgtcc 660

tacaaattcc atgtcggcac caaaataaag agttccagaa cccagttgat tcttagattg 720

tggtttacca agagcgatcg cccctacata aaactgcgat attggtaccc tagcataagt 780

tgcggctacg ggtagtaatt gaatcattaa cgtactaata ttagtaccaa gtcgatcaat 840

ccaagatgcg acaacacttg agtcaattac agcatgttgg gcaagaattg tccttaactc 900

tgattgaatg gaacgtggaa ccttggcaat cgcctgttct aatgctacat gggtcat 957

<210> 13
<211> 318
<212> PRT
<213> Cylindrospermopsis raciborskii T3

<400> 13

Met Thr His Val Ala Leu Glu Gln Ala Ile Ala Lys Val Pro Arg Ser
1 5 10 15

Ile Gln Ser Glu Leu Arg Thr Ile Leu Ala Gln His Ala Val Ile Asp
20 25 30

Ser Ser Val Val Ala Ser Trp Ile Asp Arg Leu Gly Thr Asn Ile Ser
35 40 45

Thr Leu Met Ile Gln Leu Leu Pro Val Ala Ala Thr Tyr Ala Arg Val
50 55 60

Pro Ile Ser Gln Phe Tyr Val Gly Ala Ile Ala Leu Gly Lys Pro Gln
65 70 75 80

Ser Lys Asn Gln Leu Gly Ser Gly Thr Leu Tyr Phe Gly Ala Asp Met
85 90 95

Glu Phe Val Gly Gln Ala Leu Ser Phe Ser Val His Ala Glu Gln Ser
100 105 110

Ala Thr Ile Asn Ala Trp Leu His Gly Glu Thr Gly Leu Gln Ala Leu
115 120 125

Ala Ile His Glu Ala Pro Cys Gly Tyr Cys Arg Gln Phe Leu Tyr Glu
130 135 140

Met Ala Thr Val Asn Gln Asn Phe Val Leu Leu Val Lys Ser Asn Glu
145 150 155 160

Ser Gln Pro Glu Gln Thr Tyr Thr Ser Asn Lys Leu Pro His Phe Leu
165 170 175

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

Gln Thr Val Phe His Asp Leu Glu Thr Tyr Ser Thr Asp Asp Val Val
195 200 205

Leu Ala Ala Leu Ser Ala Ala Asn Gln Ser Tyr Ala Pro Tyr Thr Lys
210 215 220

Asn Phe Ala Gly Val Ala Leu Lys Asp Ser His Gly Asn Ile Phe Thr
225 230 235 240

Gly Arg Tyr Ala Glu Asn Ala Ala Phe Asn Ser Ser Met Ser Pro Met
245 250 255

Glu Ser Ala Leu Thr Phe Met Asn Met Asn Arg Tyr Ser Gln Ser Leu
260 265 270

Phe Asp Ile Cys Asp Ala Val Leu Val Glu Val Glu Thr Gly Ile Ser
275 280 285

Gln Arg Pro Val Thr Glu Ala Phe Leu Ser Ser Ile Ala Pro Lys Val
290 295 300

Lys Leu Arg Tyr Ala Pro Ala Thr Pro Ser Ser Asn Lys Leu

305 310 315

<210> 14
<211> 3738
<212> DNA
<213> Cylindrospermopsis raciborskii T3

<400> 14
ttaatgcttg agtatgtttt cctcctgctt acaaggcaaa gctttccttt tttgtagcaa 60

atcccaaact gctttgagag atttaattgc ttggtctatc tcctcttcgg tattggcggc 120

tgtaatcgaa aaccttaaag cacttttatt taaaggtacg attggaaaaa tagcaggagt 180

aattaaaata ccatattccc aaaggagttg acacacatca atcatgtgtt gagcatctcc 240

cactaacacg cctacgatgg gaacgtaacc atagttatcc acttcgaatc caatggctct 300

tgcttgtgta accaatttgt gagttaggtg ataaatttgt tttcttaact gctccccctc 360

ctgacgattc acctgtaatc cggctaaggc acttgccaaa ctcgcaacag gagaaggacc 420

agaaaatatg gcagtccaag cgttgcggaa gttggttttg atccggcgat cgccacaagt 480

taagaatgct gcgtaagaag aataggcttt ggacaaacca gctacataga tgatattatc 540

ctctgcaaac cgcaggtcaa aataattcac catcccgttt cctttgtaac cgtaaggcat 600

atcgctgctg ggattttcgc ccaaaatgcc aaaaccatga gcatcatcca tgtaaattaa 660

ggcattgtac tcttttgcca gatgcacgta agctggcaga tcgggaaaat ctgccgacat 720

ggaatacacg ccatcaatga caataatctt tacttgttca ggcggatatt ttgctagttt 780

ttcggctaaa tcgttcaaat cattatgtcg atattggatg aactgggctc ctttgtgctg 840

agccagacag cacgcttcat aaatacaacg atgtgcagct atgtcaccaa agatgacacc 900

attattccca gttaatagtg gtaaaattcc tatctgaagc agtgttacag ctggaaatac 960

taaaacatca ggtacgccta aaagtttgga caattcttcc tccaattcct cataaattgc 1020

tggggaagca acaagccgag tccagcttgg atgtgtgccc catttatcca aagctggtgg 1080

aattgcttcc ttaacttttg gatgcaagtc aagacctaaa tagttgcaag aagcaaagtc 1140

tatcacccaa tgtccgtcaa ttagcacctt gcgaccttgt tgttctgtga cgactcttgt 1200

gacttgagga atttttgtt ggttaactac gttttccaga gtgttgattt cgttggctga 1260

gtcaacaggt ggagctagat cagattgttt ctcttgtacc acttggtttt ggaaataagt 1320

gatgatggca gttggagtgt tcttttgtaa aaagaacgtt ccagacagat tgatccctaa 1380

acgttcctct aggagcgttt gcagttctaa taaatctaaa gaatctaatc ccatatccag 1440

cagtttttgt tgtggagcgt aggctgcctg acgttgggaa cccattactt ttaagatgca 1500

ttctttaacg agatccgcta cagttttgtt ttccttagtt gcagatgttg cttttggtac 1560

caatgaacca attgctgagt taatatacgg tcctttgcga tcaccaggcg agtgcaaagc 1620

actgtcgcgc aggttatatt caatcaaaat acccatgccg agattatctg tatcttccgg 1680

acgataatta gcaataattc ccctaatttc ggctcctccc gacacatgga aacccacaat 1740

tggatccaga agctgtcgtt gctcattgtg tagctttaaa tactccatca tcggcatttg 1800

ggaataattg acataatttc gacagcgagt tacacccacc acgctctcaa tgccgccttt 1860

cagggtacag tagtaaagca taaagtcccg caattcattt cctaaccccc gcgcctgaaa 1920

ctcaggtaga atatttagtg cgagcagttg aataactgac ccttggggag tatgtaacgt 1980

cggcacttgc gcatatttta cattctctaa tgcctcagtg ctggtaattg tttgggaata 2040

aatcgcacca ataatttgat cttctataat cagcactaaa ttaccttgcg ggtttagctc 2100

aagtcttcgc cgaatttcat gagtagatgc ccgtaaattt tctggccaac acttgacctc 2160

caagtcaact aaggcaggta aatctgacaa ataggcatga ctaattttgt aaggtctttt 2220

ctcgaagtaa ttaagcgtaa tgcgagtaaa aggaaatgtt tttgggtatc ttttagaaag 2280

ctctagtttt ggaaatagac ctacttgtgc agcagacatg agaaaaacct cagcttccac 2340

aagatactgc tgagaaaatc cctgaaacgc atcgaaatgt aagttttcgc ttttgtctaa 2400

aaactgatag actacccttg gttccaaaca atggacctcc aaaatcatta aaccgtgttt 2460

attgaccact tgagaccatc tttctaagtg ttccaccaaa ctttgcacca taacatgagg 2520

aggaataagc tctccttgat catcgacaca gactgattgg taaggtaagt gagcacgttc 2580

tttcaattcg tttcttttct gaggaggaat aaagagacga tcatggtcga ggaacgaacg 2640

gatgtgcagg atattttcgg gatcatgaat gccatgagct tctaaagaac gcaccatttg 2700

ttctgggttc ccaatatctc cctgtaaaac taagtgggga aggctagcaa gggtgcgtgt 2760

ggtagctttt aaagaagctt cgttataatc tacacctata agacgcaggg gatactgttc 2820

gagtgctttt cccctagcag acttaaattg aatggtttcc cagactcgtt tcaggagagt 2880

tccatcgcca caccccatgt cagtaatgta tttgggttgt tcttctaatg gcaactgatt 2940

gaatactgag aggatacttt cttctaaatc ggcaaaatat ttctggtgtt gaaatccact 3000

cccgatcacg ttaagggtgc gatcaatgtg cctttcgtga ccggaagcat ctctttggaa 3060

tacggagaga caattgccaa acaatacatc atgaatgcgg gacaacatag gagtgtagga 3120

cgccactatg gctgtattca aggctcgctc tcccataaat cgaccaagtt cggttatggt 3180

caaacgacct gctgtaaggt cagcccagcc aaggtggaga aataacttac ccaactcttc 3240

ttgcactgtt gagcttaatg aggagagcaa aggtttgtcc tccgaatctg caagcaagtt 3300

gtgtttgtgc agtgccagca ggagtgggat gaccagtaat ccatctaaaa aatctgccat 3360

taggggattg tccaggttcc acaattggca agaacgctca atccatcttc ccagcaaatt 3420

tccttgtttc ccttctaaat aagactgaat tggtaggttg tacaattgaa gaatgtcttc 3480

cgaaattttg ttgtgaatcg ctgcttctgc ggttagagag tatttaagct ccttatttcg 3540

ggaaagccaa tgtaaagact cgagcatcct caaagcaact tgaaaatgtc cgctgttagc 3600

tcccagatgt tccaccattt ggtttaaaga gagaggactt tcatcggcga gtaattcaaa 3660

aacacctttt tctcgacacg caagaataac gggaaccgcc acaaagccgt gagtataacg 3720

attaatcttt tgtaacat 3738

<210> 15
<211> 1245
<212> PRT
<213> Cylindrospermopsis raciborskii T3

<400> 15

Met Leu Gln Lys Ile Asn Arg Tyr Thr His Gly Phe Val Ala Val Pro
1 5 10 15

Val Ile Leu Ala Cys Arg Glu Lys Gly Val Phe Glu Leu Leu Ala Asp
20 25 30

Glu Ser Pro Leu Ser Leu Asn Gln Met Val Glu His Leu Gly Ala Asn
35 40 45

Ser Gly His Phe Gln Val Ala Leu Arg Met Leu Glu Ser Leu His Trp
50 55 60

Leu Ser Arg Asn Lys Glu Leu Lys Tyr Ser Leu Thr Ala Glu Ala Ala
65 70 75 80

Ile His Asn Lys Ile Ser Glu Asp Ile Leu Gln Leu Tyr Asn Leu Pro
85 90 95

Ile Gln Ser Tyr Leu Glu Gly Lys Gln Gly Asn Leu Leu Gly Arg Trp
100 105 110

Ile Glu Arg Ser Cys Gln Leu Trp Asn Leu Asp Asn Pro Leu Met Ala
115 120 125

Asp Phe Leu Asp Gly Leu Leu Val Ile Pro Leu Leu Leu Ala Leu His
130 135 140

Lys His Asn Leu Leu Ala Asp Ser Glu Asp Lys Pro Leu Leu Ser Ser
145 150 155 160

Leu Ser Ser Thr Val Gln Glu Glu Leu Gly Lys Leu Phe Leu His Leu
165 170 175

Gly Trp Ala Asp Leu Thr Ala Gly Arg Leu Thr Ile Thr Glu Leu Gly
180 185 190

Arg Phe Met Gly Glu Arg Ala Leu Asn Thr Ala Ile Val Ala Ser Tyr
195 200 205

Thr Pro Met Leu Ser Arg Ile His Asp Val Leu Phe Gly Asn Cys Leu
210 215 220

Ser Val Phe Gln Arg Asp Ala Ser Gly His Glu Arg His Ile Asp Arg

225 230 235 240

Thr Leu Asn Val Ile Gly Ser Gly Phe Gln His Gln Lys Tyr Phe Ala
245 250 255

Asp Leu Glu Glu Ser Ile Leu Ser Val Phe Asn Gln Leu Pro Leu Glu
260 265 270

Glu Gln Pro Lys Tyr Ile Thr Asp Met Gly Cys Gly Asp Gly Thr Leu
275 280 285

Leu Lys Arg Val Trp Glu Thr Ile Gln Phe Lys Ser Ala Arg Gly Lys
290 295 300

Ala Leu Glu Gln Tyr Pro Leu Arg Leu Ile Gly Val Asp Tyr Asn Glu
305 310 315 320

Ala Ser Leu Lys Ala Thr Thr Arg Thr Leu Ala Ser Leu Pro His Leu
325 330 335

Val Leu Gln Gly Asp Ile Gly Asn Pro Glu Gln Met Val Arg Ser Leu
340 345 350

Glu Ala His Gly Ile His Asp Pro Glu Asn Ile Leu His Ile Arg Ser
355 360 365

Phe Leu Asp His Asp Arg Leu Phe Ile Pro Pro Gln Lys Arg Asn Glu
370 375 380

Leu Lys Glu Arg Ala His Leu Pro Tyr Gln Ser Val Cys Val Asp Asp
385 390 395 400

Gln Gly Glu Leu Ile Pro Pro His Val Met Val Gln Ser Leu Val Glu
405 410 415

His Leu Glu Arg Trp Ser Gln Val Val Asn Lys His Gly Leu Met Ile
420 425 430

Leu Glu Val His Cys Leu Glu Pro Arg Val Val Tyr Gln Phe Leu Asp
435 440 445

Lys Ser Glu Asn Leu His Phe Asp Ala Phe Gln Gly Phe Ser Gln Gln
450 455 460

Tyr Leu Val Glu Ala Glu Val Phe Leu Met Ser Ala Ala Gln Val Gly
465 470 475 480

Leu Phe Pro Lys Leu Glu Leu Ser Lys Arg Tyr Pro Lys Thr Phe Pro
485 490 495

Phe Thr Arg Ile Thr Leu Asn Tyr Phe Glu Lys Arg Pro Tyr Lys Ile
500 505 510

Ser His Ala Tyr Leu Ser Asp Leu Pro Ala Leu Val Asp Leu Glu Val
515 520 525

Lys Cys Trp Pro Glu Asn Leu Arg Ala Ser Thr His Glu Ile Arg Arg
530 535 540

Arg Leu Glu Leu Asn Pro Gln Gly Asn Leu Val Leu Ile Ile Glu Asp
545 550 555 560

Gln Ile Ile Gly Ala Ile Tyr Ser Gln Thr Ile Thr Ser Thr Glu Ala
565 570 575

Leu Glu Asn Val Lys Tyr Ala Gln Val Pro Thr Leu His Thr Pro Gln
580 585 590

Gly Ser Val Ile Gln Leu Leu Ala Leu Asn Ile Leu Pro Glu Phe Gln
595 600 605

Ala Arg Gly Leu Gly Asn Glu Leu Arg Asp Phe Met Leu Tyr Tyr Cys
610 615 620

Thr Leu Lys Gly Gly Ile Glu Ser Val Val Gly Val Thr Arg Cys Arg

625 630 635 640

Asn Tyr Val Asn Tyr Ser Gln Met Pro Met Met Glu Tyr Leu Lys Leu
645 650 655

His Asn Glu Gln Arg Gln Leu Leu Asp Pro Ile Val Gly Phe His Val
660 665 670

Ser Gly Gly Ala Glu Ile Arg Gly Ile Ile Ala Asn Tyr Arg Pro Glu
675 680 685

Asp Thr Asp Asn Leu Gly Met Gly Ile Leu Ile Glu Tyr Asn Leu Arg
690 695 700

Asp Ser Ala Leu His Ser Pro Gly Asp Arg Lys Gly Pro Tyr Ile Asn
705 710 715 720

Ser Ala Ile Gly Ser Leu Val Pro Lys Ala Thr Ser Ala Thr Lys Glu
725 730 735

Asn Lys Thr Val Ala Asp Leu Val Lys Glu Cys Ile Leu Lys Val Met
740 745 750

Gly Ser Gln Arg Gln Ala Ala Tyr Ala Pro Gln Gln Lys Leu Leu Asp
755 760 765

Met Gly Leu Asp Ser Leu Asp Leu Leu Glu Leu Gln Thr Leu Leu Glu
770 775 780

Glu Arg Leu Gly Ile Asn Leu Ser Gly Thr Phe Phe Leu Gln Lys Asn
785 790 795 800

Thr Pro Thr Ala Ile Ile Thr Tyr Phe Gln Asn Gln Val Val Gln Glu
805 810 815

Lys Gln Ser Asp Leu Ala Pro Pro Val Asp Ser Ala Asn Glu Ile Asn
820 825 830

Thr Leu Glu Asn Val Val Asn Gln Gln Lys Ile Pro Gln Val Thr Arg
835 840 845

Val Val Thr Glu Gln Gln Gly Arg Lys Val Leu Ile Asp Gly His Trp
850 855 860

Val Ile Asp Phe Ala Ser Cys Asn Tyr Leu Gly Leu Asp Leu His Pro
865 870 875 880

Lys Val Lys Glu Ala Ile Pro Pro Ala Leu Asp Lys Trp Gly Thr His
885 890 895

Pro Ser Trp Thr Arg Leu Val Ala Ser Pro Ala Ile Tyr Glu Glu Leu
900 905 910

Glu Glu Glu Leu Ser Lys Leu Leu Gly Val Pro Asp Val Leu Val Phe
915 920 925

Pro Ala Val Thr Leu Leu Gln Ile Gly Ile Leu Pro Leu Leu Thr Gly
930 935 940

Asn Asn Gly Val Ile Phe Gly Asp Ile Ala Ala His Arg Cys Ile Tyr
945 950 955 960

Glu Ala Cys Cys Leu Ala Gln His Lys Gly Ala Gln Phe Ile Gln Tyr
965 970 975

Arg His Asn Asp Leu Asn Asp Leu Ala Glu Lys Leu Ala Lys Tyr Pro
980 985 990

Pro Glu Gln Val Lys Ile Ile Val Ile Asp Gly Val Tyr Ser Met Ser
995 1000 1005

Ala Asp Phe Pro Asp Leu Pro Ala Tyr Val His Leu Ala Lys Glu
1010 1015 1020

Tyr Asn Ala Leu Ile Tyr Met Asp Asp Ala His Gly Phe Gly Ile

1025 1030 1035

Leu Gly Glu Asn Pro Ser Ser Asp Met Pro Tyr Gly Tyr Lys Gly
1040 1045 1050

Asn Gly Met Val Asn Tyr Phe Asp Leu Arg Phe Ala Glu Asp Asn
1055 1060 1065

Ile Ile Tyr Val Ala Gly Leu Ser Lys Ala Tyr Ser Ser Tyr Ala
1070 1075 1080

Ala Phe Leu Thr Cys Gly Asp Arg Arg Ile Lys Thr Asn Phe Arg
1085 1090 1095

Asn Ala Trp Thr Ala Ile Phe Ser Gly Pro Ser Pro Val Ala Ser
1100 1105 1110

Leu Ala Ser Ala Leu Ala Gly Leu Gln Val Asn Arg Gln Glu Gly
1115 1120 1125

Glu Gln Leu Arg Lys Gln Ile Tyr His Leu Thr His Lys Leu Val
1130 1135 1140

Thr Gln Ala Arg Ala Ile Gly Phe Glu Val Asp Asn Tyr Gly Tyr
1145 1150 1155

Val Pro Ile Val Gly Val Leu Val Gly Asp Ala Gln His Met Ile
1160 1165 1170

Asp Val Cys Gln Leu Leu Trp Glu Tyr Gly Ile Leu Ile Thr Pro
1175 1180 1185

Ala Ile Phe Pro Ile Val Pro Leu Asn Lys Ser Ala Leu Arg Phe
1190 1195 1200

Ser Ile Thr Ala Ala Asn Thr Glu Glu Glu Ile Asp Gln Ala Ile
1205 1210 1215

Lys Ser Leu Lys Ala Val Trp Asp Leu Leu Gln Lys Arg Lys Ala
1220 1225 1230

Leu Pro Cys Lys Gln Glu Glu Asn Ile Leu Lys His
1235 1240 1245

<210> 16
<211> 387
<212> DNA
<213> Cylindrospermopsis raciborskii T3

<400> 16
atgttgaaag atttcaacca gtttttaatc agaacactag cattcgtatt cgcatttggt 60

attttcttaa ccactggagt tggcattgct aaagctgact acctagttaa aggtggaaag 120

attaccaatg ttcaaaatac ttcttctaac ggtgataatt atgccgttag tatcagcggt 180

gggtttggtc cttgcgcaga tagagtgatt atcctaccaa cttcaggagt gataaatcga 240

gacattcata tgcgtggcta tgaagccgca ttaactgcac tatccaatgg ctttttagta 300

gatatttacg actatactgg ctcttcttgc agcaatggtg gccaactaac tattaccaac 360

caattaggta agctaatcag caattag 387

<210> 17
<211> 128
<212> PRT
<213> Cylindrospermopsis raciborskii T3

<400> 17

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

Phe Ala Phe Gly Ile Phe Leu Thr Thr Gly Val Gly Ile Ala Lys Ala
20 25 30

Asp Tyr Leu Val Lys Gly Gly Lys Ile Thr Asn Val Gln Asn Thr Ser
35 40 45

Ser Asn Gly Asp Asn Tyr Ala Val Ser Ile Ser Gly Gly Phe Gly Pro

50 55 60

Cys Ala Asp Arg Val Ile Ile Leu Pro Thr Ser Gly Val Ile Asn Arg
65 70 75 80

Asp Ile His Met Arg Gly Tyr Glu Ala Ala Leu Thr Ala Leu Ser Asn
85 90 95

Gly Phe Leu Val Asp Ile Tyr Asp Tyr Thr Gly Ser Ser Cys Ser Asn
100 105 110

Gly Gly Gln Leu Thr Ile Thr Asn Gln Leu Gly Lys Leu Ile Ser Asn
115 120 125

<210> 18
<211> 1416
<212> DNA
<213> Cylindrospermopsis raciborskii T3

<400> 18
atggaaacaa cctcaaaaaa atttaagtca gatctgatat tagaagcacg agcaagccta 60

aagttgggaa tccccttagt catttcacaa atgtgcgaaa cgggtattta tacagcgaat 120

gcagtcatga tgggtttact tggtacgcaa gttttggccg ccggtgcttt gggcgcgctc 180

gctttttga ccttattatt tgcctgccat ggtattctct cagtaggagg atcactagca 240

gccgaagctt ttggggcaaa taaaatagat gaagttagtc gtattgcttc cgggcaaata 300

tggctagcag ttaccttgtc tttacctgca atgcttctgc tttggcatgg cgatactatc 360

ttgctgctat tcggtcaaga ggaaagcaat gtgttattga caaaaacgta tttacactca 420

attttatggg gctttcccgc tgcgcttagt attttgacat taagaggcat tgcctctgct 480

ctcaacgttc cccgattgat aactattact atgctcactc agctgatatt gaataccgcc 540

gccgattatg tgttaatatt cggtaaattt ggtcttcctc aacttggttt ggctggaata 600

ggctgggcaa ctgctctggg tttttgggtt agttttacat tggggcttat cttgctgatt 660

ttctccctga aagttagaga ttataaactt ttccgctact tgcatcagtt tgataaacag 720

atctttgtca aaatttttca aactggatgg cccatggggt ttcaatgggg ggcggaaacg 780

gcactattta acgtcaccgc ttgggtagca gggtatttag gaacggtaac attagcagcc 840

catgatattg gcttccaaac ggcagaactg gcgatggtta taccactcgg agtcggcaat 900

gtcgctatga caagagtagg tcagagtata ggagaaaaaa acccttggg tgcaagaagg 960

gtagcatcga ttggaattac aatagttggc atttatgcca gtattgtagc acttgttttc 1020

tggttgtttc catatcaaat tgccggaatt tatttaaata taaacaatcc cgagaatatc 1080

gaagcaatta agaaagcaac tacttttatc cccttggcgg gactattcca aatgttttac 1140

agtattcaaa taattattgt tggggctttg gtcggtctgc gggatacatt tgttccagta 1200

tcaatgaact taattgtctg gggtcttgga ttggcaggaa gctatttcat ggcaatcatt 1260

ttaggatggg gggggatcgg gatttggttg gctatggttt tgagtccact cctctcggca 1320

gttattttaa ctgttcgttt ttatcgagtg attgacaatc ttcttgccaa cagtgatgat 1380

atgttacaga atgcgtctgt tactactcta ggctga 1416

<210> 19
<211> 471
<212> PRT
<213> Cylindrospermopsis raciborskii T3

<400> 19

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

Arg Ala Ser Leu Lys Leu Gly Ile Pro Leu Val Ile Ser Gln Met Cys
20 25 30

Glu Thr Gly Ile Tyr Thr Ala Asn Ala Val Met Met Gly Leu Leu Gly
35 40 45

Thr Gln Val Leu Ala Ala Gly Ala Leu Gly Ala Leu Ala Phe Leu Thr
50 55 60

Leu Leu Phe Ala Cys His Gly Ile Leu Ser Val Gly Gly Ser Leu Ala
65 70 75 80

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

Ser Gly Gln Ile Trp Leu Ala Val Thr Leu Ser Leu Pro Ala Met Leu
100 105 110

Leu Leu Trp His Gly Asp Thr Ile Leu Leu Leu Phe Gly Gln Glu Glu
115 120 125

Ser Asn Val Leu Leu Thr Lys Thr Tyr Leu His Ser Ile Leu Trp Gly
130 135 140

Phe Pro Ala Ala Leu Ser Ile Leu Thr Leu Arg Gly Ile Ala Ser Ala
145 150 155 160

Leu Asn Val Pro Arg Leu Ile Thr Ile Thr Met Leu Thr Gln Leu Ile
165 170 175

Leu Asn Thr Ala Ala Asp Tyr Val Leu Ile Phe Gly Lys Phe Gly Leu
180 185 190

Pro Gln Leu Gly Leu Ala Gly Ile Gly Trp Ala Thr Ala Leu Gly Phe
195 200 205

Trp Val Ser Phe Thr Leu Gly Leu Ile Leu Leu Ile Phe Ser Leu Lys
210 215 220

Val Arg Asp Tyr Lys Leu Phe Arg Tyr Leu His Gln Phe Asp Lys Gln
225 230 235 240

Ile Phe Val Lys Ile Phe Gln Thr Gly Trp Pro Met Gly Phe Gln Trp
245 250 255

Gly Ala Glu Thr Ala Leu Phe Asn Val Thr Ala Trp Val Ala Gly Tyr
260 265 270

Leu Gly Thr Val Thr Leu Ala Ala His Asp Ile Gly Phe Gln Thr Ala

275 280 285

Glu Leu Ala Met Val Ile Pro Leu Gly Val Gly Asn Val Ala Met Thr
290 295 300

Arg Val Gly Gln Ser Ile Gly Glu Lys Asn Pro Leu Gly Ala Arg Arg
305 310 315 320

Val Ala Ser Ile Gly Ile Thr Ile Val Gly Ile Tyr Ala Ser Ile Val
325 330 335

Ala Leu Val Phe Trp Leu Phe Pro Tyr Gln Ile Ala Gly Ile Tyr Leu
340 345 350

Asn Ile Asn Asn Pro Glu Asn Ile Glu Ala Ile Lys Lys Ala Thr Thr
355 360 365

Phe Ile Pro Leu Ala Gly Leu Phe Gln Met Phe Tyr Ser Ile Gln Ile
370 375 380

Ile Ile Val Gly Ala Leu Val Gly Leu Arg Asp Thr Phe Val Pro Val
385 390 395 400

Ser Met Asn Leu Ile Val Trp Gly Leu Gly Leu Ala Gly Ser Tyr Phe
405 410 415

Met Ala Ile Ile Leu Gly Trp Gly Gly Ile Gly Ile Trp Leu Ala Met
420 425 430

Val Leu Ser Pro Leu Leu Ser Ala Val Ile Leu Thr Val Arg Phe Tyr
435 440 445

Arg Val Ile Asp Asn Leu Leu Ala Asn Ser Asp Asp Met Leu Gln Asn
450 455 460

Ala Ser Val Thr Thr Leu Gly
465 470

<210> 20
<211> 1134
<212> DNA
<213> Cylindrospermopsis raciborskii T3

<400> 20
atgaccaatc aaaataacca agaattagag aacgatttac caatcgccaa gcagccttgt 60

ccggtcaatt cttataatga gtgggacaca cttgaggagg tcattgttgg tagtgttgaa 120

ggtgcaatgt taccggccct agaaccaatc aacaaatgga cattcccttt tgaagaattg 180

gaatctgccc aaaagatact ctctgagagg ggaggagttc cttatccacc agagatgatt 240

acattagcac acaaagaact aaatgaattt attcacattc ttgaagcaga aggggtcaaa 300

gttcgtcgag ttaaacctgt agatttctct gtccccttct ccacaccagc ttggcaagta 360

ggaagtggtt tttgtgccgc caatcctcgc gatgtttttt tggtgattgg gaatgagatt 420

attgaagcac caatggcaga tcgcaaccgc tattttgaaa cttgggcgta tcgagagatg 480

ctcaaggaat attttcaggc aggagctaag tggactgcag cgccgaagcc acaattattc 540

gacgcacagt atgacttcaa tttccagttt cctcaactgg gggagccgcc gcgtttcgtc 600

gttacagagt ttgaaccgac ttttgatgcg gcagattttg tgcgctgtgg acgagatatt 660

tttggtcaaa aaagtcatgt gactaatggt ttgggcatag aatggttaca acgtcacttg 720

gaagacgaat accgtattca tattattgaa tcgcattgtc cggaagcact gcacatcgat 780

accaccttaa tgcctcttgc acctggcaaa atactagtaa atccagaatt tgtagatgtt 840

aataaattgc caaaaatcct gaaaagctgg gacattttgg ttgcacctta ccccaaccat 900

atacctcaaa accagctgag actggtcagt gaatgggcag gtttgaatgt actgatgtta 960

gatgaagagc gagtcattgt agaaaaaaac caggagcaga tgattaaagc actgaaagat 1020

tggggattta agcctattgt ttgccatttt gaaagctact atccattttt aggatcattt 1080

cactgtgcaa cattagacgt tcgccgacgc ggaactcttc agtcctattt ttaa 1134

<210> 21
<211> 377
<212> PRT
<213> Cylindrospermopsis raciborskii T3

<400> 21

Met Thr Asn Gln Asn Asn Gln Glu Leu Glu Asn Asp Leu Pro Ile Ala
1 5 10 15

Lys Gln Pro Cys Pro Val Asn Ser Tyr Asn Glu Trp Asp Thr Leu Glu
20 25 30

Glu Val Ile Val Gly Ser Val Glu Gly Ala Met Leu Pro Ala Leu Glu
35 40 45

Pro Ile Asn Lys Trp Thr Phe Pro Phe Glu Glu Leu Glu Ser Ala Gln
50 55 60

Lys Ile Leu Ser Glu Arg Gly Gly Val Pro Tyr Pro Pro Glu Met Ile
65 70 75 80

Thr Leu Ala His Lys Glu Leu Asn Glu Phe Ile His Ile Leu Glu Ala
85 90 95

Glu Gly Val Lys Val Arg Arg Val Lys Pro Val Asp Phe Ser Val Pro
100 105 110

Phe Ser Thr Pro Ala Trp Gln Val Gly Ser Gly Phe Cys Ala Ala Asn
115 120 125

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

Met Ala Asp Arg Asn Arg Tyr Phe Glu Thr Trp Ala Tyr Arg Glu Met
145 150 155 160

Leu Lys Glu Tyr Phe Gln Ala Gly Ala Lys Trp Thr Ala Ala Pro Lys
165 170 175

Pro Gln Leu Phe Asp Ala Gln Tyr Asp Phe Asn Phe Gln Phe Pro Gln
180 185 190

Leu Gly Glu Pro Pro Arg Phe Val Val Thr Glu Phe Glu Pro Thr Phe
195 200 205

Asp Ala Ala Asp Phe Val Arg Cys Gly Arg Asp Ile Phe Gly Gln Lys
210 215 220

Ser His Val Thr Asn Gly Leu Gly Ile Glu Trp Leu Gln Arg His Leu
225 230 235 240

Glu Asp Glu Tyr Arg Ile His Ile Ile Glu Ser His Cys Pro Glu Ala
245 250 255

Leu His Ile Asp Thr Thr Leu Met Pro Leu Ala Pro Gly Lys Ile Leu
260 265 270

Val Asn Pro Glu Phe Val Asp Val Asn Lys Leu Pro Lys Ile Leu Lys
275 280 285

Ser Trp Asp Ile Leu Val Ala Pro Tyr Pro Asn His Ile Pro Gln Asn
290 295 300

Gln Leu Arg Leu Val Ser Glu Trp Ala Gly Leu Asn Val Leu Met Leu
305 310 315 320

Asp Glu Glu Arg Val Ile Val Glu Lys Asn Gln Glu Gln Met Ile Lys
325 330 335

Ala Leu Lys Asp Trp Gly Phe Lys Pro Ile Val Cys His Phe Glu Ser
340 345 350

Tyr Tyr Pro Phe Leu Gly Ser Phe His Cys Ala Thr Leu Asp Val Arg
355 360 365

Arg Arg Gly Thr Leu Gln Ser Tyr Phe
370 375

<210> 22

<211> 1005
<212> DNA
<213> Cylindrospermopsis raciborskii T3

<400> 22
atgacaactg ctgacctaat cttaattaac aactggtacg tagtcgcaaa ggtggaagat 60

tgtaaaccag gaagtatcac cacggctctt ttattgggag ttaagttggt actatggcgc 120

agtcgtgaac agaattcccc catacagata tggcaagact actgccctca ccgaggtgtg 180

gctctgtcta tgggagaaat tgttaataat actttggttt gtccgtatca cggatggaga 240

tataatcaag caggtaaatg cgtacatatc ccggctcacc ctgacatgac acccccagca 300

agtgcccaag ccaagatcta tcattgccag gagcgatacg gattagtatg ggtgtgctta 360

ggtgatcctg tcaatgatat accttcatta cccgaatggg acgatccgaa ttatcataat 420

acttgtacta aatcttattt tattcaagct agtgcgtttc gtgtaatgga taatttcata 480

gatgtatctc attttccttt tgtccacgac ggtgggttag gtgatcgcaa ccacgcacaa 540

attgaagaat ttgaggtaaa agtagacaaa gatggcatta gcataggtaa ccttaaactc 600

cagatgccaa ggtttaacag cagtaacgaa gatgactcat ggactcttta ccaaaggatt 660

agtcatccct tgtgtcaata ctatattact gaatcctctg aaattcggac tgcggatttg 720

atgctggtaa caccgattga tgaagacaac agcttagtgc gaatgttagt aacgtggaac 780

cgctccgaaa tattagagtc aacggtacta gaggaatttg acgaaacaat agaacaagat 840

attccgatta tacactctca acagccagcg cgtttaccac tgttaccttc aaagcagata 900

aacatgcaat ggttgtcaca ggaaatacat gtaccgtcag atcgatgcac agttgcctat 960

cgtcgatggc taaaggaact gggcgttacc tatggtgttt gttaa 1005

<210> 23
<211> 334
<212> PRT
<213> Cylindrospermopsis raciborskii T3

<400> 23

Met Thr Thr Ala Asp Leu Ile Leu Ile Asn Asn Trp Tyr Val Val Ala
1 5 10 15

Lys Val Glu Asp Cys Lys Pro Gly Ser Ile Thr Thr Ala Leu Leu Leu
20 25 30

Gly Val Lys Leu Val Leu Trp Arg Ser Arg Glu Gln Asn Ser Pro Ile
35 40 45

Gln Ile Trp Gln Asp Tyr Cys Pro His Arg Gly Val Ala Leu Ser Met
50 55 60

Gly Glu Ile Val Asn Asn Thr Leu Val Cys Pro Tyr His Gly Trp Arg
65 70 75 80

Tyr Asn Gln Ala Gly Lys Cys Val His Ile Pro Ala His Pro Asp Met
85 90 95

Thr Pro Pro Ala Ser Ala Gln Ala Lys Ile Tyr His Cys Gln Glu Arg
100 105 110

Tyr Gly Leu Val Trp Val Cys Leu Gly Asp Pro Val Asn Asp Ile Pro
115 120 125

Ser Leu Pro Glu Trp Asp Asp Pro Asn Tyr His Asn Thr Cys Thr Lys
130 135 140

Ser Tyr Phe Ile Gln Ala Ser Ala Phe Arg Val Met Asp Asn Phe Ile
145 150 155 160

Asp Val Ser His Phe Pro Phe Val His Asp Gly Gly Leu Gly Asp Arg
165 170 175

Asn His Ala Gln Ile Glu Glu Phe Glu Val Lys Val Asp Lys Asp Gly
180 185 190

Ile Ser Ile Gly Asn Leu Lys Leu Gln Met Pro Arg Phe Asn Ser Ser
195 200 205

Asn Glu Asp Asp Ser Trp Thr Leu Tyr Gln Arg Ile Ser His Pro Leu

210 215 220

Cys Gln Tyr Tyr Ile Thr Glu Ser Ser Glu Ile Arg Thr Ala Asp Leu
225 230 235 240

Met Leu Val Thr Pro Ile Asp Glu Asp Asn Ser Leu Val Arg Met Leu
245 250 255

Val Thr Trp Asn Arg Ser Glu Ile Leu Glu Ser Thr Val Leu Glu Glu
260 265 270

Phe Asp Glu Thr Ile Glu Gln Asp Ile Pro Ile Ile His Ser Gln Gln
275 280 285

Pro Ala Arg Leu Pro Leu Leu Pro Ser Lys Gln Ile Asn Met Gln Trp
290 295 300

Leu Ser Gln Glu Ile His Val Pro Ser Asp Arg Cys Thr Val Ala Tyr
305 310 315 320

Arg Arg Trp Leu Lys Glu Leu Gly Val Thr Tyr Gly Val Cys
325 330

<210> 24
<211> 1839
<212> DNA
<213> Cylindrospermopsis raciborskii T3

<400> 24
atgcagatct taggaatttc agcttactac cacgatagtg ctgccgcgat ggttatcgat 60

ggcgaaattg ttgctgcagc tcaggaagaa cgtttctcaa gacgaaagca cgatgctggg 120

tttccgactg gagcgattac ttactgtcta aaacaagtag gaaccaagtt acaatatatc 180

gatcaaattg ttttttacga caagccatta gtcaaatttg agcggttgct agaaacatat 240

ttagcatatg ccccaaaggg atttggctcg tttattactg ctatgcccgt ttggctcaaa 300

gaaaagcttt acctaaaaac acttttaaaa aaagaattgg cgcttttggg ggagtgcaaa 360

gcttctcaat tgcctcctct actgtttacc tcacatcacc aagcccatgc ggccgctgct 420

tttttccca gtccttttca gcgtgctgcc gttctgtgct tagatggtgt aggagagtgg 480

gcaactactt ctgtctggtt gggagaagga aataaactca caccacaatg ggaaattgat 540

tttccccatt ccctcggttt gctttactca gcgtttacct actacactgg gttcaaagtt 600

aactcaggtg agtacaaact catgggttta gcaccctacg gggaacccaa atatgtggac 660

caaattctca agcatttgtt ggatctcaaa gaagatggta cttttaggtt gaatatggac 720

tacttcaact acacggtggg gctaaccatg accaatcata agttccatag tatgtttgga 780

ggaccaccac gccaggcgga aggaaaaatc tcccaaagag acatggatct ggcaagttcg 840

atccaaaagg tgactgaaga agtcatactg cgtctggcta gaactatcaa aaaagaactg 900

ggtgtagagt atctatgttt agcaggtggt gtcggtctca attgcgtggc taacggacga 960

attctccgag aaagtgattt caaagatatt tggattcaac ccgcagcagg agatgccggt 1020

agtgcagtgg gagcagcttt agcgatttgg catgaatacc ataagaaacc tcgcacttca 1080

acagcaggcg atcgcatgaa aggttcttat ctgggaccta gctttagcga ggcggagatt 1140

ctccagtttc ttaattctgt taacataccc taccatcgat gcgttgataa cgaacttatg 1200

gctcgtcttg cagaaatttt agaccaggga aatgttgtag gctggttttc tggacgaatg 1260

gagtttggtc cgcgtgcttt gggtggccgt tcgattattg gcgattcacg cagtccaaaa 1320

atgcaatcgg tcatgaacct gaaaattaaa tatcgtgagt ccttccgtcc atttgctcct 1380

tcagtcttgg ctgaacgagt ctccgactac ttcgatcttg atcgtcctag tccttatatg 1440

cttttggtag cacaagtcaa agagaatctg cacattccta tgacacaaga gcaacacgag 1500

ctatttggga tcgagaagct gaatgttcct cgttcccaaa ttcccgcagt cactcacgtt 1560

gattactcag ctcgtattca gacagttcac aaagaaacga atcctcgtta ctacgagtta 1620

attcgtcatt ttgaggcacg aactggttgt gctgtcttgg tcaatacttc gtttaatgtc 1680

cgcggcgaac caattgtttg tactcccgaa gacgcttatc gatgctttat gagaactgaa 1740

atggactatt tggttatgga gaatttcttg ttggtcaaat ctgaacagcc acggggaaat 1800

agtgatgagt catggcaaaa agaattcgag ttagattaa 1839

<210> 25
<211> 612
<212> PRT
<213> Cylindrospermopsis raciborskii T3

<400> 25

Met Gln Ile Leu Gly Ile Ser Ala Tyr Tyr His Asp Ser Ala Ala Ala
1 5 10 15

Met Val Ile Asp Gly Glu Ile Val Ala Ala Ala Gln Glu Glu Arg Phe
20 25 30

Ser Arg Arg Lys His Asp Ala Gly Phe Pro Thr Gly Ala Ile Thr Tyr
35 40 45

Cys Leu Lys Gln Val Gly Thr Lys Leu Gln Tyr Ile Asp Gln Ile Val
50 55 60

Phe Tyr Asp Lys Pro Leu Val Lys Phe Glu Arg Leu Leu Glu Thr Tyr
65 70 75 80

Leu Ala Tyr Ala Pro Lys Gly Phe Gly Ser Phe Ile Thr Ala Met Pro
85 90 95

Val Trp Leu Lys Glu Lys Leu Tyr Leu Lys Thr Leu Leu Lys Lys Glu
100 105 110

Leu Ala Leu Leu Gly Glu Cys Lys Ala Ser Gln Leu Pro Pro Leu Leu
115 120 125

Phe Thr Ser His His Gln Ala His Ala Ala Ala Ala Phe Phe Pro Ser
130 135 140

Pro Phe Gln Arg Ala Ala Val Leu Cys Leu Asp Gly Val Gly Glu Trp
145 150 155 160

Ala Thr Thr Ser Val Trp Leu Gly Glu Gly Asn Lys Leu Thr Pro Gln
165 170 175

Trp Glu Ile Asp Phe Pro His Ser Leu Gly Leu Leu Tyr Ser Ala Phe
180 185 190

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

Gly Leu Ala Pro Tyr Gly Glu Pro Lys Tyr Val Asp Gln Ile Leu Lys
210 215 220

His Leu Leu Asp Leu Lys Glu Asp Gly Thr Phe Arg Leu Asn Met Asp
225 230 235 240

Tyr Phe Asn Tyr Thr Val Gly Leu Thr Met Thr Asn His Lys Phe His
245 250 255

Ser Met Phe Gly Gly Pro Pro Arg Gln Ala Glu Gly Lys Ile Ser Gln
260 265 270

Arg Asp Met Asp Leu Ala Ser Ser Ile Gln Lys Val Thr Glu Glu Val
275 280 285

Ile Leu Arg Leu Ala Arg Thr Ile Lys Lys Glu Leu Gly Val Glu Tyr
290 295 300

Leu Cys Leu Ala Gly Gly Val Gly Leu Asn Cys Val Ala Asn Gly Arg
305 310 315 320

Ile Leu Arg Glu Ser Asp Phe Lys Asp Ile Trp Ile Gln Pro Ala Ala
325 330 335

Gly Asp Ala Gly Ser Ala Val Gly Ala Ala Leu Ala Ile Trp His Glu
340 345 350

Tyr His Lys Lys Pro Arg Thr Ser Thr Ala Gly Asp Arg Met Lys Gly
355 360 365

Ser Tyr Leu Gly Pro Ser Phe Ser Glu Ala Glu Ile Leu Gln Phe Leu

370 375 380

Asn Ser Val Asn Ile Pro Tyr His Arg Cys Val Asp Asn Glu Leu Met
385 390 395 400

Ala Arg Leu Ala Glu Ile Leu Asp Gln Gly Asn Val Val Gly Trp Phe
405 410 415

Ser Gly Arg Met Glu Phe Gly Pro Arg Ala Leu Gly Gly Arg Ser Ile
420 425 430

Ile Gly Asp Ser Arg Ser Pro Lys Met Gln Ser Val Met Asn Leu Lys
435 440 445

Ile Lys Tyr Arg Glu Ser Phe Arg Pro Phe Ala Pro Ser Val Leu Ala
450 455 460

Glu Arg Val Ser Asp Tyr Phe Asp Leu Asp Arg Pro Ser Pro Tyr Met
465 470 475 480

Leu Leu Val Ala Gln Val Lys Glu Asn Leu His Ile Pro Met Thr Gln
485 490 495

Glu Gln His Glu Leu Phe Gly Ile Glu Lys Leu Asn Val Pro Arg Ser
500 505 510

Gln Ile Pro Ala Val Thr His Val Asp Tyr Ser Ala Arg Ile Gln Thr
515 520 525

Val His Lys Glu Thr Asn Pro Arg Tyr Tyr Glu Leu Ile Arg His Phe
530 535 540

Glu Ala Arg Thr Gly Cys Ala Val Leu Val Asn Thr Ser Phe Asn Val
545 550 555 560

Arg Gly Glu Pro Ile Val Cys Thr Pro Glu Asp Ala Tyr Arg Cys Phe
565 570 575

Met Arg Thr Glu Met Asp Tyr Leu Val Met Glu Asn Phe Leu Leu Val
580 585 590

Lys Ser Glu Gln Pro Arg Gly Asn Ser Asp Glu Ser Trp Gln Lys Glu
595 600 605

Phe Glu Leu Asp
610

<210> 26
<211> 444
<212> DNA
<213> Cylindrospermopsis raciborskii T3

<400> 26
atgagtgaat ttttcccaca aaaaagtggt aaattaaaga tggaacagat aaaagaactt 60

gacaaaaaag gattgcgtga gtttggactg attggcggtt ctatagtggc ggttttattc 120

ggctttttac tgccagttat acgccatcat tccttatcag ttatcccttg ggttgttgct 180

ggatttctct ggatttgggc aataatcgca cctacgactt taagttttat ttaccaaata 240

tggatgagga ttggacttgt tttaggatgg atacaaacac gaattatttt gggagtttta 300

ttttatataa tgatcacacc aataggattc ataagacggc tgttgaatca agatccaatg 360

acgcgaatct tcgagccaga gttgccaact tatcgccaat tgagtaagtc aagaactaca 420

caaagtatgg agaaaccatt ctaa 444

<210> 27
<211> 147
<212> PRT
<213> Cylindrospermopsis raciborskii T3

<400> 27

Met Ser Glu Phe Phe Pro Gln Lys Ser Gly Lys Leu Lys Met Glu Gln
1 5 10 15

Ile Lys Glu Leu Asp Lys Lys Gly Leu Arg Glu Phe Gly Leu Ile Gly
20 25 30

Gly Ser Ile Val Ala Val Leu Phe Gly Phe Leu Leu Pro Val Ile Arg
35 40 45

His His Ser Leu Ser Val Ile Pro Trp Val Val Ala Gly Phe Leu Trp
50 55 60

Ile Trp Ala Ile Ile Ala Pro Thr Thr Leu Ser Phe Ile Tyr Gln Ile
65 70 75 80

Trp Met Arg Ile Gly Leu Val Leu Gly Trp Ile Gln Thr Arg Ile Ile
85 90 95

Leu Gly Val Leu Phe Tyr Ile Met Ile Thr Pro Ile Gly Phe Ile Arg
100 105 110

Arg Leu Leu Asn Gln Asp Pro Met Thr Arg Ile Phe Glu Pro Glu Leu
115 120 125

Pro Thr Tyr Arg Gln Leu Ser Lys Ser Arg Thr Thr Gln Ser Met Glu
130 135 140

Lys Pro Phe
145

<210> 28
<211> 165
<212> DNA
<213> Cylindrospermopsis raciborskii T3

<400> 28
atgctaaaag acacttggga ttttattaaa gacattgccg gatttattaa agaacaaaaa 60

aactatttgt tgattcccct aattatcacc ctggtatcct tgggggcgct gattgtcttt 120

gctcaatctt ctgcgatcgc acctttcatt tacactcttt tttaa 165

<210> 29
<211> 54
<212> PRT
<213> Cylindrospermopsis raciborskii T3

<400> 29

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

Lys Glu Gln Lys Asn Tyr Leu Leu Ile Pro Leu Ile Ile Thr Leu Val
20 25 30

Ser Leu Gly Ala Leu Ile Val Phe Ala Gln Ser Ser Ala Ile Ala Pro
35 40 45

Phe Ile Tyr Thr Leu Phe
50

<210> 30
<211> 1299
<212> DNA
<213> Cylindrospermopsis raciborskii T3

<400> 30
atgagtaact tcaagggttc ggtaaagata gcattgatgg gaatattgat tttttgtggg 60

ctaatctttg gcgtagcatt tgttgaaatt gggttacgta ttgccgggat cgaacacata 120

gcattccata gcattgatga acacaggggg tgggtagggc gacctcatgt ttccgggtgg 180

tatagaaccg aaggtgaagc tcacatccaa atgaatagtg atggctttcg agatcgagaa 240

cacatcaagg tcaaaccaga aaataccttc aggatagcgc tgttgggaga ttcctttgta 300

gagtccatgc aagtaccgtt ggagcaaaat ttggcagcag ttatagaagg agaaatcagt 360

agttgtatag ctttagctgg acgaaaggcg gaagtgatta attttggagt gactggttat 420

ggaacagacc aagaactaat tactctacgg gagaaagttt gggactattc acctgatata 480

gtagtgctag atttttatac tggcaacgac attgttgata actcccgtgc gctgagtcag 540

aaattctatc ctaatgaact aggttcacta aagccgtttt ttatacttag agatggtaat 600

ctggtggttg atgcttcgtt tatcaatacg gataattatc gctcaaagct gacatggtgg 660

ggcaaaactt atatgaaaat aaaagaccac tcacggattt tacaggtttt aaacatggta 720

cgggatgctc ttaacaactc tagtagaggg ttttcttctc aagctataga ggaaccgtta 780

tttagtgatg gaaaacagga tacaaaattg agcgggtttt ttgatatcta caaaccacct 840

actgaccctg aatggcaaca ggcatggcaa gtcacagaga aactgattag ctcaatgcaa 900

cacgaggtga ctgcgaagaa agcagatttt ttagttgtta cttttggcgg tccctttcaa 960

cgagaacctt tagtgcgtca aaaagaaatg caagaattgg gtctgactga ttggttttac 1020

ccagagaagc gaattacacg tttgggtgag gatgaggggt tcagtgtact caatctcagc 1080

ccaaatttgc aggtttattc tgagcagaac aatgcttgcc tatatgggtt tgatgatact 1140

caaggctgtg tagggcattg gaatgcttta ggacatcagg tagcaggaaa aatgattgca 1200

tcgaagattt gtcaacagca gatgagagaa agtatattgc ctcataagca cgacccttca 1260

agccaaagct cacctattac ccaatcagtg atccaataa 1299

<210> 31
<211> 432
<212> PRT
<213> Cylindrospermopsis raciborskii T3

<400> 31

Met Ser Asn Phe Lys Gly Ser Val Lys Ile Ala Leu Met Gly Ile Leu
1 5 10 15

Ile Phe Cys Gly Leu Ile Phe Gly Val Ala Phe Val Glu Ile Gly Leu
20 25 30

Arg Ile Ala Gly Ile Glu His Ile Ala Phe His Ser Ile Asp Glu His
35 40 45

Arg Gly Trp Val Gly Arg Pro His Val Ser Gly Trp Tyr Arg Thr Glu
50 55 60

Gly Glu Ala His Ile Gln Met Asn Ser Asp Gly Phe Arg Asp Arg Glu
65 70 75 80

His Ile Lys Val Lys Pro Glu Asn Thr Phe Arg Ile Ala Leu Leu Gly
85 90 95

Asp Ser Phe Val Glu Ser Met Gln Val Pro Leu Glu Gln Asn Leu Ala
100 105 110

Ala Val Ile Glu Gly Glu Ile Ser Ser Cys Ile Ala Leu Ala Gly Arg
115 120 125

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

Glu Leu Ile Thr Leu Arg Glu Lys Val Trp Asp Tyr Ser Pro Asp Ile
145 150 155 160

Val Val Leu Asp Phe Tyr Thr Gly Asn Asp Ile Val Asp Asn Ser Arg
165 170 175

Ala Leu Ser Gln Lys Phe Tyr Pro Asn Glu Leu Gly Ser Leu Lys Pro
180 185 190

Phe Phe Ile Leu Arg Asp Gly Asn Leu Val Val Asp Ala Ser Phe Ile
195 200 205

Asn Thr Asp Asn Tyr Arg Ser Lys Leu Thr Trp Trp Gly Lys Thr Tyr
210 215 220

Met Lys Ile Lys Asp His Ser Arg Ile Leu Gln Val Leu Asn Met Val
225 230 235 240

Arg Asp Ala Leu Asn Asn Ser Ser Arg Gly Phe Ser Ser Gln Ala Ile
245 250 255

Glu Glu Pro Leu Phe Ser Asp Gly Lys Gln Asp Thr Lys Leu Ser Gly
260 265 270

Phe Phe Asp Ile Tyr Lys Pro Pro Thr Asp Pro Glu Trp Gln Gln Ala
275 280 285

Trp Gln Val Thr Glu Lys Leu Ile Ser Ser Met Gln His Glu Val Thr

290 295 300

Ala Lys Lys Ala Asp Phe Leu Val Val Thr Phe Gly Gly Pro Phe Gln
305 310 315 320

Arg Glu Pro Leu Val Arg Gln Lys Glu Met Gln Glu Leu Gly Leu Thr
325 330 335

Asp Trp Phe Tyr Pro Glu Lys Arg Ile Thr Arg Leu Gly Glu Asp Glu
340 345 350

Gly Phe Ser Val Leu Asn Leu Ser Pro Asn Leu Gln Val Tyr Ser Glu
355 360 365

Gln Asn Asn Ala Cys Leu Tyr Gly Phe Asp Asp Thr Gln Gly Cys Val
370 375 380

Gly His Trp Asn Ala Leu Gly His Gln Val Ala Gly Lys Met Ile Ala
385 390 395 400

Ser Lys Ile Cys Gln Gln Gln Met Arg Glu Ser Ile Leu Pro His Lys
405 410 415

His Asp Pro Ser Ser Gln Ser Ser Pro Ile Thr Gln Ser Val Ile Gln
420 425 430

<210> 32
<211> 1449
<212> DNA
<213> Cylindrospermopsis raciborskii T3

<400> 32
atgacaaata ccgaaagagg attagcagaa ataacatcaa caggatataa gtcagagctt 60

agatcggagg cacgagttag cctccaactg gcaattccct tagtccttgt cgaaatatgc 120

ggaacgagta ttaatgtggt ggatgtagtc atgatgggct tacttggtac tcaagttttg 180

gctgctggtg ccttgggtgc gatcgctttt ttatctgtat cgaatacttg ttataatatg 240

cttttgtcgg gggtagcaaa ggcatctgag gcttttgggg caaacaaaat agatcaggtt 300

agtcgtattg cttctgggca aatatggctg gcactcacct tgtctttgcc tgcaatgctt 360

ttgctttggt atatggatac tatattggtg ctatttggtc aagttgaaag caacacatta 420

attgcaaaaa cgtatttaca ctcaattgtg tggggatttc cggcggcagt tggtattttg 480

atattaagag gcattgcctc tgctgtgaac gtcccccaat tggtaactgt gacgatgcta 540

gtagggctgg tcttgaatgc cccggccaat tatgtattaa tgttcggtaa atttggtctt 600

cctgaacttg gtttagctgg aataggctgg gcaagtactt tggttttttg gattagtttt 660

ctagtggggg ttgtcttgct gattttctcc ccaaaagtta gagattataa acttttccgc 720

tacttgcatc agtttgatcg acagacggtt gtggaaattt ttcaaactgg atggcctatg 780

ggttttctac tgggagtgga atcagtagta ttgagcctca ccgcttggtt aacaggctat 840

ttgggaacag taacattagc agctcatgag atcgcgatcc aaacagcaga actggcgata 900

gtgataccac tcggaatcgg gaatgttgcc gtcacgagag taggtcagac tataggagaa 960

aaaaaccctt tgggtgctag aagggcagca ttgattggga ttatgattgg tggcatttat 1020

gccagtcttg tggcagtcat tttctggttg tttccatatc agattgcggg actttattta 1080

aaaataaacg atccagagag tatggaagca gttaagacag caactaattt tctcttcttg 1140

gcgggattat tccaattttt tcatagcgtt caaataattg ttgttggggt tttaataggg 1200

ttgcaggata cgtttatccc attgttaatg aatttggtag gctggggtct tggcttggca 1260

gtaagctatt acatgggaat cattttatgt tggggaggta tgggtatctg gttaggtctg 1320

gttttgagtc cactcctgtc cggacttatt ttaatggttc gtttttatca agagattgcc 1380

aataggattg ccaatagtga tgatgggcaa gagagtatat ctattgacaa cgttgaagaa 1440

ctctcctga 1449

<210> 33
<211> 482
<212> PRT
<213> Cylindrospermopsis raciborskii T3

<400> 33

Met Thr Asn Thr Glu Arg Gly Leu Ala Glu Ile Thr Ser Thr Gly Tyr

1 5 10 15

Lys Ser Glu Leu Arg Ser Glu Ala Arg Val Ser Leu Gln Leu Ala Ile
20 25 30

Pro Leu Val Leu Val Glu Ile Cys Gly Thr Ser Ile Asn Val Val Asp
35 40 45

Val Val Met Met Gly Leu Leu Gly Thr Gln Val Leu Ala Ala Gly Ala
50 55 60

Leu Gly Ala Ile Ala Phe Leu Ser Val Ser Asn Thr Cys Tyr Asn Met
65 70 75 80

Leu Leu Ser Gly Val Ala Lys Ala Ser Glu Ala Phe Gly Ala Asn Lys
85 90 95

Ile Asp Gln Val Ser Arg Ile Ala Ser Gly Gln Ile Trp Leu Ala Leu
100 105 110

Thr Leu Ser Leu Pro Ala Met Leu Leu Leu Trp Tyr Met Asp Thr Ile
115 120 125

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

Tyr Leu His Ser Ile Val Trp Gly Phe Pro Ala Ala Val Gly Ile Leu
145 150 155 160

Ile Leu Arg Gly Ile Ala Ser Ala Val Asn Val Pro Gln Leu Val Thr
165 170 175

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

Leu Met Phe Gly Lys Phe Gly Leu Pro Glu Leu Gly Leu Ala Gly Ile
195 200 205

Gly Trp Ala Ser Thr Leu Val Phe Trp Ile Ser Phe Leu Val Gly Val
210 215 220

Val Leu Leu Ile Phe Ser Pro Lys Val Arg Asp Tyr Lys Leu Phe Arg
225 230 235 240

Tyr Leu His Gln Phe Asp Arg Gln Thr Val Val Glu Ile Phe Gln Thr
245 250 255

Gly Trp Pro Met Gly Phe Leu Leu Gly Val Glu Ser Val Val Leu Ser
260 265 270

Leu Thr Ala Trp Leu Thr Gly Tyr Leu Gly Thr Val Thr Leu Ala Ala
275 280 285

His Glu Ile Ala Ile Gln Thr Ala Glu Leu Ala Ile Val Ile Pro Leu
290 295 300

Gly Ile Gly Asn Val Ala Val Thr Arg Val Gly Gln Thr Ile Gly Glu
305 310 315 320

Lys Asn Pro Leu Gly Ala Arg Arg Ala Ala Leu Ile Gly Ile Met Ile
325 330 335

Gly Gly Ile Tyr Ala Ser Leu Val Ala Val Ile Phe Trp Leu Phe Pro
340 345 350

Tyr Gln Ile Ala Gly Leu Tyr Leu Lys Ile Asn Asp Pro Glu Ser Met
355 360 365

Glu Ala Val Lys Thr Ala Thr Asn Phe Leu Phe Leu Ala Gly Leu Phe
370 375 380

Gln Phe Phe His Ser Val Gln Ile Ile Val Val Gly Val Leu Ile Gly
385 390 395 400

Leu Gln Asp Thr Phe Ile Pro Leu Leu Met Asn Leu Val Gly Trp Gly

405 410 415

Leu Gly Leu Ala Val Ser Tyr Tyr Met Gly Ile Ile Leu Cys Trp Gly
420 425 430

Gly Met Gly Ile Trp Leu Gly Leu Val Leu Ser Pro Leu Leu Ser Gly
435 440 445

Leu Ile Leu Met Val Arg Phe Tyr Gln Glu Ile Ala Asn Arg Ile Ala
450 455 460

Asn Ser Asp Asp Gly Gln Glu Ser Ile Ser Ile Asp Asn Val Glu Glu
465 470 475 480

Leu Ser

<210> 34
<211> 831
<212> DNA
<213> Cylindrospermopsis raciborskii T3

<400> 34
atgaaaacaa acaaacatat agctatgtgg gcttgtccta gaagtcgttc tactgtaatt 60

acccgtgctt ttgagaactt agatgggtgt gttgtttatg atgagcctct agaggctccg 120

aatgtcttga tgacaactta cacgatgagt aacagtcgta cgttagcaga agaagactta 180

aagcaattaa tactgcaaaa taatgtagaa acagacctca agaaagttat agaacaattg 240

actggagatt taccggacgg aaaattattc tcatttcaaa aaatgataac aggtgactat 300

agatctgaat ttggaataga ttgggcaaaa aagctaacta acttcttttt aataaggcat 360

ccccaagata ttatttttc tttcgatata gcggagagaa agacaggtat cacagaacca 420

ttcacacaac aaaatcttgg catgaaaaca ctttatgaag ttttccaaca aattgaagtt 480

attacagggc aaacaccttt agttattcac tcagatgata taattaaaaa ccctccttct 540

gctttgaaat ggctgtgtaa aaacttaggg cttgcatttg atgaaaagat gctgacatgg 600

aaagcaaatc tagaagactc caatttaaag tatacaaaat tatatgctaa ttctgcgtct 660

ggcagttcag aaccttggtt tgaaacttta agatcgacca aaacatttct cgcctatgaa 720

aagaaggaga aaaaattacc agctcggtta atacctctac tagatgaatc tattccttac 780

tatgaaaaac tcttacagca ttgtcatatt tttgaatggt cagaacactg a 831

<210> 35
<211> 276
<212> PRT
<213> Cylindrospermopsis raciborskii T3

<400> 35

Met Lys Thr Asn Lys His Ile Ala Met Trp Ala Cys Pro Arg Ser Arg
1 5 10 15

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

Tyr Asp Glu Pro Leu Glu Ala Pro Asn Val Leu Met Thr Thr Tyr Thr
35 40 45

Met Ser Asn Ser Arg Thr Leu Ala Glu Glu Asp Leu Lys Gln Leu Ile
50 55 60

Leu Gln Asn Asn Val Glu Thr Asp Leu Lys Lys Val Ile Glu Gln Leu
65 70 75 80

Thr Gly Asp Leu Pro Asp Gly Lys Leu Phe Ser Phe Gln Lys Met Ile
85 90 95

Thr Gly Asp Tyr Arg Ser Glu Phe Gly Ile Asp Trp Ala Lys Lys Leu
100 105 110

Thr Asn Phe Phe Leu Ile Arg His Pro Gln Asp Ile Ile Phe Ser Phe
115 120 125

Asp Ile Ala Glu Arg Lys Thr Gly Ile Thr Glu Pro Phe Thr Gln Gln
130 135 140

Asn Leu Gly Met Lys Thr Leu Tyr Glu Val Phe Gln Gln Ile Glu Val
145 150 155 160

Ile Thr Gly Gln Thr Pro Leu Val Ile His Ser Asp Asp Ile Ile Lys
165 170 175

Asn Pro Pro Ser Ala Leu Lys Trp Leu Cys Lys Asn Leu Gly Leu Ala
180 185 190

Phe Asp Glu Lys Met Leu Thr Trp Lys Ala Asn Leu Glu Asp Ser Asn
195 200 205

Leu Lys Tyr Thr Lys Leu Tyr Ala Asn Ser Ala Ser Gly Ser Ser Glu
210 215 220

Pro Trp Phe Glu Thr Leu Arg Ser Thr Lys Thr Phe Leu Ala Tyr Glu
225 230 235 240

Lys Lys Glu Lys Lys Leu Pro Ala Arg Leu Ile Pro Leu Leu Asp Glu
245 250 255

Ser Ile Pro Tyr Tyr Glu Lys Leu Leu Gln His Cys His Ile Phe Glu
260 265 270

Trp Ser Glu His
275

<210> 36
<211> 774
<212> DNA
<213> Cylindrospermopsis raciborskii T3

<400> 36
ctaaaaattt ttttctactc ttttcaggat agaattccag tttctagagc cgttgtaacc 60

gtacatatct tgatagtacg tatcgatgag gtactcattt tcgtggagca ttaaccagct 120

ttttaactcc gctaatttct gctctccttt ttctattaat tcttgctcat ccaaatcatc 180

cctgtccaac tcctccctgt ccaactccca catagttttg ttggtatctt cgacaatcaa 240

gtagtctcca ctttttagac cgttttcgtg aaaatattca actactccca ccgcattagc 300

atgggcatct tctacgatca accagggatg agcaagccca gaaagcagtt ccgacgacat 360

tattgcaccc atattgttac aatccccctc taaaaaatga acgcgagagt cagtttttgc 420

tttctcgtcg agtagggaaa gatcgatatc gatacagtag acacaacctt ctatttggaa 480

cagttctaag tgatcggcta gccaaatcgc gctgccaccg cttaatgctc ctatttcgat 540

tattgttttc gggcgaagct catacaggag cattgaataa agagctattt cggtgcaccc 600

tttcaggaag ggtatccctt tccaagtgaa caaatcgcgg tttgccaaga gcgctctcca 660

agctggcact ggaatagcac atttatcttc tctttcagaa attttggcaa accgattagg 720

tttgaaaggt gcaactttat aggcggcttc ttgaacaaat ttttggaagc tcat 774

<210> 37
<211> 257
<212> PRT
<213> Cylindrospermopsis raciborskii T3

<400> 37

Met Ser Phe Gln Lys Phe Val Gln Glu Ala Ala Tyr Lys Val Ala Pro
1 5 10 15

Phe Lys Pro Asn Arg Phe Ala Lys Ile Ser Glu Arg Glu Asp Lys Cys
20 25 30

Ala Ile Pro Val Pro Ala Trp Arg Ala Leu Leu Ala Asn Arg Asp Leu
35 40 45

Phe Thr Trp Lys Gly Ile Pro Phe Leu Lys Gly Cys Thr Glu Ile Ala
50 55 60

Leu Tyr Ser Met Leu Leu Tyr Glu Leu Arg Pro Lys Thr Ile Ile Glu
65 70 75 80

Ile Gly Ala Leu Ser Gly Gly Ser Ala Ile Trp Leu Ala Asp His Leu
85 90 95

Glu Leu Phe Gln Ile Glu Gly Cys Val Tyr Cys Ile Asp Ile Asp Leu
100 105 110

Ser Leu Leu Asp Glu Lys Ala Lys Thr Asp Ser Arg Val His Phe Leu
115 120 125

Glu Gly Asp Cys Asn Asn Met Gly Ala Ile Met Ser Ser Glu Leu Leu
130 135 140

Ser Gly Leu Ala His Pro Trp Leu Ile Val Glu Asp Ala His Ala Asn
145 150 155 160

Ala Val Gly Val Val Glu Tyr Phe His Glu Asn Gly Leu Lys Ser Gly
165 170 175

Asp Tyr Leu Ile Val Glu Asp Thr Asn Lys Thr Met Trp Glu Leu Asp
180 185 190

Arg Glu Glu Leu Asp Arg Asp Asp Leu Asp Glu Gln Glu Leu Ile Glu
195 200 205

Lys Gly Glu Gln Lys Leu Ala Glu Leu Lys Ser Trp Leu Met Leu His
210 215 220

Glu Asn Glu Tyr Leu Ile Asp Thr Tyr Tyr Gln Asp Met Tyr Gly Tyr
225 230 235 240

Asn Gly Ser Arg Asn Trp Asn Ser Ile Leu Lys Arg Val Glu Lys Asn
245 250 255

Phe

<210> 38
<211> 327
<212> DNA
<213> Cylindrospermopsis raciborskii T3

<400> 38
ttattcaaat agccgtagtt tatgatcggt atccaattcg ctattgtttt ttctgccata 60

tccccaacct aagatgcgac gatattcacc cataatgcca ctgtcaatta aatcatcctc 120

gttgactgca acattggtat gagattgcgg cgcaacatag agcgcatccg caggacaata 180

tgcttcacag atgaaacaag tttgacagtc ttcctgtcgg gcgatcgcag gcggttggtt 240

gggaactgca tcaaagacat tggtagggca tacttggacg caaacattac aattaataca 300

gagtttatgg ctgacaagct cgatcat 327

<210> 39
<211> 108
<212> PRT
<213> Cylindrospermopsis raciborskii T3

<400> 39

Met Ile Glu Leu Val Ser His Lys Leu Cys Ile Asn Cys Asn Val Cys
1 5 10 15

Val Gln Val Cys Pro Thr Asn Val Phe Asp Ala Val Pro Asn Gln Pro
20 25 30

Pro Ala Ile Ala Arg Gln Glu Asp Cys Gln Thr Cys Phe Ile Cys Glu
35 40 45

Ala Tyr Cys Pro Ala Asp Ala Leu Tyr Val Ala Pro Gln Ser His Thr
50 55 60

Asn Val Ala Val Asn Glu Asp Asp Leu Ile Asp Ser Gly Ile Met Gly
65 70 75 80

Glu Tyr Arg Arg Ile Leu Gly Trp Gly Tyr Gly Arg Lys Asn Asn Ser
85 90 95

Glu Leu Asp Thr Asp His Lys Leu Arg Leu Phe Glu
100 105

<210> 40

<211> 1653
<212> DNA
<213> Cylindrospermopsis raciborskii T3

<400> 40
ttaagtggtt aatactggtg gtgtagcgct cgcatccttc acccaatccc gtctcaccca 60

aagcctttct aagccgcccg tggcttggta ataaagctga tttggatcgg tttcaggata 120

gtctatgcga atatgttcgc tacgcgtttc cttgcgatgt aaagcgctaa aatatgccca 180

tcgtgctaca gacacaagag cagccgctcg acgagaaaat tccagatcgc gcactgtatc 240

ttgtttcggg ttcccttgta cttgctgcca cagcatttct aatttggcga gggaatccaa 300

aagtccctgc tcacagcgca agtaattctt ctctaatggg aacatctcgg cttgtacacc 360

gcggacaact gcctcgctat cgaatgtttc ggaaccaggg tactgggaac gtaatccggc 420

ttgacctgct ggacgcacaa cccgttcatg gacatgagcg cccaaactct tggcaaaggc 480

ggctgcacct tcccctgccc attgtcctgt agagattgcc caagcagcat taggaccatc 540

acccccagaa gctatcccag ctaaaaactc ccgcgatgct gcatctccgg cggcatacag 600

tccaggaact tttgtaccac aactatcatt cacaatccga attccacctg taccacggac 660

tgtaccttct aaaaccagtg ttacaggtac tcgttctgta taagggtcaa tgccagcttt 720

tttatagggt agaaaggcga tgaagtgaga cttttcaacc aatgcttgga tttcaggtgt 780

ggctcgatcc aaacgagcat aaacgggacc tttcaggagg gcattgggca ggaacgatgg 840

atcgcgacga ccattgatat agccaccaag atcgttacct gcctcatcgg tgtaactagc 900

ccagtaaaag ggagcagccc ttgtcactgt ggcattgaaa gcggtcgaga tggtatagtg 960

actggaagct tccatactgg agagttcgcc gccagcttcc accgccatca gcagtccatc 1020

gcctgtattg gtattgcaac ctaaagcttt acttaggaat gcacaaccgc cattcgctag 1080

aactactgca ccagcgcgaa cggtataggt gcgatgattt tgcctctgta cacctctagc 1140

tccagccacg gagccgtcct gggctaataa cagttctaga gccggacttt ggtcgaaaat 1200

ttgcacaccc acacgcaaca ggttcttgcg aagtacccgc atatattccg gaccataata 1260

actctggcgc acggattccc cattttcttt ggggaaacga tagccccaat cttccactaa 1320

gggcaaactc agccaagctt tttcaattac acgttcaatc caacgtaagt tagcgaggtt 1380

atttcctttg ctgtaacatt cggatacatc tttctcccaa ttctctggag aaggtgccat 1440

gacgctattg ccactggcag cagctgcacc gctcgtacct agaaaacctt tatcaacaat 1500

gatgactttg acaccttggg ctccagccgc ccatgctgcc catgcggcgg caggaccacc 1560

accaattacc agcacgtcag cagttaattg tagttcagtg ccgctatagg ctgtaagcaa 1620

ttgcttttcc tccttgttta aagtcaagtt cat 1653

<210> 41
<211> 550
<212> PRT
<213> Cylindrospermopsis raciborskii T3

<400> 41

Met Asn Leu Thr Leu Asn Lys Glu Glu Lys Gln Leu Leu Thr Ala Tyr
1 5 10 15

Ser Gly Thr Glu Leu Gln Leu Thr Ala Asp Val Leu Val Ile Gly Gly
20 25 30

Gly Pro Ala Ala Ala Trp Ala Ala Trp Ala Ala Gly Ala Gln Gly Val
35 40 45

Lys Val Ile Ile Val Asp Lys Gly Phe Leu Gly Thr Ser Gly Ala Ala
50 55 60

Ala Ala Ser Gly Asn Ser Val Met Ala Pro Ser Pro Glu Asn Trp Glu
65 70 75 80

Lys Asp Val Ser Glu Cys Tyr Ser Lys Gly Asn Asn Leu Ala Asn Leu
85 90 95

Arg Trp Ile Glu Arg Val Ile Glu Lys Ala Trp Leu Ser Leu Pro Leu
100 105 110

Val Glu Asp Trp Gly Tyr Arg Phe Pro Lys Glu Asn Gly Glu Ser Val
115 120 125

Arg Gln Ser Tyr Tyr Gly Pro Glu Tyr Met Arg Val Leu Arg Lys Asn
130 135 140

Leu Leu Arg Val Gly Val Gln Ile Phe Asp Gln Ser Pro Ala Leu Glu
145 150 155 160

Leu Leu Leu Ala Gln Asp Gly Ser Val Ala Gly Ala Arg Gly Val Gln
165 170 175

Arg Gln Asn His Arg Thr Tyr Thr Val Arg Ala Gly Ala Val Val Leu
180 185 190

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

Asn Thr Gly Asp Gly Leu Leu Met Ala Val Glu Ala Gly Gly Glu Leu
210 215 220

Ser Ser Met Glu Ala Ser Ser His Tyr Thr Ile Ser Thr Ala Phe Asn
225 230 235 240

Ala Thr Val Thr Arg Ala Ala Pro Phe Tyr Trp Ala Ser Tyr Thr Asp
245 250 255

Glu Ala Gly Asn Asp Leu Gly Gly Tyr Ile Asn Gly Arg Arg Asp Pro
260 265 270

Ser Phe Leu Pro Asn Ala Leu Leu Lys Gly Pro Val Tyr Ala Arg Leu
275 280 285

Asp Arg Ala Thr Pro Glu Ile Gln Ala Leu Val Glu Lys Ser His Phe
290 295 300

Ile Ala Phe Leu Pro Tyr Lys Lys Ala Gly Ile Asp Pro Tyr Thr Glu
305 310 315 320

Arg Val Pro Val Thr Leu Val Leu Glu Gly Thr Val Arg Gly Thr Gly

325 330 335

Gly Ile Arg Ile Val Asn Asp Ser Cys Gly Thr Lys Val Pro Gly Leu
340 345 350

Tyr Ala Ala Gly Asp Ala Ala Ser Arg Glu Phe Leu Ala Gly Ile Ala
355 360 365

Ser Gly Gly Asp Gly Pro Asn Ala Ala Trp Ala Ile Ser Thr Gly Gln
370 375 380

Trp Ala Gly Glu Gly Ala Ala Ala Phe Ala Lys Ser Leu Gly Ala His
385 390 395 400

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

Gln Tyr Pro Gly Ser Glu Thr Phe Asp Ser Glu Ala Val Val Arg Gly
420 425 430

Val Gln Ala Glu Met Phe Pro Leu Glu Lys Asn Tyr Leu Arg Cys Glu
435 440 445

Gln Gly Leu Leu Asp Ser Leu Ala Lys Leu Glu Met Leu Trp Gln Gln
450 455 460

Val Gln Gly Asn Pro Lys Gln Asp Thr Val Arg Asp Leu Glu Phe Ser
465 470 475 480

Arg Arg Ala Ala Ala Leu Val Ser Val Ala Arg Trp Ala Tyr Phe Ser
485 490 495

Ala Leu His Arg Lys Glu Thr Arg Ser Glu His Ile Arg Ile Asp Tyr
500 505 510

Pro Glu Thr Asp Pro Asn Gln Leu Tyr Tyr Gln Ala Thr Gly Gly Leu
515 520 525

Glu Arg Leu Trp Val Arg Arg Asp Trp Val Lys Asp Ala Ser Ala Thr
530 535 540

Pro Pro Val Leu Thr Thr
545 550

<210> 42
<211> 750
<212> DNA
<213> Cylindrospermopsis raciborskii T3

<400> 42
ttaattatct tctgcagtcg gtcgaatcaa aatttcattt acatttacat gatcgggttg 60

tgtcactgca taaattatag ctcttgcaat atcctcactt tgtaaaggtg ttattgtact 120

aagttgttct ttactaagct gtttcgtgat cgggtcagaa attaagtcat taaatggcgt 180

atcgactaaa cctggctcaa tgatggtaac gcgaatgttg tctaaagata cctcctggcg 240

taatgcttct gaaagagcat tgacgcctga tttggcagca ctataaacga ccgcaccgga 300

ctgcgctatc ctgccatcga cagaagatat attgactata tgaccggatt tttgggcctt 360

cagaagaggc aaaactgcgt ggatagcata taaaactccc agaacattca catcgaatgc 420

tcgcctccag tctgcgggat ttccagtatc aattgcacca aacacaccaa ttcctgcatt 480

attcaccaaa atatctacat gtcctagctc aaccttggtc ttttggacta gatgatttac 540

ttgagattcg tctgtaatat ctgtaacaat aggcaatgct tgaccaccac tggcttcaat 600

ccgttttgct agtgcatgca aaagctcagc acgtcttgcg gcgatcgcaa cttttgcccc 660

ctccgcagct aaagcaaatg ctgtagcctc tccaatccca gaggaagctc cagtaataat 720

cgccactttt ccatccaatt tacctgccat 750

<210> 43
<211> 249
<212> PRT
<213> Cylindrospermopsis raciborskii T3

<400> 43

Met Ala Gly Lys Leu Asp Gly Lys Val Ala Ile Ile Thr Gly Ala Ser

1 5 10 15

Ser Gly Ile Gly Glu Ala Thr Ala Phe Ala Leu Ala Ala Glu Gly Ala
20 25 30

Lys Val Ala Ile Ala Ala Arg Arg Ala Glu Leu Leu His Ala Leu Ala
35 40 45

Lys Arg Ile Glu Ala Ser Gly Gly Gln Ala Leu Pro Ile Val Thr Asp
50 55 60

Ile Thr Asp Glu Ser Gln Val Asn His Leu Val Gln Lys Thr Lys Val
65 70 75 80

Glu Leu Gly His Val Asp Ile Leu Val Asn Asn Ala Gly Ile Gly Val
85 90 95

Phe Gly Ala Ile Asp Thr Gly Asn Pro Ala Asp Trp Arg Arg Ala Phe
100 105 110

Asp Val Asn Val Leu Gly Val Leu Tyr Ala Ile His Ala Val Leu Pro
115 120 125

Leu Leu Lys Ala Gln Lys Ser Gly His Ile Val Asn Ile Ser Ser Val
130 135 140

Asp Gly Arg Ile Ala Gln Ser Gly Ala Val Val Tyr Ser Ala Ala Lys
145 150 155 160

Ser Gly Val Asn Ala Leu Ser Glu Ala Leu Arg Gln Glu Val Ser Leu
165 170 175

Asp Asn Ile Arg Val Thr Ile Ile Glu Pro Gly Leu Val Asp Thr Pro
180 185 190

Phe Asn Asp Leu Ile Ser Asp Pro Ile Thr Lys Gln Leu Ser Lys Glu
195 200 205

Gln Leu Ser Thr Ile Thr Pro Leu Gln Ser Glu Asp Ile Ala Arg Ala
210 215 220

Ile Ile Tyr Ala Val Thr Gln Pro Asp His Val Asn Val Asn Glu Ile
225 230 235 240

Leu Ile Arg Pro Thr Ala Glu Asp Asn
245

<210> 44
<211> 1005
<212> DNA
<213> Cylindrospermopsis raciborskii T3

<400> 44
ttaacaaacc ccataagtaa cacctagttg ctttagccat cgacgatagg caagtgtgca 60

tctatctgat ggtacgtgga tttcgtgtga aaacaattgt gtatttatct gctttggagt 120

taacagtggt aaacgtaccg gctgttgtgc atgtaagatc cgaatatctt gttctattgt 180

ttcgtcatat tcagttagca tctttgactc taacgtttca tacccgttcc acattatcaa 240

catacgcaat acactatttt cctcatcaat cggtgtgatc gtcattaaat ccacaatcct 300

catttcaggg gattctgaaa cgcagtattg acataaagga tgactaagcc tgaaccaatt 360

aacccaagag tcatcttcga tatggctgac aatccttgat gtctggaatt gatacttacc 420

catagtaagg ccatctttat ctaatttcac ctcaaattct tccacttttg tataattgcg 480

atcacctaac caaccgtcat ggataaaagg aaaatgagac acgtctaagg aattatccat 540

cacacgaaac gcactagctt taatcaagta agacttggta taagtcttgt gataattcgg 600

atcatcccat tcaggaaatg aaggtatatc attaacagga tcgcccaagc acacccacac 660

taagccatag cgctcctggg agtgatatgt cctggcttca gcacttgccg gtggtaccat 720

gccagggtga gctgggatct gtatgcattt accagcctca ttgtatctcc atccgtgata 780

cggacaaact aaagtattat tcgtaatttc tcccatagac agaggaacac ctcggtgggg 840

gcagtagtca agccatacct gtatgggtga attttgttca taactgcgcc ataataccaa 900

cttcactccc aacaaacgag atctggtgat acttccaggt ttacagtctt ctacattggc 960

gactacgtgc cagttattga ttaagattgg gtcggtagtt gtcat 1005

<210> 45
<211> 334
<212> PRT
<213> Cylindrospermopsis raciborskii T3

<400> 45

Met Thr Thr Thr Asp Pro Ile Leu Ile Asn Asn Trp His Val Val Ala
1 5 10 15

Asn Val Glu Asp Cys Lys Pro Gly Ser Ile Thr Arg Ser Arg Leu Leu
20 25 30

Gly Val Lys Leu Val Leu Trp Arg Ser Tyr Glu Gln Asn Ser Pro Ile
35 40 45

Gln Val Trp Leu Asp Tyr Cys Pro His Arg Gly Val Pro Leu Ser Met
50 55 60

Gly Glu Ile Thr Asn Asn Thr Leu Val Cys Pro Tyr His Gly Trp Arg
65 70 75 80

Tyr Asn Glu Ala Gly Lys Cys Ile Gln Ile Pro Ala His Pro Gly Met
85 90 95

Val Pro Pro Ala Ser Ala Glu Ala Arg Thr Tyr His Ser Gln Glu Arg
100 105 110

Tyr Gly Leu Val Trp Val Cys Leu Gly Asp Pro Val Asn Asp Ile Pro
115 120 125

Ser Phe Pro Glu Trp Asp Asp Pro Asn Tyr His Lys Thr Tyr Thr Lys
130 135 140

Ser Tyr Leu Ile Lys Ala Ser Ala Phe Arg Val Met Asp Asn Ser Leu
145 150 155 160

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

Asn Tyr Thr Lys Val Glu Glu Phe Glu Val Lys Leu Asp Lys Asp Gly
180 185 190

Leu Thr Met Gly Lys Tyr Gln Phe Gln Thr Ser Arg Ile Val Ser His
195 200 205

Ile Glu Asp Asp Ser Trp Val Asn Trp Phe Arg Leu Ser His Pro Leu
210 215 220

Cys Gln Tyr Cys Val Ser Glu Ser Pro Glu Met Arg Ile Val Asp Leu
225 230 235 240

Met Thr Ile Thr Pro Ile Asp Glu Glu Asn Ser Val Leu Arg Met Leu
245 250 255

Ile Met Trp Asn Gly Tyr Glu Thr Leu Glu Ser Lys Met Leu Thr Glu
260 265 270

Tyr Asp Glu Thr Ile Glu Gln Asp Ile Arg Ile Leu His Ala Gln Gln
275 280 285

Pro Val Arg Leu Pro Leu Leu Thr Pro Lys Gln Ile Asn Thr Gln Leu
290 295 300

Phe Ser His Glu Ile His Val Pro Ser Asp Arg Cys Thr Leu Ala Tyr
305 310 315 320

Arg Arg Trp Leu Lys Gln Leu Gly Val Thr Tyr Gly Val Cys
325 330

<210> 46
<211> 726
<212> DNA
<213> Cylindrospermopsis raciborskii T3

<400> 46
ctaaattatc cttttcaagg catccaccaa cagtggtttg atgttgtttt ttgtaaaaat 60

cagagttagc atcctgtaat cggtaattga agtgttggca gctgcggtat gccatacagt 120

tggtgtataa aacattgctg cccctcctgg aagtgaaaga catatttctg catttagtga 180

attggcagaa gatgaatcta atgagtgttc ccattggtgg ctacttggta taactcgcat 240

tgtacccata gtattatctg tatcctgtaa gtatatagtt atgaatacca tggcttgatt 300

ggctactgga accaacaacc gaagcgcgtc gtcatttaac tcgtttttg acatggatgc 360

aagtgcgttc aatacttcaa ctacatatcc atggtcttga tgccaagcaa tgtatcctgt 420

acctgcacga attatggcta gatcggtgat caataggaag atatcagacc caattagagc 480

ctgtactggt cccatcacag ttggaagctc taaaagcctc tgaattatct tttgatacct 540

aactggatct gggatagtat gctcagacca ccactcatag tcacccgcca atactccccc 600

acgtttttgt tcggtaataa gttctacttc atgccgtatt tcttcaatta acgcttttgg 660

tacagcttct tcaactgtga aataaccatc atttgtgtaa gcttgttttt gttccgctgt 720

gagcat 726

<210> 47
<211> 241
<212> PRT
<213> Cylindrospermopsis raciborskii T3

<400> 47

Met Leu Thr Ala Glu Gln Lys Gln Ala Tyr Thr Asn Asp Gly Tyr Phe
1 5 10 15

Thr Val Glu Glu Ala Val Pro Lys Ala Leu Ile Glu Glu Ile Arg His
20 25 30

Glu Val Glu Leu Ile Thr Glu Gln Lys Arg Gly Gly Val Leu Ala Gly
35 40 45

Asp Tyr Glu Trp Trp Ser Glu His Thr Ile Pro Asp Pro Val Arg Tyr
50 55 60

Gln Lys Ile Ile Gln Arg Leu Leu Glu Leu Pro Thr Val Met Gly Pro
65 70 75 80

Val Gln Ala Leu Ile Gly Ser Asp Ile Phe Leu Leu Ile Thr Asp Leu
85 90 95

Ala Ile Ile Arg Ala Gly Thr Gly Tyr Ile Ala Trp His Gln Asp His
100 105 110

Gly Tyr Val Val Glu Val Leu Asn Ala Leu Ala Ser Met Ser Lys Asn
115 120 125

Glu Leu Asn Asp Asp Ala Leu Arg Leu Leu Val Pro Val Ala Asn Gln
130 135 140

Ala Met Val Phe Ile Thr Ile Tyr Leu Gln Asp Thr Asp Asn Thr Met
145 150 155 160

Gly Thr Met Arg Val Ile Pro Ser Ser His Gln Trp Glu His Ser Leu
165 170 175

Asp Ser Ser Ser Ala Asn Ser Leu Asn Ala Glu Ile Cys Leu Ser Leu
180 185 190

Pro Gly Gly Ala Ala Met Phe Tyr Thr Pro Thr Val Trp His Thr Ala
195 200 205

Ala Ala Asn Thr Ser Ile Thr Asp Tyr Arg Met Leu Thr Leu Ile Phe
210 215 220

Thr Lys Asn Asn Ile Lys Pro Leu Leu Val Asp Ala Leu Lys Arg Ile
225 230 235 240

Ile

<210> 48

<211> 576
<212> DNA
<213> Cylindrospermopsis raciborskii T3

<400> 48
tcaatggtta gtaggaatta tcctatagct gttctttctc tggatagaag aaaggttgtg 60

agaagctcgc tccgacttca tttcagccaa tttttctgca gaccaatact gaaaatatcc 120

caatcttaat aattcatcac tagcctcttg taactggctg aatgactgta ctgatgctaa 180

aacatactta gggtgagtta tgattacgtt attcacattc tccgcgtcat caccaacata 240

ttgtttgtct ggatgcgatc ctaaagctac caaatcgtat tctggtaata cataattcgc 300

cttggtaatg tacctttcca acctctgtgc atctaggttt tgagggtcgc agccaaaaat 360

caccatttca aagtcattat tccatgttct tatctgttcc attagaagct ctggcagttc 420

aggtccatga aaccaacgaa cactaacacg gttatttaac caagctgcct tcgcgtaagg 480

acagggtgga aaatttcctg ttagaggatt gggaatgctg acaacattga taatccaatc 540

ctctatttct tggcgaaatt gttcgatatt tatcat 576

<210> 49
<211> 191
<212> PRT
<213> Cylindrospermopsis raciborskii T3

<400> 49

Met Ile Asn Ile Glu Gln Phe Arg Gln Glu Ile Glu Asp Trp Ile Ile
1 5 10 15

Asn Val Val Ser Ile Pro Asn Pro Leu Thr Gly Asn Phe Pro Pro Cys
20 25 30

Pro Tyr Ala Lys Ala Ala Trp Leu Asn Asn Arg Val Ser Val Arg Trp
35 40 45

Phe His Gly Pro Glu Leu Pro Glu Leu Leu Met Glu Gln Ile Arg Thr
50 55 60

Trp Asn Asn Asp Phe Glu Met Val Ile Phe Gly Cys Asp Pro Gln Asn

65 70 75 80

Leu Asp Ala Gln Arg Leu Glu Arg Tyr Ile Thr Lys Ala Asn Tyr Val
85 90 95

Leu Pro Glu Tyr Asp Leu Val Ala Leu Gly Ser His Pro Asp Lys Gln
100 105 110

Tyr Val Gly Asp Asp Ala Glu Asn Val Asn Asn Val Ile Ile Thr His
115 120 125

Pro Lys Tyr Val Leu Ala Ser Val Gln Ser Phe Ser Gln Leu Gln Glu
130 135 140

Ala Ser Asp Glu Leu Leu Arg Leu Gly Tyr Phe Gln Tyr Trp Ser Ala
145 150 155 160

Glu Lys Leu Ala Glu Met Lys Ser Glu Arg Ala Ser His Asn Leu Ser
165 170 175

Ser Ile Gln Arg Lys Asn Ser Tyr Arg Ile Ile Pro Thr Asn His
180 185 190

<210> 50
<211> 777
<212> DNA
<213> Cylindrospermopsis raciborskii T3

<400> 50
ttaatctagg tcatagtata accatatatt aggctcgatg tatattccca tattgttggg 60

atagtcaatt ttgacaggta ctaagccttt gggaataata tagtcaccag tttctggaaa 120

acgcatccca actctatctt cccaaccgtc aatagtatca ttaattgttg tggatttaaa 180

acagatccct gcaattttag ccccatgttt gacattaact cgtaaccaag ggtcaaatat 240

aagaccattt ttatctcgcc aggtaatata ccgctctatg ggtataagtg ggtaaagata 300

ttttaggctt ggacgtgcag ccatgatcaa agaattaaga ccgtggtatt gagcaagttc 360

tttcatgtat ccaatcagat actgactcaa gtttttgcct tgatactctg gtaggattga 420

aatcgatact acacataacg cattaggcag gcggttctgt tctcggtctt caagccactt 480

ggctaaagcc cagtcacaac cttcgtccgg taactcatca aaacggcttt cataagttaa 540

agggatacag tttccttgcg ctatcataag ctgtgtggta gcttctacta acccaaactg 600

gaattctgga taaatttcaa atagagctaa ggaagctgga tctgcccaga catcatgtat 660

caaaaatttt gggtatgctt gatcaaagac actcatcgtc ctttccacaa aatcagaagt 720

ttcttttggg gttacaaagc tatactctaa attatgctgt acaatttgaa tggtcat 777

<210> 51
<211> 258
<212> PRT
<213> Cylindrospermopsis raciborskii T3

<400> 51

Met Thr Ile Gln Ile Val Gln His Asn Leu Glu Tyr Ser Phe Val Thr
1 5 10 15

Pro Lys Glu Thr Ser Asp Phe Val Glu Arg Thr Met Ser Val Phe Asp
20 25 30

Gln Ala Tyr Pro Lys Phe Leu Ile His Asp Val Trp Ala Asp Pro Ala
35 40 45

Ser Leu Ala Leu Phe Glu Ile Tyr Pro Glu Phe Gln Phe Gly Leu Val
50 55 60

Glu Ala Thr Thr Gln Leu Met Ile Ala Gln Gly Asn Cys Ile Pro Leu
65 70 75 80

Thr Tyr Glu Ser Arg Phe Asp Glu Leu Pro Asp Glu Gly Cys Asp Trp
85 90 95

Ala Leu Ala Lys Trp Leu Glu Asp Arg Glu Gln Asn Arg Leu Pro Asn
100 105 110

Ala Leu Cys Val Val Ser Ile Ser Ile Leu Pro Glu Tyr Gln Gly Lys

115 120 125

Asn Leu Ser Gln Tyr Leu Ile Gly Tyr Met Lys Glu Leu Ala Gln Tyr
130 135 140

His Gly Leu Asn Ser Leu Ile Met Ala Ala Arg Pro Ser Leu Lys Tyr
145 150 155 160

Leu Tyr Pro Leu Ile Pro Ile Glu Arg Tyr Ile Thr Trp Arg Asp Lys
165 170 175

Asn Gly Leu Ile Phe Asp Pro Trp Leu Arg Val Asn Val Lys His Gly
180 185 190

Ala Lys Ile Ala Gly Ile Cys Phe Lys Ser Thr Thr Ile Asn Asp Thr
195 200 205

Ile Asp Gly Trp Glu Asp Arg Val Gly Met Arg Phe Pro Glu Thr Gly
210 215 220

Asp Tyr Ile Ile Pro Lys Gly Leu Val Pro Val Lys Ile Asp Tyr Pro
225 230 235 240

Asn Asn Met Gly Ile Tyr Ile Glu Pro Asn Ile Trp Leu Tyr Tyr Asp
245 250 255

Leu Asp

<210> 52
<211> 777
<212> DNA
<213> Cylindrospermopsis raciborskii T3

<400> 52
ctaatcctta aatttatact ggaagtcaaa tgagatctca ctatcgttat tatctggaag 60

tacttgcact gtcaattcat taccgacttt cccattccca ggcataatta ataagttagg 120

gtgaggtgga atgccgtcgt actgtcggac gcggcgaaaa atgctcgaat tctcgccacc 180

atgtttattc aagaggactt caactggtgt gatgacaaaa gtcattcctg acccaaggtg 240

gcgcgatcgc cgcttttgat ttgctggagt ggaaacacta acaaataagg cacaccctcc 300

tagagaataa gaccagttag cagactgcgg atcggcagac caatggcagg gacaagacac 360

cgcatcaagg ctatgtaacg cattcaaaaa atcaaatgct tgacctgcat attcctctac 420

tgtaagaact gttggttcag gtgggaaaaa gatgacaagt gtcagaagat ccgcattttc 480

gtgctgaagc aattcgtttt cattaacttc atcaatgtat ttgtagatac cctcaagcgt 540

atgctcaacc aagatcgggt cagttaaaga tgagactatc aggtatctaa tcattccctt 600

ctgttccccg atagttcccc agaagcaagg gaaggcagaa tcgctgattg tttcaacaaa 660

tgttgagtag ctagtgcgta cccaagcagg aaggcactcc tctagaagag aggattccat 720

ctggcttttg ttccagattg gtgtaactcc gtcaggacat aaattcttga ttaccat 777

<210> 53
<211> 258
<212> PRT
<213> Cylindrospermopsis raciborskii T3

<400> 53

Met Val Ile Lys Asn Leu Cys Pro Asp Gly Val Thr Pro Ile Trp Asn
1 5 10 15

Lys Ser Gln Met Glu Ser Ser Leu Leu Glu Glu Cys Leu Pro Ala Trp
20 25 30

Val Arg Thr Ser Tyr Ser Thr Phe Val Glu Thr Ile Ser Asp Ser Ala
35 40 45

Phe Pro Cys Phe Trp Gly Thr Ile Gly Glu Gln Lys Gly Met Ile Arg
50 55 60

Tyr Leu Ile Val Ser Ser Leu Thr Asp Pro Ile Leu Val Glu His Thr
65 70 75 80

Leu Glu Gly Ile Tyr Lys Tyr Ile Asp Glu Val Asn Glu Asn Glu Leu

85 90 95

Leu Gln His Glu Asn Ala Asp Leu Leu Thr Leu Val Ile Phe Phe Pro
100 105 110

Pro Glu Pro Thr Val Leu Thr Val Glu Glu Tyr Ala Gly Gln Ala Phe
115 120 125

Asp Phe Leu Asn Ala Leu His Ser Leu Asp Ala Val Ser Cys Pro Cys
130 135 140

His Trp Ser Ala Asp Pro Gln Ser Ala Asn Trp Ser Tyr Ser Leu Gly
145 150 155 160

Gly Cys Ala Leu Phe Val Ser Val Ser Thr Pro Ala Asn Gln Lys Arg
165 170 175

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

Glu Val Leu Leu Asn Lys His Gly Gly Glu Asn Ser Ser Ile Phe Arg
195 200 205

Arg Val Arg Gln Tyr Asp Gly Ile Pro Pro His Pro Asn Leu Leu Ile
210 215 220

Met Pro Gly Asn Gly Lys Val Gly Asn Glu Leu Thr Val Gln Val Leu
225 230 235 240

Pro Asp Asn Asn Asp Ser Glu Ile Ser Phe Asp Phe Gln Tyr Lys Phe
245 250 255

Lys Asp

<210> 54
<211> 1227
<212> DNA

<213> Cylindrospermopsis raciborskii T3

<400> 54
ctatatctta ttttttggaa gtccctgaaa attattcaac aagatcgaga cgttgttgtt 60

gccagaattt gtgacagcca ggtcaagctt gctgtcgccg ttgaaatccg caattgctat 120

agattcagga ttagtaccga ctggaaagtt agtagctatg ccaaaagacc cattaccatt 180

tcctggtaag accgagacgt tattgctact ataatttgta acagccaggt caagtttact 240

gtcgccattc acatctctaa tcgctacaga gtagggatta gtaccggctg gaaagttagt 300

ggctgcgcca aaagacccat taccatttcc cagtaagacc gagacgttat tgctgctagt 360

atttgcaaca gccaggtcaa gcttgctgtc gccatttaca tccccagttg ctacaaatat 420

gggattagta ccgactggaa agttagtggc tgcgccaaaa gacccattac catttcccag 480

taagaccgag acgttattgc tgacccaatt tgtaatagca aggtcgagct tactgtcgct 540

attaaaatcc gcaatcgcta cggaaatcga ataagtatcg acagggaagc tgctggctgc 600

gccaaaagac ccattaccat ttcccagtaa aaccaagacc ttattgtcga accaatttgt 660

aaaagcaagg tcaagctcac tatcgttatt cacatctcca atggctacag aataagggtt 720

agtaccaact gaaaagttag tggctgcgcc aaaagaccca ttaccatttc ctagtaagac 780

cgagacgtta ttgctactaa aatttgcaac agccaggtca agcttgctgt cgccatttac 840

atccccagtc actacaaaga cgggattagt accgactgga aagttagtgg ctgcgccaaa 900

agacccatta ccatttccca gtaagaccga gacgttattg tcgaaccaat ttgtaacagc 960

caggtcgagc ttactatcgc tattgaaatc cccaactgct acagagtcag catcaagacc 1020

agttgggaag ttaatagcag tagcataact actcctgtgg gcaaatctca ctcctacgga 1080

caaattaacc ggaacactaa attgcccaga aagcttttca ttcttcagat aatagtcagt 1140

tatatttgct aatgcaacag gagttataca taaaaatgta ctaacagata atatccccgc 1200

tataattagt aaagtgagcc ttttcac 1227

<210> 55
<211> 408
<212> PRT
<213> Cylindrospermopsis raciborskii T3

<400> 55

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

Thr Phe Leu Cys Ile Thr Pro Val Ala Leu Ala Asn Ile Thr Asp Tyr
20 25 30

Tyr Leu Lys Asn Glu Lys Leu Ser Gly Gln Phe Ser Val Pro Val Asn
35 40 45

Leu Ser Val Gly Val Arg Phe Ala His Arg Ser Ser Tyr Ala Thr Ala
50 55 60

Ile Asn Phe Pro Thr Gly Leu Asp Ala Asp Ser Val Ala Val Gly Asp
65 70 75 80

Phe Asn Ser Asp Ser Lys Leu Asp Leu Ala Val Thr Asn Trp Phe Asp
85 90 95

Asn Asn Val Ser Val Leu Leu Gly Asn Gly Asn Gly Ser Phe Gly Ala
100 105 110

Ala Thr Asn Phe Pro Val Gly Thr Asn Pro Val Phe Val Val Thr Gly
115 120 125

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

Ser Asn Asn Val Ser Val Leu Leu Gly Asn Gly Asn Gly Ser Phe Gly
145 150 155 160

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

Gly Asp Val Asn Asn Asp Ser Glu Leu Asp Leu Ala Phe Thr Asn Trp
180 185 190

Phe Asp Asn Lys Val Leu Val Leu Leu Gly Asn Gly Asn Gly Ser Phe
195 200 205

Gly Ala Ala Ser Ser Phe Pro Val Asp Thr Tyr Ser Ile Ser Val Ala
210 215 220

Ile Ala Asp Phe Asn Ser Asp Ser Lys Leu Asp Leu Ala Ile Thr Asn
225 230 235 240

Trp Val Ser Asn Asn Val Ser Val Leu Leu Gly Asn Gly Asn Gly Ser
245 250 255

Phe Gly Ala Ala Thr Asn Phe Pro Val Gly Thr Asn Pro Ile Phe Val
260 265 270

Ala Thr Gly Asp Val Asn Gly Asp Ser Lys Leu Asp Leu Ala Val Ala
275 280 285

Asn Thr Ser Ser Asn Asn Val Ser Val Leu Leu Gly Asn Gly Asn Gly
290 295 300

Ser Phe Gly Ala Ala Thr Asn Phe Pro Ala Gly Thr Asn Pro Tyr Ser
305 310 315 320

Val Ala Ile Arg Asp Val Asn Gly Asp Ser Lys Leu Asp Leu Ala Val
325 330 335

Thr Asn Tyr Ser Ser Asn Asn Val Ser Val Leu Pro Gly Asn Gly Asn
340 345 350

Gly Ser Phe Gly Ile Ala Thr Asn Phe Pro Val Gly Thr Asn Pro Glu
355 360 365

Ser Ile Ala Ile Ala Asp Phe Asn Gly Asp Ser Lys Leu Asp Leu Ala
370 375 380

Val Thr Asn Ser Gly Asn Asn Asn Val Ser Ile Leu Leu Asn Asn Phe

385 390 395 400

Gln Gly Leu Pro Lys Asn Lys Ile
405

<210> 56
<211> 603
<212> DNA
<213> Cylindrospermopsis raciborskii T3

<400> 56
ctattgtttg aaaattgtga atttgttttc cacgtatttg agtagttgtt ctaggctttc 60

ctcgacggtg agttcggatg tttccaccca taaatctggg ctattgggtg gttcataagg 120

ggcgctgatt cccgtaaatc catctatttc cccactgcgt gcttttagat aaagaccttt 180

cggatcacgc tgctcacaaa gttccagtgg agttgcaatg tatacttcat gaaatagatc 240

tccagctagt ctacgcacct gttctcggtc attcctgtag ggtgagatga aggcagtgat 300

cactaggcat cctgactccg caaagagttt ggcaacctca cccaaacgac ggatattttc 360

tgagcgatca ctagcagaaa atcctaaatc ggaacacagt ccatgacgaa cactatcacc 420

atctaaaaca aaggtagacc atcctttctc gaacaaagtc tgctctaatt ttaaagccaa 480

tgttgtttta ccagccccgg acagtccagt aaaccataga atcccgcttt tatgaccatt 540

ctttagataa cgatcatatg gagatataag atgttttgta tagtgaatat tagttgattt 600

cat 603

<210> 57
<211> 200
<212> PRT
<213> Cylindrospermopsis raciborskii T3

<400> 57

Met Lys Ser Thr Asn Ile His Tyr Thr Lys His Leu Ile Ser Pro Tyr
1 5 10 15

Asp Arg Tyr Leu Lys Asn Gly His Lys Ser Gly Ile Leu Trp Phe Thr
20 25 30

Gly Leu Ser Gly Ala Gly Lys Thr Thr Leu Ala Leu Lys Leu Glu Gln
35 40 45

Thr Leu Phe Glu Lys Gly Trp Ser Thr Phe Val Leu Asp Gly Asp Ser
50 55 60

Val Arg His Gly Leu Cys Ser Asp Leu Gly Phe Ser Ala Ser Asp Arg
65 70 75 80

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

Ser Gly Cys Leu Val Ile Thr Ala Phe Ile Ser Pro Tyr Arg Asn Asp
100 105 110

Arg Glu Gln Val Arg Arg Leu Ala Gly Asp Leu Phe His Glu Val Tyr
115 120 125

Ile Ala Thr Pro Leu Glu Leu Cys Glu Gln Arg Asp Pro Lys Gly Leu
130 135 140

Tyr Leu Lys Ala Arg Ser Gly Glu Ile Asp Gly Phe Thr Gly Ile Ser
145 150 155 160

Ala Pro Tyr Glu Pro Pro Asn Ser Pro Asp Leu Trp Val Glu Thr Ser
165 170 175

Glu Leu Thr Val Glu Glu Ser Leu Glu Gln Leu Leu Lys Tyr Val Glu
180 185 190

Asn Lys Phe Thr Ile Phe Lys Gln
195 200

<210> 58
<211> 1350
<212> DNA
<213> Cylindrospermopsis raciborskii T3

<400> 58
ttaagaaaaa attatttcaa actcgctcgc caaacgctcc ataatcaaat taatttcaga 60

cgaaaaagga cagtaatatg gtagctctac caacaccctt cttgcggaaa ctgtcacctt 120

cgctgctatt ttgataatcg tttcccttaa cctaggaacc tgggctttag ccagttttgt 180

tccctgtgct gcttgccgaa ttcccaacat taaaatgtaa gctgcttgag ataaaaataa 240

ccgaaactga ttgacaataa atttctcaca gctgagtcta tctgatttta tccccagttt 300

taattcctta attctatgct ctgaagtagc tcctctttga acataaaatt tatcgtataa 360

atcctgagct tctgtttcca agctagtaat tataaatcta ggattgggtc ctttttctag 420

ccattctgct ttcataatta ctcgccgagg ttctgaccaa ctccgagctg cgtaatacac 480

atcatcaaat aaacgaactt tttctcctgt gcgacaatat tccagtctgg ctcggtcaag 540

aaggtaatta atttttcgtt ttaagacatc attattgctg aatccaaaaa catatccaac 600

cccgcttttt tcacaaacct caatgatttc tggtaacgag aaaccccccgt ctcccctcag 660

aacaattcta atttcaggta aggctctttt gattcgcaaa aataaccatt ttagaatgcc 720

agctactcct ttaccagagt gagaatttcc cgcccttagt tgtagaacta atggataacc 780

actggaagct tcattaatca gaactggaaa gtagatatca tgcctatggt aaccattaaa 840

taagctcagt tgttgatgac catgagttag agcatcccac gcatctatgt ccaggacaat 900

ctcttttgat tcccgaggat aggattctag gaatttatca acaaataacc gacgaatttg 960

tttgatatct ttttgagtca cctgattttc taaacgactc atagttggtt gactagctaa 1020

taagttttct cctactgtgg gaacttgatt acaaactagc ttaaaaattg gatcttggcg 1080

caatttatta ctatcgttgc tatcttcata gccagcaatt atttgataaa ttcgttggct 1140

aattaattga gaaagagaat gtttgacttt agtttggtcc cgattatccg tcaaacaatc 1200

tgccatatct tgacaaattt ttacctttc ttctacttgt cgtgccagaa taattccgcc 1260

atcactactt aaactcatat cagaaaaagt cagatctaaa gtttttttat cgaagaaatt 1320

taaagataat cttgaggaag atttagtcat 1350

<210> 59
<211> 449

<212> PRT
<213> Cylindrospermopsis raciborskii T3

<400> 59

Met Thr Lys Ser Ser Ser Arg Leu Ser Leu Asn Phe Phe Asp Lys Lys
1 5 10 15

Thr Leu Asp Leu Thr Phe Ser Asp Met Ser Leu Ser Ser Asp Gly Gly
20 25 30

Ile Ile Leu Ala Arg Gln Val Glu Glu Lys Val Lys Ile Cys Gln Asp
35 40 45

Met Ala Asp Cys Leu Thr Asp Asn Arg Asp Gln Thr Lys Val Lys His
50 55 60

Ser Leu Ser Gln Leu Ile Ser Gln Arg Ile Tyr Gln Ile Ile Ala Gly
65 70 75 80

Tyr Glu Asp Ser Asn Asp Ser Asn Lys Leu Arg Gln Asp Pro Ile Phe
85 90 95

Lys Leu Val Cys Asn Gln Val Pro Thr Val Gly Glu Asn Leu Leu Ala
100 105 110

Ser Gln Pro Thr Met Ser Arg Leu Glu Asn Gln Val Thr Gln Lys Asp
115 120 125

Ile Lys Gln Ile Arg Arg Leu Phe Val Asp Lys Phe Leu Glu Ser Tyr
130 135 140

Pro Arg Glu Ser Lys Glu Ile Val Leu Asp Ile Asp Ala Trp Asp Ala
145 150 155 160

Leu Thr His Gly His Gln Gln Leu Ser Leu Phe Asn Gly Tyr His Arg
165 170 175

His Asp Ile Tyr Phe Pro Val Leu Ile Asn Glu Ala Ser Ser Gly Tyr

180 185 190

Pro Leu Val Leu Gln Leu Arg Ala Gly Asn Ser His Ser Gly Lys Gly
195 200 205

Val Ala Gly Ile Leu Lys Trp Leu Phe Leu Arg Ile Lys Arg Ala Leu
210 215 220

Pro Glu Ile Arg Ile Val Leu Arg Gly Asp Gly Gly Phe Ser Leu Pro
225 230 235 240

Glu Ile Ile Glu Val Cys Glu Lys Ser Gly Val Gly Tyr Val Phe Gly
245 250 255

Phe Ser Asn Asn Asp Val Leu Lys Arg Lys Ile Asn Tyr Leu Leu Asp
260 265 270

Arg Ala Arg Leu Glu Tyr Cys Arg Thr Gly Glu Lys Val Arg Leu Phe
275 280 285

Asp Asp Val Tyr Tyr Ala Ala Arg Ser Trp Ser Glu Pro Arg Arg Val
290 295 300

Ile Met Lys Ala Glu Trp Leu Glu Lys Gly Pro Asn Pro Arg Phe Ile
305 310 315 320

Ile Thr Ser Leu Glu Thr Glu Ala Gln Asp Leu Tyr Asp Lys Phe Tyr
325 330 335

Val Gln Arg Gly Ala Thr Ser Glu His Arg Ile Lys Glu Leu Lys Leu
340 345 350

Gly Ile Lys Ser Asp Arg Leu Ser Cys Glu Lys Phe Ile Val Asn Gln
355 360 365

Phe Arg Leu Phe Leu Ser Gln Ala Ala Tyr Ile Leu Met Leu Gly Ile
370 375 380

Arg Gln Ala Ala Gln Gly Thr Lys Leu Ala Lys Ala Gln Val Pro Arg
385 390 395 400

Leu Arg Glu Thr Ile Ile Lys Ile Ala Ala Lys Val Thr Val Ser Ala
405 410 415

Arg Arg Val Leu Val Glu Leu Pro Tyr Tyr Cys Pro Phe Ser Ser Glu
420 425 430

Ile Asn Leu Ile Met Glu Arg Leu Ala Ser Glu Phe Glu Ile Ile Phe
435 440 445

Ser

<210> 60
<211> 666
<212> DNA
<213> Cylindrospermopsis raciborskii T3

<400> 60
ctatctttgc cctgtaacaa tgtatgctac cctttgacca atattagtag catgatctgc 60

cattctctct aaacactgaa ttgctaatgt taatagtaaa atgggctcca ctaccccggg 120

aacatctttc tgctgcgcca aattacgata taacttttg taagcatcat ctactgtatc 180

atctaataat ttaatccttc taccactaat ctcgtctaaa tccgctaaag ctactaggct 240

ggtagccaac atagattggg catgatcgga cataatggca acctccccca aagtaggatg 300

gggggatag ggaaatattt tcattgctat ttctgccaaa tctttggcat agtccccaat 360

acgttccaag tctctaacta attgcatgaa tgagcttaaa caccgagatt cttggtctgt 420

gggagcttga ctgctcataa ttgtggcaca atcgacttct atttgtctgt agaagcgatc 480

aatttttttg tctaatctcc gtatttgctc agctgctgtt aaatcccgat tgaatagagc 540

ttggtgactc agacggaatg actgctctac taaagcaccc atacgcaaaa catctcgttc 600

cagtctttta atggcacgta taggttgagg tttttcaaaa attgtatatt tcacaacagc 660

tttcat 666

<210> 61
<211> 221
<212> PRT
<213> Cylindrospermopsis raciborskii T3

<400> 61

Met Lys Ala Val Val Lys Tyr Thr Ile Phe Glu Lys Pro Gln Pro Ile
1 5 10 15

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

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

Leu Thr Ala Ala Glu Gln Ile Arg Arg Leu Asp Lys Lys Ile Asp Arg
50 55 60

Phe Tyr Arg Gln Ile Glu Val Asp Cys Ala Thr Ile Met Ser Ser Gln
65 70 75 80

Ala Pro Thr Asp Gln Glu Ser Arg Cys Leu Ser Ser Phe Met Gln Leu
85 90 95

Val Arg Asp Leu Glu Arg Ile Gly Asp Tyr Ala Lys Asp Leu Ala Glu
100 105 110

Ile Ala Met Lys Ile Phe Pro Tyr Pro Pro His Pro Thr Leu Gly Glu
115 120 125

Val Ala Ile Met Ser Asp His Ala Gln Ser Met Leu Ala Thr Ser Leu
130 135 140

Val Ala Leu Ala Asp Leu Asp Glu Ile Ser Gly Arg Arg Ile Lys Leu
145 150 155 160

Leu Asp Asp Thr Val Asp Asp Ala Tyr Lys Lys Leu Tyr Arg Asn Leu

165 170 175

Ala Gln Gln Lys Asp Val Pro Gly Val Val Glu Pro Ile Leu Leu Leu
180 185 190

Thr Leu Ala Ile Gln Cys Leu Glu Arg Met Ala Asp His Ala Thr Asn
195 200 205

Ile Gly Gln Arg Val Ala Tyr Ile Val Thr Gly Gln Arg
210 215 220

<210> 62
<211> 1353
<212> DNA
<213> Cylindrospermopsis raciborskii T3

<400> 62
tcagaaatat ccgccatcat gttgaaccac ctggggaaga tgaatttgta tccaagcacc 60

accggtatca ggatggttca tggccctgat tttgccacca tgagctataa ttatttggcg 120

gacaatggat aaccctaaac cactaccagt aatttctact gtttcattct cagagcggga 180

ctcgcggtgt ctagctttgt ccccccgata aaatctttga aagacatggg gtagatccat 240

gggagcaaat ccaaccccgg aatcaataat gttaatttct aaaatctgat ttgatacttg 300

gtttaatatt gtatctgctt ctggatcaac cccattaata gacttctccc cacaaactgg 360

attcatttca atgaaaatag taccgttcag gttgctgtat ttaatacagt tatctaacag 420

attaagaaac acttgataaa ttctggactt atcagcacat atatagacct tttccgggcc 480

ggagtaagaa atactaagat gctgattagc ggctaggggc tctaaattct cccagactga 540

aaaaattagg gagcggactt ctagcatttc caaattcagt tgtatggagg aggttatttc 600

catctgggtc aggtctaacc aattttggac taaattaatt agtctgtcaa cctcctgcat 660

caagcggatg acccaacggt ttagaggggg atctaagcga gtttgcaggg tttctgcgac 720

cagacgaatg gaagtcagag gtgttctcag ttcatgggcc aggtctgaaa aagagcggtc 780

acgttgctga tgaatgtcta caaattgttg gtgactttct agaaacacac ccacttgtcc 840

ccccggtagg ggaaaactgt tagctgctaa agacaatggc tttaatccta aaataccctg 900

accatgatct cgggaagggt gaaaaatcca ctcttgcatt tgcggttttt gccaatcccg 960

ggtttgctca attaactgat ccagctcata ggatctcact aattccagta gcaggcgcac 1020

ttgacccggt tgccatcttt gtaaatacag catttcccgc gcgcactgat tacaccatag 1080

tagttggttt tcttcatcta cttgtaaata tcccaaaggc gcagcatcca gcaactgttc 1140

ataagctttg agtgacaagc gtaagttttg ttgctcatct ctaacggtag atattttacg 1200

atgtaatcca gctaataggg gtaataatat cttttcagcg tgagggttta agggttgggt 1260

taactgctcc aaatgactgt taagttgaaa ttgttgccaa agccaaaaac caaaaccgac 1320

tgccaaaccc agaagaaatc ccaataagaa cat 1353

<210> 63
<211> 450
<212> PRT
<213> Cylindrospermopsis raciborskii T3

<400> 63

Met Phe Leu Leu Gly Phe Leu Leu Gly Leu Ala Val Gly Phe Gly Phe
1 5 10 15

Trp Leu Trp Gln Gln Phe Gln Leu Asn Ser His Leu Glu Gln Leu Thr
20 25 30

Gln Pro Leu Asn Pro His Ala Glu Lys Ile Leu Leu Pro Leu Leu Ala
35 40 45

Gly Leu His Arg Lys Ile Ser Thr Val Arg Asp Glu Gln Gln Asn Leu
50 55 60

Arg Leu Ser Leu Lys Ala Tyr Glu Gln Leu Leu Asp Ala Ala Pro Leu
65 70 75 80

Gly Tyr Leu Gln Val Asp Glu Glu Asn Gln Leu Leu Trp Cys Asn Gln
85 90 95

Cys Ala Arg Glu Met Leu Tyr Leu Gln Arg Trp Gln Pro Gly Gln Val

100 105 110

Arg Leu Leu Leu Glu Leu Val Arg Ser Tyr Glu Leu Asp Gln Leu Ile
115 120 125

Glu Gln Thr Arg Asp Trp Gln Lys Pro Gln Met Gln Glu Trp Ile Phe
130 135 140

His Pro Ser Arg Asp His Gly Gln Gly Ile Leu Gly Leu Lys Pro Leu
145 150 155 160

Ser Leu Ala Ala Asn Ser Phe Pro Leu Pro Gly Gly Gln Val Gly Val
165 170 175

Phe Leu Glu Ser His Gln Gln Phe Val Asp Ile His Gln Gln Arg Asp
180 185 190

Arg Ser Phe Ser Asp Leu Ala His Glu Leu Arg Thr Pro Leu Thr Ser
195 200 205

Ile Arg Leu Val Ala Glu Thr Leu Gln Thr Arg Leu Asp Pro Pro Leu
210 215 220

Asn Arg Trp Val Ile Arg Leu Met Gln Glu Val Asp Arg Leu Ile Asn
225 230 235 240

Leu Val Gln Asn Trp Leu Asp Leu Thr Gln Met Glu Ile Thr Ser Ser
245 250 255

Ile Gln Leu Asn Leu Glu Met Leu Glu Val Arg Ser Leu Ile Phe Ser
260 265 270

Val Trp Glu Asn Leu Glu Pro Leu Ala Ala Asn Gln His Leu Ser Ile
275 280 285

Ser Tyr Ser Gly Pro Glu Lys Val Tyr Ile Cys Ala Asp Lys Ser Arg
290 295 300

Ile Tyr Gln Val Phe Leu Asn Leu Leu Asp Asn Cys Ile Lys Tyr Ser
305 310 315 320

Asn Leu Asn Gly Thr Ile Phe Ile Glu Met Asn Pro Val Cys Gly Glu
325 330 335

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

Val Ser Asn Gln Ile Leu Glu Ile Asn Ile Ile Asp Ser Gly Val Gly
355 360 365

Phe Ala Pro Met Asp Leu Pro His Val Phe Gln Arg Phe Tyr Arg Gly
370 375 380

Asp Lys Ala Arg His Arg Glu Ser Arg Ser Glu Asn Glu Thr Val Glu
385 390 395 400

Ile Thr Gly Ser Gly Leu Gly Leu Ser Ile Val Arg Gln Ile Ile Ile
405 410 415

Ala His Gly Gly Lys Ile Arg Ala Met Asn His Pro Asp Thr Gly Gly
420 425 430

Ala Trp Ile Gln Ile His Leu Pro Gln Val Val Gln His Asp Gly Gly
435 440 445

Tyr Phe
450

<210> 64
<211> 819
<212> DNA
<213> Cylindrospermopsis raciborskii T3

<400> 64
tcaaccaaat ctatagccaa aacccctaac tgtgacaata tattctggat ggctagggtc 60

taactctaat ttttccctca gccatcgaat gtgaacatcc accgttttac tgtcaccaac 120

aaaatcagga ccccaaacct ggtctaataa ctgttcccgt gaccacaccc tgcgagcata 180

actcataaat agttctagta accggaattc tttcggtgac aagctcacct ccctccctct 240

cactaacacc cgacattcct gaggatttaa actgatatcc ttatatttta aagtgggtat 300

caagggcaaa ttagaaaacc gctgacgacg taacagggcg cgacacctag ccaccatttc 360

ccgtacgcta aaaggcttag ttaggtaatc atccgcccct acctctaaac ccagcacccg 420

gtcagtttca ctacctttcg cactcagaat taaaatcggt atggaattac cctggtgacg 480

taacaaacga caaatatcta atccgttgat ttgtggcaac atcaagtcta gcacaagcag 540

gtcgaaggat aactcaccag gttgggtctc taaattcctg attaattcca cagcacaacg 600

accatcctta gcagtcacaa cttcataacc ttcaccctct aaggctacta caagcatctc 660

tcggatcagt tcttcgtctt ccactattaa aacgcgacta actggttcaa tatccgattt 720

agtgaagtat ctagggtaat tcagtagtat acattgataa caaaaatttg taagaatgta 780

ctggtctggg tttcccacta gtatatgatc ctcactcat 819

<210> 65
<211> 272
<212> PRT
<213> Cylindrospermopsis raciborskii T3

<400> 65

Met Ser Glu Asp His Ile Leu Val Gly Asn Pro Asp Gln Tyr Ile Leu
1 5 10 15

Thr Asn Phe Cys Tyr Gln Cys Ile Leu Leu Asn Tyr Pro Arg Tyr Phe
20 25 30

Thr Lys Ser Asp Ile Glu Pro Val Ser Arg Val Leu Ile Val Glu Asp
35 40 45

Glu Glu Leu Ile Arg Glu Met Leu Val Val Ala Leu Glu Gly Glu Gly
50 55 60

Tyr Glu Val Val Thr Ala Lys Asp Gly Arg Cys Ala Val Glu Leu Ile

65 70 75 80

Arg Asn Leu Glu Thr Gln Pro Gly Glu Leu Ser Phe Asp Leu Leu Val
85 90 95

Leu Asp Leu Met Leu Pro Gln Ile Asn Gly Leu Asp Ile Cys Arg Leu
100 105 110

Leu Arg His Gln Gly Asn Ser Ile Pro Ile Leu Ile Leu Ser Ala Lys
115 120 125

Gly Ser Glu Thr Asp Arg Val Leu Gly Leu Glu Val Gly Ala Asp Asp
130 135 140

Tyr Leu Thr Lys Pro Phe Ser Val Arg Glu Met Val Ala Arg Cys Arg
145 150 155 160

Ala Leu Leu Arg Arg Gln Arg Phe Ser Asn Leu Pro Leu Ile Pro Thr
165 170 175

Leu Lys Tyr Lys Asp Ile Ser Leu Asn Pro Gln Glu Cys Arg Val Leu
180 185 190

Val Arg Gly Arg Glu Val Ser Leu Ser Pro Lys Glu Phe Arg Leu Leu
195 200 205

Glu Leu Phe Met Ser Tyr Ala Arg Arg Val Trp Ser Arg Glu Gln Leu
210 215 220

Leu Asp Gln Val Trp Gly Pro Asp Phe Val Gly Asp Ser Lys Thr Val
225 230 235 240

Asp Val His Ile Arg Trp Leu Arg Glu Lys Leu Glu Leu Asp Pro Ser
245 250 255

His Pro Glu Tyr Ile Val Thr Val Arg Gly Phe Gly Tyr Arg Phe Gly
260 265 270

<210> 66
<211> 774
<212> DNA
<213> Cylindrospermopsis raciborskii T3

<400> 66
tcaggcaaaa cgagagaagt ctaaagtggg tggaatatcc tgaattcttc caggacctat 60

agcccgtagt gcttctggta aactaatatc cccagtatat agggctttac ccacaattac 120

tcctgtaacc ccctgatgtt ctaaagataa taaggttaat aggtcagtaa cagaacccac 180

acccccagag gcaatcacgg gtatggaaat agcagatacc aagtctctta atgctcgcaa 240

gtttggtccc tgaagcgtac catcacggtt tatatccgta taaataatag ctgccgcacc 300

caattcctgc atttgggttg ctagttgggg ggccaaaatt tgagaagttt ctaaccaacc 360

cctggtagca actagaccat tccgcgcatc aatcccaatt ataatttgct gggggaattg 420

ttcacacagt ccttgaacca gatctggttg ctctactgct acagttccca gaattgccca 480

ctgtacccca agattaaata actgtataac gctggagcta tcacgtattc ctccgccaac 540

ttcaataggt atggaaatag cattggtaat agcttctata gtagataaat taactatttt 600

accagttttt gctccatcta aatctactaa atgtagtctt gttgctcctt ggtctgccca 660

cattttagcg gtttccacag ggttatggct gtaaacctgg gattgtgcat agtcaccttt 720

gtagagtctt acacaacgcc cctctaatag atctattgct gggataactt ccat 774

<210> 67
<211> 257
<212> PRT
<213> Cylindrospermopsis raciborskii T3

<400> 67

Met Glu Val Ile Pro Ala Ile Asp Leu Leu Glu Gly Arg Cys Val Arg
1 5 10 15

Leu Tyr Lys Gly Asp Tyr Ala Gln Ser Gln Val Tyr Ser His Asn Pro
20 25 30

Val Glu Thr Ala Lys Met Trp Ala Asp Gln Gly Ala Thr Arg Leu His

35 40 45

Leu Val Asp Leu Asp Gly Ala Lys Thr Gly Lys Ile Val Asn Leu Ser
50 55 60

Thr Ile Glu Ala Ile Thr Asn Ala Ile Ser Ile Pro Ile Glu Val Gly
65 70 75 80

Gly Gly Ile Arg Asp Ser Ser Ser Val Ile Gln Leu Phe Asn Leu Gly
85 90 95

Val Gln Trp Ala Ile Leu Gly Thr Val Ala Val Glu Gln Pro Asp Leu
100 105 110

Val Gln Gly Leu Cys Glu Gln Phe Pro Gln Gln Ile Ile Ile Gly Ile
115 120 125

Asp Ala Arg Asn Gly Leu Val Ala Thr Arg Gly Trp Leu Glu Thr Ser
130 135 140

Gln Ile Leu Ala Pro Gln Leu Ala Thr Gln Met Gln Glu Leu Gly Ala
145 150 155 160

Ala Ala Ile Ile Tyr Thr Asp Ile Asn Arg Asp Gly Thr Leu Gln Gly
165 170 175

Pro Asn Leu Arg Ala Leu Arg Asp Leu Val Ser Ala Ile Ser Ile Pro
180 185 190

Val Ile Ala Ser Gly Gly Val Gly Ser Val Thr Asp Leu Leu Thr Leu
195 200 205

Leu Ser Leu Glu His Gln Gly Val Thr Gly Val Ile Val Gly Lys Ala
210 215 220

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

Pro Gly Arg Ile Gln Asp Ile Pro Pro Thr Leu Asp Phe Ser Arg Phe
245 250 255

Ala

<210> 68
<211> 396
<212> DNA
<213> Cylindrospermopsis raciborskii T3

<400> 68
atgagttggt ccacaatgaa ggacgtcttg attttaatag tcaaatccct ccaaatccat 60

tataatccca tgaatgctct ttcaattcct acctggatta tccatatttc tagtgtcatt 120

gaatgggtag ttgccatttc cctcatctgg aaatatggcg aactgaccca aaaccatagt 180

tggaggggat ttgccttagg tatgataccc gccttaatta gcgccctatc cgcttgtacc 240

tggcattatt tcgataatcc ccagtcccta gaatggttag tcaccctcca ggctactact 300

acgttaatag gtaattttac tctttgggca gcagcagtct gggtttggcg ttctactcga 360

ccgaatgagg ttctcagtat ctcaaataag gagtag 396

<210> 69
<211> 131
<212> PRT
<213> Cylindrospermopsis raciborskii T3

<400> 69

Met Ser Trp Ser Thr Met Lys Asp Val Leu Ile Leu Ile Val Lys Ser
1 5 10 15

Leu Gln Ile His Tyr Asn Pro Met Asn Ala Leu Ser Ile Pro Thr Trp
20 25 30

Ile Ile His Ile Ser Ser Val Ile Glu Trp Val Val Ala Ile Ser Leu
35 40 45

Ile Trp Lys Tyr Gly Glu Leu Thr Gln Asn His Ser Trp Arg Gly Phe

50 55 60

Ala Leu Gly Met Ile Pro Ala Leu Ile Ser Ala Leu Ser Ala Cys Thr
65 70 75 80

Trp His Tyr Phe Asp Asn Pro Gln Ser Leu Glu Trp Leu Val Thr Leu
85 90 95

Gln Ala Thr Thr Thr Leu Ile Gly Asn Phe Thr Leu Trp Ala Ala Ala
100 105 110

Val Trp Val Trp Arg Ser Thr Arg Pro Asn Glu Val Leu Ser Ile Ser
115 120 125

Asn Lys Glu
130

<210> 70
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 70
ttaattgctt ggtctatctc 20

<210> 71
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 71
caataccgaa gaggagatag 20

<210> 72
<211> 20
<212> DNA

<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 72
taggcgtgtt agtgggagat 20

<210> 73
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 73
tgtgtaacca atttgtgagt 20

<210> 74
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 74
ttagccggat tacaggtgaa 20

<210> 75
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 75
ctggactcgg cttgttgctt 20

<210> 76
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 76
cagcgagtta cacccaccac 20

<210> 77
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 77
ctcgcactaa atattctacc 20

<210> 78
<211> 19
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 78
aaaacctcag cttccacaa 19

<210> 79
<211> 22
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 79
atgattttgg aggtccattg tt 22

<210> 80
<211> 42156
<212> DNA
<213> Cylindrospermopsis raciborskii AWT205

<400> 80
gtttttactg caaaagcata ttcatattat attctaatag ggttggtgga atattcaagg 60

ggaggttaga aaatgcgatc gctcttatga atgaggttgt ctatccgaat atcaaatatt 120

ggtggttgaa aaaagacctt atatgcggac acagattccc atgatgaaaa tatatcattg 180

tcaagtcaat tagtcaaccc cccaatagac atctccgaaa aagaatcaaa gtgtgataaa 240

atttgcagta cagcaggata taaaatagtt tttcctctat acttctgagt gtaggcttgc 300

gtccgccccc gggcgcacgt ttgcggtttg ctaaggagtt aaacacggtg cgttaatatg 360

tatcagcaac ctgagataac agctcgttga atgcttagcg gttaagtcca gtcattgctc 420

gtagcagtcg ctcttgattc aggatgcggt ctaagttcaa cattaatgtc accctacttg 480

tctgcttgat tattatccct tattttccaa caactctaat gaaagtacct ataacagcaa 540

acgaagatgc agctacatta cttcagcgtg ttggactgtc cctaaaggaa gcacaccaac 600

aacttgaggc aatgcaacgc cgagcgcacg aaccgatcgc aattgtgggg ctggggctgc 660

ggtttccggg agctgattca ccacagacat tctggaaact acttcagaat ggtgttgata 720

tggtcaccga aatccctagc gatcgctggg cagttgatga atactatgat ccccaacctg 780

ggtgtccagg caaaatgtat attcgtgaag ccgcttttgt tgatgcagtg gataaattcg 840

atgcctcgtt ttttgatatt tcgccacgtg aagcggccaa tatagatccc cagcatagaa 900

tgttgctgga ggtagcttgg gaggcactcg aaagggctgg cattgctccc agccaattga 960

tggatagcca aacgggggta tttgtcggga tgagcgaaaa tgactattat gctcacctag 1020

aaaatacagg ggatcatcat aatgtctatg cggcaacggg caatagcaat tactatgctc 1080

cggggcgttt atcctatcta ttggggcttc aaggacctaa catggtcgtt gatagtgcct 1140

gttcctcctc cttagtggct gtacatcttg cctgtaatag tttgcggatg ggagaatgtg 1200

atctggcact ggctggtggc gttcagctta tgttaatccc agaccctatg attgggactg 1260

cccagttaaa tgcctttgcg accgatggtc gtagtaaaac atttgacgct gccgccgatg 1320

gctatggacg cggcgaaggt tgtggcatga ttgtacttaa aagaataagt gacgcgatcg 1380

tggcagacga tccaatttta gccgtaatcc ggggtagtgc agtcaatcat ggcgggcgta 1440

gcagtggttt aactgcccct aataagctgt ctcaagaagc cttactgcgt caggcactac 1500

aaaacgccaa ggttcagccg gaagcagtca gttatatcga agcccatggc acagggacac 1560

aactgggcga cccgattgag gtgggagcat taacgaccgt ctttggatct tctcgttcag 1620

aacccttgtg gattggctct gtcaaaacta atatcggaca cctagaacca gccgctggta 1680

ttgcggggtt aataaaagtc attttatcat tacaagaaaa acagattcct cccagtctcc 1740

attttcaaaa ccctaatccc ttcattgatt gggaatcttc gccagttcaa gtgccgacac 1800

agtgtgtacc ctggactggg aaagagcgcg tcgctggagt tagctcgttt ggtatgagcg 1860

gtacaaactg tcatctagtt gtcgcagaag cacctgtccg ccaaaacgaa aaatctgaaa 1920

atgcaccgga gcgtccttgt cacattctga ccctttcagc caaaaccgaa gcggcactca 1980

acgcattggt agcccgttac atggcatttc tcagggaagc gcccgccata tccctagctg 2040

atctttgtta tagtgccaat gtcgggcgta atctttttgc ccatcgctta agttttatct 2100

ccgagaacat cgcgcagtta tcagaacaat tagaacactg cccacagcag gctacaatgc 2160

caacgcaaca taatgtgata ctagataatc aactcagccc tcaaatcgct tttctgttta 2220

ctggacaagg ttcgcagtac atcaacatgg ggcgtgagct ttacgaaact cagcccacct 2280

tccgtcggat tatggacgaa tgtgacgaca ttctgcatcc attgttgggt gaatcaattc 2340

tgaacatact ctacacttcc cctagcaaac ttaatcaaac cgtttatacc caacctgccc 2400

tttttgcttt tgaatatgcc ctagcaaaac tatggatatc atggggtatt gagcctgatg 2460

tcgtactggg tcacagcgtg ggtgaatatg tagccgcttg tctggcgggt gtctttagtt 2520

tagaagatgg gttaaaactc attgcatctc gtggatgttt gatgcaagcc ttaccgccgg 2580

ggaaaatgct tagtatcaga agcaatgaga tcggagtgaa agcgctcatc gcgccttata 2640

gtgcagaagt atcaattgca gcaatcaatg gacagcaaag cgtggtgatc tccggcaaag 2700

ctgaaattat agataattta gcagcagagt ttgcatcgga aggcatcaaa acacacctaa 2760

ttacagtctc ccacgctttc cactcgccaa tgatgacccc catgctgaaa gcattccgag 2820

acgttgccag caccatcagc tataggtcac ccagtttatc actgatttct aacggtacag 2880

ggcaattggc aacaaaggag gttgctacac ctgattattg ggtgcgtcat gtccattcta 2940

ccgtccgttt tgccgatggt attgccacat tggcagaaca gaatactgac atcctcctag 3000

aagtaggacc caaaccaata ttgttgggta tggcaaagca gatttatagt gaaaacggtt 3060

cagctagtca tccgctcatg ctacccagtt tgcgtgaaga tggcaacgat tggcagcaga 3120

tgctttctac ttgtggacaa cttgtagtta atggagtcaa gattgactgg gcgggttttg 3180

acaaggatta ttcacgacac aaaatattgt tgcccaccta tccgtttcag agagaacgat 3240

attggattga aagctccgtc aaaaagcccc aaaaacagga gctgcgccca atgttggata 3300

agatgatccg gctaccatca gagaacaaag tggtgtttga aaccgagttt ggcgtgcgac 3360

agatgcctca tatctccgat catcagatat acggtgaagt cattgtaccg ggggcagtat 3420

tagcttcctt aatcttcaat gcagcgcagg ttttataccc agactatcag catgaattaa 3480

ctgatattgc tttttatcag ccaattatct ttcatgacga cgatacggtg atcgtgcagg 3540

cgattttcag ccctgataag tcacaggaga atcaaagcca tcaaacattt ccacccatga 3600

gcttccagat tattagcttc atgccggatg gtcccttaga gaacaaaccg aaagtccatg 3660

tcacagggtg tctgagaatg ttgcgcgatg cccaaccgcc aacactctcc ccgaccgaaa 3720

tacgtcagcg ctgtccacat accgtaaatg gtcatgactg gtacaatagc ttagtcaaac 3780

aaaaatttga aatgggtcct tcctttaggt gggtacagca actttggcat ggggaaaatg 3840

aagcattgac ccgtcttcac ataccagatg tggtcggctc tgtatcagga catcaacttc 3900

acggcatatt gctcgatggt tcactttcaa ccaccgctgt catggagtac gagtacggag 3960

actccgcgac cagagttcct ttgtcatttg cttctctgca actgtacaaa cccgtcacgg 4020

gaacagagtg gtggtgctac gcgaggaaga ttggggaatt caaatatgac ttccagatta 4080

tgaatgaaat cggggaaacc ttggtgaaag caattggctt tgtacttcgt gaagcctctc 4140

ccgaaaaatt cctcagaaca acatacgtac acaactggct tgtagacatt gaatggcaag 4200

ctcaatcaac ttccctagtc ccttctgatg gcactatctc tggcagttgt ttggttttat 4260

cagatcagca tggaacaggg gctgcattgg cacaaaggct agacaatgct ggagtgccag 4320

tgaccatgat ctatgctgat ctgatactgg acaattacga attaatattc cgtactttgc 4380

cagatttaca acaagtcgtc tatttatggg ggttggatca aaaagaggat tgtcacccca 4440

tgaagcaagc agaggataac tgtacatcgg tgctatatct tgtgcaagca ttactcaata 4500

cctactcaac cccgccatcc ctgcttattg tcacctgtga tgcacaagcg gtggttgaac 4560

aagatcgagt aaatggcttc gcccaatcgt ctttgttggg acttgccaaa gttatcatgc 4620

tagaacaccc agaattgtcc tgtgtttaca tggatgtgga agccggatat ttacagcaag 4680

atgtggcgaa cacgatattt acacagctaa aaagaggcca tctatcaaag gacggagaag 4740

agagtcagtt ggcttggcgc aatggacaag catacgtagc acgtcttagt caatataaac 4800

ccaaatccga acaactggtt gagatccgca gcgatcgcag ctatttgatc actggtggac 4860

ggggcggtgt cggcttacaa atcgcacggt ggttagtgga aaaggggget aaacatctcg 4920

ttttgttggg gcgcagtcag accagttccg aagtcagtct ggtgttggat gagctagaat 4980

cagccggggc gcaaatcatt gtggctcaag ctgatattag cgatgagaag gtattagcgc 5040

agattctgac caatctaacc gtacctctgt gtggtgtaat ccacgccgca ggagtgcttg 5100

atgatgcgag tctactccaa caaactccag ccaagctcaa aaaagttcta ttgccaaaag 5160

cagagggggc ttggattctg cataatttga ccctggagca gcgactagac ttctttgttc 5220

tcttttcttc tgccagttct ctattaggtg cgccagggca ggccaactat tcagcagcca 5280

atgctttcct agatggttta gctgcctatc ggcgagggcg aggactcccc tgtttgtcta 5340

tctgctgggg ggcatgggat caagtcggta tggctgcacg acaagggcta ctggacaagt 5400

taccgcaaag aggtgaagag gccatcccgt tacagaaagg cttagacctc ttcggcgaat 5460

tactgaacga gccagccgct caaattggtg tgatcccaat tcaatggact cgcttcttgg 5520

atcatcaaaa aggtaatttg ccttttttatg agaagttttc taagtctagc cggaaagcgc 5580

agagttacga ttcgatggca gtcagtcaca cagaagatat tcagaggaaa ctgaagcaag 5640

ctgctgtgca agatcgacca aaattattag aagtgcatct tcgctctcaa gtcgctcaac 5700

tgttaggaat aaacgtggca gagctaccaa atgaagaagg aattggtttt gttacattag 5760

gtcttgactc gctcacctct attgaactgc gtaacagttt acaacgcaca ttagattgtt 5820

cattacctgt caccttttgct tttgactacc caactataga aatagcggtt aagtacctaa 5880

cacaagttgt aattgcaccg atggaaagca cagcatcgca gcaaacagac tctttatcag 5940

caatgttcac agatacttcg tccatcggga gaattcttga caacgaaaca gatgtgttag 6000

acagcgaaat gcaaagtgat gaagatgaat ctttgtctac acttatacaa aaattatcaa 6060

cacatttgga ttaggagtga tcaataatta tacattgcgg acgtgagcat acaagtaaag 6120

gaaaaatgaa tgaacgcttt gtcagaaaat caggtaactt ctatagtcaa gaaggcattg 6180

aacaaaatag aggagttaca agccgaactt gaccgtttaa aatacgcgca acgggaacca 6240

atcgccatca ttggaatggg ctgtcgcttt cctggtgcag acacacctga agctttttgg 6300

aaattattgc acaatggggt tgatgctatc caagagattc caaaaagccg ttgggatatt 6360

gacgactatt atgatcccac accagcaaca cccggcaaaa tgtatacacg ttttggtggt 6420

tttctcgacc aaatagcagc cttcgaccct gagttctttc gcatttctac tcgtgaggca 6480

atcagcttag accctcaaca gagattgctt ctggaagtga gttgggaagc cttagaacgg 6540

gctgggctga caggcaataa actgactaca caaacaggtg tctttgttgg catcagtgaa 6600

agtgattatc gtgatttgat tatgcgtaat ggttctgacc tagatgtata ttctggttca 6660

ggtaactgcc atagtacagc cagcgggcgt ttatcttatt atttgggact tactggaccc 6720

aatttgtccc ttgataccgc ctgttcgtcc tctttggttt gtgtggcatt ggctgtcaag 6780

agcctacgtc aacaggagtg tgatttggca ttggcgggtg gtgtacagat acaagtgata 6840

ccagatggct ttatcaaagc ctgtcaatcc cgtatgttgt cgcctgatgg acggtgcaaa 6900

acatttgatt tccaggcaga tggttatgcc cgtgctgagg ggtgtgggat ggtagttctc 6960

aaacgcctat ccgatgcaat tgctgacaat gataatatcc tggccttgat tcgtggtgcc 7020

gcagtcaatc atgatggcta cacgagtgga ttaaccgttc ccagtggtcc ctcacaacgg 7080

gcggtgatcc aacaggcatt agcggatgct ggaatacacc cggatcaaat tagctatatt 7140

gaggcacatg gcacaggtac atccttaggc gatcctattg aaatgggtgc gattgggcaa 7200

gtctttggtc aacgctcaca gatgcttttc gtcggttcgg tcaagacgaa tattggtcat 7260

actgaggctg ctgctggtat tgctggtctc atcaaggttg tactctcaat gcagcacggt 7320

gaaatcccag caaacttaca cttcgaccag ccaagtcctt atattaactg ggatcaatta 7380

ccagtcagta tcccaacaga aacaatacct tggtctacta gcgatcgctt tgcaggagtc 7440

agtagctttg gctttagtgg cacaaactct catatcgtac tagaggcagc cccaaacata 7500

gagcaaccta ctgatgatat taatcaaacg ccgcatattt tgaccttagc tgcaaaaaca 7560

cccgcagccc tgcaagaact ggctcggcgt tatgcgactc agatagagac ctctcccgat 7620

gttcctctgg cggacatttg tttcacagca cacatagggc gtaaacattt taaacatagg 7680

tttgcggtag tcacggaatc taaagagcaa ctgcgtttgc aattggatgc atttgcacaa 7740

tcaggggtg tggggcgaga agtcaaatcg ctaccaaaga tagcctttct ttttacaggt 7800

caaggctcac agtatgtggg aatgggtcgt caactttacg aaaaccaacc taccttccga 7860

aaagcactcg cccattgtga tgacatcttg cgtgctggtg catatttcga ccgatcacta 7920

ctttcgattc tctacccaga gggaaaatca gaagccattc accaaaccgc ttatactcag 7980

cccgcgcttt ttgctcttga gtatgcgatc gctcagttgt ggcactcctg gggtatcaaa 8040

ccagatatcg tgatggggca tagtgtaggt gaatacgtcg ccgcttgtgt ggcgggcata 8100

ttttctttag aggatgggct gaaactaatt gctactcgtg gtcgtctgat gcaatcccta 8160

cctcaagacg gaacgatggt ttcttctttg gcaagtgaag ctcgtatcca ggaagctatt 8220

acaccttacc gagatgatgt gtcaatcgca gcgataaatg ggacagaaag cgtggttatc 8280

tctggcaaac gcacctctgt gatggcaatt gctgaacaac tcgccaccgt tggcatcaag 8340

acacgccaac tgacggtttc ccatgccttc cattcaccac ttatgacacc catcttggat 8400

gagttccgcc aggtggcagc cagtatcacc tatcaccagc ccaagttgct acttgtctcc 8460

aacgtctccg ggaaagtggc cggccctgaa atcaccagac cagattactg ggtacgccat 8520

gtccgtgagg cagtgcgctt tgccgatgga gtgaggacgc tgaatgaaca aggtgtcaat 8580

atctttctgg aaatcggttc taccgctacc ctgttgggca tggcactgcg agtaaatgag 8640

gaagattcaa atgcctcaaa aggaacttcg tcttgctacc tgcccagttt acgggaaagc 8700

cagaaggatt gtcagcagat gttcactagt ctgggtgagt tgtacgtaca tggatatgat 8760

attgattggg gtgcatttaa tcggggatat caaggacgca aggtgatatt gccaacctat 8820

ccgtttcagc gacaacgtta ttggcttccc gaccctaagt tggcacaaag ttccgattta 8880

gataccttc aagctcagag cagcgcatca tcacaaaatc ctagcgctgt gtccacttta 8940

ctgatggaat atttgcaagc aggtgatgtc caatctttag ttgggctttt ggatgatgaa 9000

cggaaactct ctgctgctga acgaattgca ctacccagta ttttggagtt tttggtagag 9060

gaacaacagc gacaaataag ctcaaccaca actcctcaaa cagttttaca aaaaataagt 9120

caaacttccc atgaggacag atatgaaata ttgaagaacc tgatcaaatc tgaaatcgaa 9180

acgattatca aaagtgttcc ctccgatgaa caaatgtttt ctgacttagg aattgattcc 9240

ttgatggcga tcgaactgcg taataagctc cgttctgcta tagggttgga actgccagtg 9300

gcaatagtat ttgaccatcc cacgattaag cagttaacta acttcgtact ggacagaatt 9360

gtgccgcagg cagaccaaaa ggacgttccc accgaatcct tgtttgcttc taaacaggag 9420

atatcagttg aggagcagtc ttttgcaatt accaagctgg gcttatcccc tgcttcccac 9480

tccctgcatc ttcctccatg gacggttaga cctgcggtaa tggcagatgt aacaaaacta 9540

agccaacttg aaagagaggc ctatggctgg atcggagaag gagcgatcgc cccgccccat 9600

ctcattgccg atcgcatcaa tttactcaac agtggtgata tgccttggtt ctgggtaatg 9660

gagcgatcag gagagttggg cgcgtggcag gtgctacaac cgacatctgt tgatccatat 9720

acttatggaa gttgggatga agtaactgac caaggtaaac tgcaagcaac cttcgaccca 9780

agtggacgca atgtgtatat tgtcgcgggt gggtctagca acctccccac ggtagccagc 9840

cacctcatga cgcttcagac tttattgatg ctgcgggaaa ctggtcgtga cacaatcttt 9900

gtctgtctgg caatgccagg ttatgccaaa taccacagtc aaacaggaaa atcgccggaa 9960

gagtatattg cgctgactga cgaggatggt atcccaatgg acgagtttat tgcactttct 10020

gtctacgact ggcctgttac cccatcgttt cgtgttctgc gagacggtta tccacctgat 10080

cgagattctg gtggtcacgc agttagtacg gttttccagc tcaatgattt cgatggagcg 10140

atcgaagaaa catatcgtcg tattatccgc catgccgatg tccttggtct cgaaagaggc 10200

taaatttcag gcgttggtga atagaaccca cattccgcag ataaggtctt atgaataaaa 10260

aacaggtaga cacattgtta atacacgctc atctttttac catgcagggc aatggcctgg 10320

gatatattgc cgatggggca attgcggttc agggtagcca gatcgtagca gtggattcga 10380

cagaggcttt gctgagtcat tttgaaggaa ataaaacaat taatgcggta aattgtgcag 10440

tgttgcctgg actaattgat gctcatatac atacgacttg tgctattctg cgtggagtgg 10500

cacaggatgt aaccaattgg ctaatggacg cgacaattcc ttatgcactt cagatgacac 10560

ccgcagtaaa tatagccgga acgcgcttga gtgtactcga agggctgaaa gcaggaacaa 10620

ccacattcgg cgattctgag actccttacc cgctctgggg agagtttttc gatgaaattg 10680

gggtacgtgc tattctatcc cctgccttta acgcctttcc actagaatgg tcggcatgga 10740

aggagggaga cctctatccc ttcgatatga aggcaggacg acgtggtatg gaagaggctg 10800

tggattttgc ttgtgcatgg aatggagccg cagagggacg tatcaccact atgttgggac 10860

tacaggcggc ggatatgcta ccactggaga tcctacacgc agctaaagag attgcccaac 10920

gggaaggctt aatgctgcat attcatgtgg cccagggaga tcgagaaaca aaacaaattg 10980

tcaaacgata tggtaagcgt ccgatcgcat ttctagctga aattggctac ttggacgaac 11040

agttgctggc agttcacctc accgatgcca cagatgaaga agtgatacaa gtagccaaaa 11100

gtggtgctgg catggcactc tgttcgggcg ctattggcat cattgacggt cttgttccgc 11160

ccgctcatgt ttttcgacaa gcaggcggtt ccgttgcact cggttctgat caagcctgtg 11220

gcaacaactg ttgtaacatc ttcaatgaaa tgaagctgac cgccttattc aacaaaataa 11280

aatatcatga tccaaccatt atgccggctt gggaagtcct gcgtatggct accatcgaag 11340

gagcgcaggc gattggttta gatcacaaga ttggctctct tcaagtgggc aaagaagccg 11400

acctgatctt aatagacctc agttccccta acctctcgcc caccctgctc aaccctattc 11460

gtaaccttgt acctaacttg gtgtatgctg cttcaggaca tgaagttaaa agcgtcatgg 11520

tggcgggaaa acttttagtg gaagactacc aagtcctcac ggtagatgag tccgctattc 11580

tcgctgaagc gcaagtacaa gctcaacaac tctgccaacg tgtgaccgct gaccccattc 11640

acaaaaagat ggtgttaatg gaagcgatgg ctaagggtaa attatagata caggcttatc 11700

tgcaacaaca tttctgaatc aaacctggag gggcaaacca atgaccatat atgaaaataa 11760

gttgagtagt tatcaaaaaa atcaagatgc cataatatct gcaaaagaac tcgaagaatg 11820

gcatttaatt ggacttctag accattcaat agatgcggta atagtaccga attattttct 11880

tgagcaagag tgtatgacaa tttcagagag aataaaaaag agtaaatatt ttagcgctta 11940

tcccggtcat ccatcagtaa gtagcttggg acaagagttg tatgaatgcg aaagtgagct 12000

tgaattagca aagtatcaag aagacgcacc cacattgatt aaagaaatgc ggaggctggt 12060

acatccgtac ataagtccaa ttgatagact tagggttgaa gttgatgata tttggagtta 12120

tggctgtaat ttagcaaaac ttggtgataa aaaactgttt gcgggtatcg ttagagagtt 12180

taaagaagat aaccctggcg caccacattg tgacgtaatg gcatggggtt ttctcgaata 12240

ttataaagat aaaccaaata tcataaatca aatcgcagca aatgtatatt taaaaacgtc 12300

tgcatcagga ggagaaatag tgctttggga tgaatggcca actcaaagcg aatatatagc 12360

atacaaaaca gatgatccag ctagtttcgg tcttgatagc aaaaagatcg cacaaccaaa 12420

acttgagatc caaccgaacc agggagattt aattctattc aattccatga gaattcatgc 12480

ggtgaaaaag atagaaactg gtgtacgtat gacatgggga tgtttgattg gatactctgg 12540

aactgataaa ccgcttgtta tttggactta atgtagcgtt tccatttgag tcaaggcacg 12600

agaagcttct aaagctggaa tagatacact atcattctca actacactct caaatgtcct 12660

aggtaactgt gccccaaaca tcagcattcc aatggcgttg aacaaaaaga aagccaacca 12720

caagatatgg ttactctcaa atttaacagc agctacatcc gcaggtaaaa atcctacacc 12780

aaacgcgatt aagttaacat tgcggagagt atgcccttga gccaaaccca agaagtaccc 12840

acatagtatg caacatactg aattgcatac taggacaagt accaaccagg gaataaaaat 12900

atcaatattc tcaataattt ctgcgtggtt ggttaacaac ccaaaaacat catcgggaaa 12960

tagccaacac gctccgccga aaaccagact cactagcaga gccattccca cagaaacttt 13020

tgccagaggt gctaactgtt ctgtggctcc tttcccttta aaatttcctg ccagagtttc 13080

tgtacagaat cccaatcctt caacaatgta gatgctcaaa gcccatatct gtaagagcaa 13140

ggcattttga gcgtagataa ttgtccccat ttgtgcccct tcgtagttaa acgttaagtt 13200

ggtaaacata caaactaaat tgctgacaaa gatgtttcca ttgagagtta aggtggagcg 13260

tatagctttt atgtcccaaa tttttccagc taattctttt acctcttgcc acgggatttc 13320

tttgcagaca aaaaacaatc ccaccaatag ggtgagatat tgacttgcag cagaagctac 13380

tcctgccccc atgctcgacc agtctaagtg gataataaac aagtagtcga gtgcgatatt 13440

ggcagcattg cccacaaccg acaacaacac aactaagcca ttttttttccc gtcccagaaa 13500

ccagccaagc aggacaaagt tgagcaaaat ggcaggcgct ccccaactct gggtgttaaa 13560

atacgcttga gctgaagact tcacctctgg gccgacatct agtatagaaa accccaacac 13620

ccctaacggg tactgtaaca gtatgatcgc caccccccagc accagagcaa ttaaaccatt 13680

aagcagtccc gccaacagta cgccctctcg gtcatctcgt ccgactgctt gtgctgttaa 13740

cgcagtggta cccattcgta aaaacgataa aacaaagtag agaaagttaa gcaggtttcc 13800

agcaagggct actccagcta ggtagtggat ttccgagaga tgacctaaga acatgatact 13860

gactaaatta ctcagtggta ctataatatt cgataggacg ttggtaaaag ctagtcggaa 13920

gtagcggggt ataaagtcat actggcttgg aaatgtcagg ctcataagat taatttgaca 13980

gtagagttgt tggaaaataa gggataataa tcaagcagac aagtagggtg acattaatgt 14040

tgaacttaga ccgcatcctg aatcaagagc gactgctacg agaaatgact ggacttaacc 14100

gccaagcatt caacgagctg ttatctcagt ttgctgatac ctatgaacgc accgtgttca 14160

actccttagc aaaccgcaaa cgtgcgcccg ggggcggacg caagcctaca ctcagaagta 14220

tagaggaaaa actattttat atcctgctgt actgcaaatg ttatccgacg tttgacttgc 14280

tgagtgtgtt gttcaacttt gaccgctcct gtgctcatga ttgggtacat cgactactgt 14340

ctgtgctaga aaccacttta ggagaaaagc aagttttgcc agcacgcaaa ctcaggagca 14400

tggaggaatt caccaaaagg tttccagatg tgaaggaggt gattgtggat ggtacggagc 14460

gtccagtcca gcgtcctcaa aaccgagaac gccaaaaaga gtattactct ggcaagaaaa 14520

agcggcatac atgcaagcag attacagtca gcacaaggga gaaacgagtg attattcgga 14580

cggaaaccag agcaggtaaa gtgcatgaca aacggctact ccatgaatca gagatagtgc 14640

aatacattcc tgatgaagta gcaatagagg gagatttggg ttttcatggg ttggagaaag 14700

aatttgtcaa tgtccattta ccacacaaga aaccgaaagg tatcgaagca aggaggcatg 14760

gcggcgggat gggtcagttt ttataagaga gttttgacaa tataaataaa agacttttga 14820

caaccagact tggcattact tagtttcagt ctttcatctc aagtttacgt tattctgagg 14880

cgaacatgaa tcttataaca acaaaaaaac aggtagatac attagtgata cacgctcatc 14940

tttttaccat gcagggaaat ggtgtgggat atattgcaga tggggcactt gcggttgagg 15000

gtagccgtat tgtagcagtt gattcgacgg aggcgttgct gagtcatttt gagggcagaa 15060

aggttattga gtccgcgaat tgtgccgtct tgcctgggct gattaatgct cacgtagaca 15120

caagtttggt gctgatgcgt ggggcggcgc aagatgtaac taattggcta atggacgcga 15180

ccatgcctta ttttgctcac atgacacccg tggcgagtat ggctgcaaca cgcttaaggg 15240

tggtagaaga gttgaaagca ggcacaacaa cattctgtga caataaaatt attagccccc 15300

tgtggggcga atttttcgat gaaattggtg tacgggctag tttagctcct atgttcgatg 15360

cactcccact ggagatgcca ccgcttcaag acggggagct ttatcccttc gatatcaagg 15420

cgggacggcg ggcgatggca gaggctgtgg attttgcctg tgggtggaat ggggcagcag 15480

aggggcgtat cactaccatg ttaggaatgt attcgccaga tatgatgccg cttgagatgc 15540

tacgcgcagc caaagagatt gctcaacggg aaggcttaat gctgcatttt catgtagcgc 15600

agggagatcg ggaaacagag caaatcgtta aacgatatgg taagcgtccg atcgcatttc 15660

tagctgagat tggctacttg gacgaacagt tgctggcagt tcacctcacc gatgccaccg 15720

atgaagaggt gatacaagta gccaaaagtg gcgctggcat ggtactctgt tcgggaatga 15780

ttggcactat tgacggtatc gtgccgcccg ctcatgtgtt tcggcaagca ggcggacccg 15840

ttgcgctagg cagcagctac aataatattt tccatgagat gaagctgacc gccttattca 15900

acaaaataaa atatcacgat ccaaccatta tgccggcttg ggaagtcctg cgtatggcta 15960

ccatcgaagg agcgcgggcg attggtttag atcacaagat tggctctctt gaagttggca 16020

aagaagccga cctgatctta atagacctca gcacccctaa cctctcaccc actctgctta 16080

accccattcg taaccttgta cctaatttcg tgtacgctgc ttcaggacat gaagttaaaa 16140

gtgtcatggt ggcgggaaaa ctgttattgg aagactacca agtcctcaca gtagatgagt 16200

ctgctatcat tgctgaagca caattgcaag cccaacagat ttctcaatgc gtagcatctg 16260

accctatcca caaaaaaatg gtgctgatgg cggcgatggc aaggggccaa ttgtaggaat 16320

ggtcttgagt tatctagtaa gctaagttgc caactaacaa ttaaaaatac gaagcaggtg 16380

ataaggcaga attacagcag gttgtctttc ggatcgctcg ttggatcttt gtaccttccc 16440

tagtcatggc gatcgccctc atcgtcttcg cccaacccgt gatgagcctg ttcggtgcag 16500

agtttgctgt ggctcattgg tagccgatac catccctcca actgacttgt catgatagtc 16560

atggtgcgac tttcccttcg gtactgataa actgggattg aatccctttc agagtcatca 16620

tgatagattt gggaagtcta aatgtggtcg agaagaaagt gcttttccca tgttgagaat 16680

agtcacatta acatcagcat caaaacgcct aattctagat tttacctatg gtttcagcca 16740

aggtaaagga actgagtcta aattacacgc cgtcatgaga taatatgatt attaattttc 16800

tgtatagccc agttaattat acttgattgt aggctatttt tagcctcttc taatgaagaa 16860

tccagactaa tccttatgta cgggaatatg ttatgcaaga aaaacgaatc gcaatgtggt 16920

ctgtgccacg aagtttgggt acagtgctgc tacaagcctg gtcgagtcgg ccagataccg 16980

tagtctttga tgaacttctc tcctttccct atctctttat caaagggaaa gatatgggct 17040

ttacttggac agaccttgat tctagccaaa tgccccacgc agattggcga tccgtcatcg 17100

atctgttaaa ggctcccctg cctgaaggga aatcaatcat cgatctgtta aaggctcccc 17160

tgcctgaagg gaaatcaatt tgctatcaga agcatcaagc gtatcattta atcgaagaga 17220

ccatggggat tgagtggata ttgcccttca gcaactgctt tctgattcgc caacccaaag 17280

aaatgctctt atcttttcgt aagattgtgc cacattttac ctttgaagaa acaggctgga 17340

tcgaattaaa acggctgttt gactatgtac atcaaacgag cggagtaatc ccgcctgtca 17400

tagatgcaca cgacttgctg aacgatccgc ggagaatgct ctccaagctt tgtcaggttg 17460

taggggttga gtttaccgag acaatgctca gttggccccc catggaggtc gagttgaacg 17520

aaaaactagc cccttggtac agcaccgtag caagttctac gcattttcac tcgtatcaga 17580

ataaaaatga gtcgttgccg ctatatcttg tcgatatttg taaacgctgc gatgaaatat 17640

atcaggaatt atatcaattt cgactttatt agagagtatt ggtaatgaaa attttgaatt 17700

agtgaagaaa tagaagttga gaatatagac catctaggga tagagactta tgctggacgg 17760

attcaacaac atcaggacaa ttacccacgt cagagtgatt ttagctttgc tgtttacgga 17820

caattatgga tttatggcat ggaactatag gctgatttag ctctaagctt aattagtctt 17880

aaacctcata aacgcctctt tttcaagcgt ggctttcagg ctctatccct tatgaaacaa 17940

gctgtttgac cactttgtca cccggtaagg agaaaaacct taaacccaag cagaaaaaat 18000

tagcccgtaa aaaaaaggga agtaaatcaa ggaaatatag ggtaatatat ttttcacaag 18060

tttatcaatt gtaatctact tgattcagta aattaattaa ggtgttgaag agatgcaaac 18120

aagaattgta aatagctgga atgagtggga tgaactaaag gagatggttg tcgggattgc 18180

agatggtgct tattttgaac caactgagcc aggtaaccgc cctgctttac gcgataagaa 18240

cattgccaaa atgttctctt ttcccagggg tccgaaaaag caagaggtaa cagagaaagc 18300

taatgaggag ttgaatgggc tggtagcgct tctagaatca cagggcgtaa ctgtacgccg 18360

cccagagaaa cataactttg gcctgtctgt gaagacacca ttctttgagg tagagaatca 18420

atattgtgcg gtctgcccac gtgatgttat gatcaccttt gggaacgaaa ttctcgaagc 18480

aactatgtca cggcggtcac gcttctttga gtatttaccc tatcgcaaac tagtctatga 18540

atattggcat aaagatccag atatgatctg gaatgctgcg cctaaaccga ctatgcaaaa 18600

tgccatgtac cgcgaagatt tctgggagtg tccgatggaa gatcgatttg agagtatgca 18660

tgattttgag ttctgcgtca cccaggatga ggtgattttt gacgcagcag actgtagccg 18720

ctttggccgt gatatttttg tgcaggagtc aatgacgact aatcgtgcag ggattcgctg 18780

gctcaaacgg catttagagc cgcgtcgctt ccgcgtgcat gatattcact tcccactaga 18840

tattttccca tcccacattg attgtacttt tgtcccctta gcacctgggg ttgtgttagt 18900

gaatccagat cgccccatca aagagggtga agagaaactc ttcatggata acggttggca 18960

attcatcgaa gcacccctcc ccacttccac cgacgatgag atgcctatgt tctgccagtc 19020

cagtaagtgg ttggcgatga atgtgttaag catttccccc aagaaggtca tctgtgaaga 19080

gcaagagcat ccgcttcatg agttgctaga taaacacggc tttgaggtct atccaattcc 19140

ctttcgcaat gtctttgagt ttggcggttc gctccattgt gccacctggg atatccatcg 19200

cacgggaacc tgtgaggatt acttccctaa actaaactat acgccggtaa ctgcatcaac 19260

caatggcgtt tctcgcttca tcatttagta ggttttatag ttatgcaaaa gagagaaagc 19320

ccacagatac tatttgatgg gaatggaaca caatctgagt ttccagatag ttgcattcac 19380

cacttgttcg aggatcaagc cgcaaagcga ccggatgcga tcgctctcat tgacggtgag 19440

caatccctta cctacgggga actaaatgta cgcgctaacc acctagccca gcatctcttg 19500

tccctaggct gtcaacccga tgacctcctc gccatctgca tcgagcgttc ggcagaactc 19560

tttattggtt tgttgggtat cctaaaagcc ggatgtgctt atgtgccttt ggatgtaggc 19620

tatcctggcg atcgcataga gtatatgttg cgggactcgg atgcgcgtat tttactaacc 19680

tcaacggatg tcgctaagaa acttgcctta accatacctg cattgcaaga gtgccaaacc 19740

gtctatttag atcaagagat atttgagtat gattttcatt ttttagcgat agctaaacta 19800

ttacataacc aatacttgag attattacat ttttattttt ataccttgat tcagcaatgc 19860

caggcaactt cggtttccca agggattcag acacaggttc tccccaataa tctcgcttac 19920

tgcatttaca cctctggctc taccggaaat cccaaaggga tcttgatgga acatcgctca 19980

ctggtgaata tgctttggtg gcatcagcaa acgcggcctt cggttcaggg tgttaggacg 20040

ctgcaatttt gtgcagtcag ctttgacttt tcctgccatg aaatttttc taccctctgt 20100

cttggcggga tattggtctt ggtgccagag gcagtgcgcc aaaatccctt tgcattggct 20160

gagttcatca gtcaacagaa aattgaaaaa ttgtttcttc ccgttatagc attactacag 20220

ttggccgaag ctgtaaatgg gaataaaagc acctccctcg cgctttgcga agttatcact 20280

accggggagc agatgcagat cacacctgct gtcgccaacc tctttcagaa aaccggggcg 20340

atgttgcata atcactacgg ggcaacagaa tttcaagatg ccaccactca taccctcaag 20400

ggcaatccag agggctggcc aacactggtg ccagtgggtc gtccactgca caatgttcaa 20460

gtgtatattc tggatgaggc acagcaacct gtacctcttg gtggagaggg tgaattctgt 20520

attggtggta ttggactggc tcgtggctat cacaatttgc ctgacctaac gaatgaaaaa 20580

tttattccca atccatttgg ggctaatgag aacgctaaaa aactctaccg cacaggggac 20640

ttggcacgct acctacccga cggcacgatt gagcatttag gacggataga ccaccaggtt 20700

aagatccgag gtttccgcgt ggaattgggg gaaattgagt ccgtgctggc aagtcaccaa 20760

gctgtgcgtg aatgtgccgt tgtggcacgg gagattgcag gtcatacaca gttggtaggg 20820

tatatcatag caaaggatac acttaatctc agtttcgaca aacttgaacc tatcctgcgt 20880

caatattcgg aagcggtgct gccagaatac atgataccca ctcggttcat caatatcagt 20940

aatatgccgt tgactcccag tggtaaactt gaccgcaggg cattacctga tcccaaaggc 21000

gatcgccctg cattgtctac cccacttgtc aagcctcgta cccagacaga gaaacgttta 21060

gcagagattt ggggcagtta tcttgctgta gatattgtgg gaacccacga caatttcttt 21120

gatctaggcg gtacgtcact gctattgact caagcgcaca aattcctgtg cgagaccttt 21180

aatattaatt tgtccgctgt ctcactcttt caatatccca caattcagac attggcacaa 21240

tatattgatt gccaaggaga cacaacctca agcgatacag catccaggca caagaaagta 21300

cgtaaaaagc agtccggtga cagcaacgat attgccatca tcagtgtggc aggtcgcttt 21360

ccgggtgctg aaacgattga gcagttctgg cataatctct gtaatggtgt tgaatccatc 21420

acccttttta gtgatgatga gctagagcag actttgcctg agttatttaa taatcccgct 21480

tatgtcaaag caggtgcggt gctagaaggc gttgaattat ttgatgctac ctttttggc 21540

tacagcccca aagaagctgc ggtgacagac cctcagcaac ggattttgct agagtgtgcc 21600

tgggaagcat ttgaacgggc tggctacaac cccgaaacct atccagaacc agttggtgtt 21660

tatgctggtt caagcctgag tacctatctg cttaacaata ttggctctgc tttaggcata 21720

attaccgagc aacccttttat tgaaacggat atggagcagt ttcaggctaa aattggcaat 21780

gaccggagct atcttgctac acgcatctct tacaagctga atctcaaggg tccaagcgtc 21840

aatgtgcaga ccgcctgctc aacctcgtta gttgcggttc acatggcctg tcagagtctc 21900

attagtggag agtgtcaaat ggctttagcc ggtggtattt ctgtggttgt accacagaag 21960

gggggctatc tctacgaaga aggcatggtt cgttcccagg atggtcattg tcgcgccttt 22020

gatgccgaag cccaagggac tatatttggc aatggcggcg gcttggtttt gcttaaacgg 22080

ttgcaggatg cactggacga taacgacaac attatggcag tcatcaaagc cacagccatc 22140

aacaacgacg gtgcgctcaa gatgggctac acagcaccga gcgtggatgg gcaagctgat 22200

gtaattagcg aggcgattgc tatcgctgac atagatgcaa gcaccattgg ctatgtagaa 22260

gctcatggca cagccaccca attgggtgat ccgattgaag tagcagggtt agcaagggca 22320

tttcagcgta gtacggacag cgtccttggt aaacaacaat gcgctattgg atcagttaaa 22380

actaatattg gccacttaga tgaggcggca ggcattgccg gactgataaa ggctgctcta 22440

gctctacaat atggacagat tccaccgagc ttgcactatg ccaatcctaa tccacggatt 22500

gattttgacg caaccccatt ttttgtcaac acagaactac gcgaatggtc aaggaatggt 22560

tatcctcggc gggcgggggt gagttctttt ggtgtgggtg gaactaacag ccatattgtg 22620

ctggaggagt cgcctgtaaa gcaacccaca ttgttctctt ctttgccaga acgcagtcat 22680

catctgctga cgctttctgc ccatacacaa gaggctttgc atgagttggt gcaacgctac 22740

atccaacata acgagacaca ccttgatatt aacttaggcg acctctgttt cacagccaat 22800

acgggacgca agcattttga gcatcgccta gcggttgtag ccgaatcaat ccctggctta 22860

caggcacaac tggaaactgc acagactgcg atttcagcac agaaaaaaaa tgccccgccg 22920

acgatcgcat tcctgtttac aggtcaaggc tcacaataca ttaacatggg gcgcaccctc 22980

tacgatactg aatcaacatt ccgtgcagcc cttgaccgat gtgaaaccat tctccaaaat 23040

ttagggatcg agtccattct ctccgttatt tttggttcat ctgagcatgg actctcatta 23100

gatgacacag cctataccca gcccgcactc tttgccatcg aatacgcgct ctatcaatta 23160

tggaagtcgt ggggcatcca gccctcagtg gtgataggtc atagtgtagg tgaatatgtg 23220

tccgcttgtg tggcgggagt ctttagctta gaggatgggt tgaaactgat tgcagaacga 23280

ggacgactga tacaggcact tcctcgtgat gggagcatgg tttccgtgat ggcaagcgag 23340

aagcgtattg cagatatcat tttaccttat gggggacagg tagggatcgc cgcgattaat 23400

ggcccacaaa gtgttgtaat ttctgggcaa cagcaagcga ttgatgctat ttgtgccatc 23460

ttggaaactg agggcatcaa aagcaagaag ctaaacgtct cccatgcctt ccactcgccg 23520

ctagtggaag caatgttaga ctctttcttg caggttgcac aagaggtcac ttactcgcaa 23580

cctcaaatca agcttatctc taatgtaacg ggaacattgg caagccatga atcttgtccc 23640

gatgaacttc cgatcaccac cgcagagtat tgggtacgtc atgtgcgaca gcccgtccgg 23700

tttgcggcgg gaatggagag ccttgagggt caaggggtaa acgtatttat agaaatcggt 23760

cctaaacctg ttcttttagg catgggacgc gactgcttgc ctgaacaaga gggactttgg 23820

ttgcctagtt tgcgcccaaa acaggatgat tggcaacagg tgttaagtag tttgcgtgat 23880

ctatacttag caggtgtaac cgtagattgg agcagtttcg atcaggggta tgctcgtcgc 23940

cgtgtgccac taccgactta tccttggcag cgagagcggc attgggtaga gccaattatt 24000

cgtcaacggc aatcagtatt acaagccaca aataccacca agctaactcg taacgccagc 24060

gtggcgcagc atcctctgct tggtcaacgg ctgcatttgt cgcggactca agagatttac 24120

tttcaaacct tcatccactc cgacttccca atatgggttg ctgatcataa agtatttgga 24180

aatgtcatca ttccgggtgt cgcctatttt gagatggcac tggcagcagg gaaggcactt 24240

aaaccagaca gtatattttg gctcgaagat gtatccatcg cccaagcact gattattccc 24300

gatgaagggc aaactgtgca aatagtatta agcccacagg aagagtcagc ttatttttt 24360

gaaatcctct ctttagaaaa agaaaactct tgggtgcttc atgcctctgg taagctagtc 24420

gcccaagagc aagtgctaga aaccgagcca attgacttga ttgcgttaca ggcacattgt 24480

tccgaagaag tgtcagtaga tgtgctatat caggaagaaa tggcgcgccg gctggatatg 24540

ggtccaatga tgcgtggggt gaagcagctt tggcgttatc cgctctcctt tgccaaaagt 24600

catgatgcga tcgcactcgc caaggtcagc ttgccagaaa tcttgcttca tgagtccaat 24660

gcctaccaat tccatcctgt aatcttggat gcggggctgc aaatgataac ggtctcttat 24720

cctgaagcaa accaaggcca gacttatgta cctgttggta tagagggtct acaagtctat 24780

ggtcgtccca gttcagaact ttggtgtcgc gcccaatatc ggcctccttt ggatacagat 24840

caaaggcagg gtattgattt gctgccaaag aaattgattg cagacttgca tctatttgat 24900

acccagggtc gtgtggttgc catcatgttt ggtgtgcaat ctgtccttgt gggacgggaa 24960

gcaatgttgc gatcgcaaga tacttggcga aattggcttt atcaagtcct gtggaaacct 25020

caagcctgtt ttggactttt accgaattac ctgccaaccc cagataagat tcggaaacgc 25080

ctggaaacaa agttagcgac attgatcatc gaagctaatt tggcgactta tgcgatcgcc 25140

tatacccaac tggaaaggtt aagtctagct tacgttgtgg cggctttccg acaaatgggc 25200

tggctgtttc aacccggtga gcgtttttcc accgcccaga aggtatcagc gttaggaatc 25260

gttgatcaac atcggcaact attcgctcgt ttgctcgaca ttctagccga agcagacata 25320

ctccgcagcg aaaacttgat gacgatatgg gaagtcattt catacccgga aacgattgat 25380

atacaggtac ttcttgacga cctcgaagcc aaagaagcag aagccgaagt cacactggtt 25440

tcccgttgca gtgcaaaatt ggccgaagta ttacaaggaa aatgtgaccc catacagttg 25500

ctctttcccg caggggacac aacaacgtta agcaaactct atcgtgaagc cccagttttg 25560

ggtgttacta atactctagt ccaagaagcg cttctttccg ccctggagca gttgccgccg 25620

gaacgtggtt ggcgaatttt agagattggt gctggaacag gtggaaccac agcctacttg 25680

ttaccgcatc tgcctgggga tcagacaaaa tatgtcttta ccgatattag tgccttttt 25740

cttgccaaag cggaagagcg ttttaaagat tacccgtttg tacgttatca ggtattagat 25800

atcgaacaag caccacaggc gcaaggattt gaaccccaaa tatacgattt aatcgtagca 25860

gcggatgtct tgcatgctac tagtgacctg cgtcaaactc ttgtacatat ccggcaatta 25920

ttagcgccgg gcgggatgtt gatcctgatg gaagacagcg aacccgcacg ctgggctgat 25980

ttaacctttg gcttaacaga aggctggtgg aagtttacag accatgactt acgccccaac 26040

catccgctat tgtctcctga gcagtggcaa atcttgttgt cagaaatggg atttagtcaa 26100

acaaccgcct tatggccaaa aatagatagc ccccataaat tgccacggga ggcggtgatt 26160

gtggcgcgta atgaaccagc catcagaaaa ccccgaagat ggctgatctt ggctgacgag 26220

gagattggtg gactactagc caaacagcta cgtgaagaag gagaagattg tatactcctc 26280

ttgccagggg aaaagtacac agagagagat tcacaaacgt ttacaatcaa tcctggagat 26340

attgaagagt ggcaacagtt attgaaccga gtaccgaaca tacaagaaat tgtacattgt 26400

tggagtatgg tttccactga cttagataga gccactattt tcagttgcag cagtacgctg 26460

catttagttc aagcattagc aaactatcca aaaaaccctc gcttgtcact tgtcacccta 26520

ggcgcacaag ccgttaacga acatcatgtt caaaatgtag ttggagcagc cctctggggc 26580

atgggaaagg taattgcact cgaacaccca gagctacaag tagcacaaat ggatttagac 26640

ccgaatggga aggttaaggc gcaagtagaa gtgcttaggg atgaacttct cgccagaaaa 26700

gaccctgcat cagcaatgtc tgtgcctgat ctgcaaacac gacctcatga aaagcaaata 26760

gcctttcgtg agcaaacacg ttatgtggca agactttcgc ccttagaccg ccccaatcct 26820

ggagagaaag gcacacaaga ggctcttacc ttccgtgatg atggcagcta tctgattgct 26880

ggtggtttag gcggactggg gttagtggtg gctcgttttc tggttacaaa tggggctaaa 26940

taccttgtgc tagtcggacg acgtggtgcg agggaggaac agcaagctca attaagcgaa 27000

ctagagcaac tcggagcttc cgtgaaagtt ttacaagccg atattgctga tgcagaacaa 27060

ctagcccaag cactttcagc agtaacctac ccaccattac ggggtgttat tcatgcggca 27120

ggtacattga acgatgggat tctacagcag caaagttggc aagcctttaa agaagtgatg 27180

aatcccaagg tagcaggtgc gtggaaccta catatactga caaaaaatca gcctttagac 27240

ttctttgtcc tgttctcctc cgccacctct ttgttaggta acgctggaca agccaatcac 27300

gccgccgcaa atgctttcct tgatgggtta gcctcctatc gtcgtcactt aggactaccg 27360

agcctctcga ttaattgggg gacatggagc gaagtgggaa ttgcggctcg acttgaacta 27420

gataagttgt ccagcaaaca gggagaggga accattacgc taggacaggg cttacaaatt 27480

cttgagcagt tgctcaaaga cgagaatggg gtgtatcaag tgggtgtcat gcctatcaac 27540

tggacacaat tcttagcaag gcaattgact ccgcagccgt tcttcagcga tgccatgaag 27600

agtattgaca cctctgtagg taaactaacc ttgcaggagc gggactcttg cccccaaggt 27660

tacgggcata atattcgaga gcaattagag aacgctccgc ccaaagaggg tctgactctc 27720

ttgcaggctc atgttcggga gcaggtttcc caagttttgg ggatagacac gaagacatta 27780

ttggcagaac aagacgtggg tttctttacc ctggggatgg attcgctgac ctctgtcgag 27840

ttaagaaaca ggttacaagc cagtttgggc tgctctcttt cttccacttt ggcttttgac 27900

tatccaacac aacaggctct tgtgaattat cttgccaatg aattgctggg aacccctgag 27960

cagctacaag agcctgaatc tgatgaagaa gatcagatat cgtcaatgga tgacatcgtg 28020

cagttgctgt ccgcgaaact agagatggaa atttaagccc atggatgaaa aactaagaac 28080

atacgaacga ttaatcaagc aatcctatca caagatagag gctctggaag ctgaagttaa 28140

caggttgaag caaacccaat gtgaacctat cgccatcgtc ggcatgggct gtcgttttcc 28200

tggtgcgaat agtccagaag cgttttggca gttgttgtgt gatggggttg atgctattcg 28260

tgagatacca aaaaatcgat gggttgttga tgcctacata gatgaaaatt tggaccgcgc 28320

agacaagaca tcaatgcgat ttggcgggtt tgtcgagcaa cttgagaagt ttgatgccca 28380

attctttggc atatcaccgc gagaagcggt ttctcttgac cctcagcaac gtttgttatt 28440

agaagtaagt tgggaagcac tggaaaatgc agcggtgata ccaccttcgg caacgggcgt 28500

attcgtcggt attagtaacc ttgattatcg tgaaacgctc ttgaagcaag gagcaattgg 28560

tacttatttt gcttcgggta atgcccatag cacagccagt ggtcgcttgt cttactttct 28620

cggtctgaca ggcccctgtc tctcgataga tacagcttgt tcttcgtcgt tggtcgctgt 28680

acatcagtca ctgataagtc tgcgtcagcg agaatgtgac ttagcgttgg ttgggggagt 28740

ccatcggctg atagccccag aggaaagtgt ctcgttagca aaagcccata tgttatctcc 28800

cgatggtcgt tgcaaagtct ttgatgcgtc ggcaaacggg tatgtccgag ccgaaggatg 28860

tggcatgata gtcctcaaac gattatcgga cgcgcaagct gatggggata aaatcttggc 28920

gttgattcgc gggtcagcca taaatcaaga cggtcgcacg agtggcttga ccgttccaaa 28980

tggtccccaa caagccgacg tgattcgcca agccctcgcc aatagtggca taagaccaga 29040

acaagttaac tatgtagaag ctcatggcac agggacttcc ctaggagacc cgattgaggt 29100

cggcgcgttg ggaacgatct ttaatcaacg ctcccaacct ttaattattg gttcagttaa 29160

aacaaatatt gggcatctag aagcagcagc agggattgct ggactgatta aagtcgtcct 29220

tgccatgcag catggagaaa ttccacctaa tttacacttt caccagccca atcctcgcat 29280

taactgggat aaattgccaa tcaggatccc cacagaacga acagcttggc ctactggcga 29340

tcgcatcgca gggataagtt ctttcggctt tagtggcact aattctcatg tcgtgttaga 29400

ggaagcccca aaaatagagc cgtctacttt agagattcat tcaaagcagt atgtttttac 29460

cttatcagca gcgacacctc aagcactaca agaacttact cagcgttatg taacttatct 29520

cactgaacac ttacaagaga gtctggcgga tatttgcttt acagccaaca cagggcgcaa 29580

acactttaga catcgctttg cagtagtagc agagtctaaa acccagttgc gccaacaatt 29640

ggaaacgttt gcccaatcgg gagaggggca ggggaagagg acatctctct caaaaatagc 29700

ttttctcttt acaggtcaag gctcacagta tgtggggatg gggcaagaac tttatgagag 29760

ccaacccacc ttccggcaaa ccattgaccg atgtgatgag attcttcgtt cactgttggg 29820

caaatcaatc ctctcaatac tctatcccag ccaacaaatg ggattggaaa cgccatccca 29880

aattgatgaa accgcctata ctcaacccac tctttttct cttgaatatg cactggcgca 29940

gttgtggcgc tcctggggta ttgagcctga tgtggtgatg gggcatagtg tgggagaata 30000

tgtggccgct tgtgtggcgg gtgtcttttc tttagaggat ggactcaaac taattgctga 30060

aagaggccgt ctgatgcaag aattgcctcc cgatggggcg atggtttcag ttatggccaa 30120

taaatcgcgc atagagcaag caattcaatc tgtcagccga gaggtttcta ttgcggccat 30180

caatggacct gagagtgtgg ttatctctgg taaaagggag atattacaac agattaccga 30240

acatctggtt gccgaaggca ttaagacacg ccaactgaag gtctctcatg cctttcactc 30300

accattgatg gagccaatat taggtcagtt ccgccgagtt gccaatacca tcacctatcg 30360

gccaccgcaa attaaccttg tctcaaatgt cacaggcgga caggtgtata aagaaatcgc 30420

tactcccgat tattgggtga gacatctgca agagactgtc cgttttgcgg atggggttaa 30480

ggtgttacat gaacagaatg tcaatttcat gctcgaaatt ggtcccaaac ccacactgct 30540

gggcatggtt gagttacaaa gttctgagaa tccattttct atgccaatga tgatgcccag 30600

tttgcgtcag aatcgtagcg actggcagca gatgttggag agcttgagtc aactctatgt 30660

tcatggtgtt gagattgact ggatcggttt taataaagac tatgtgcgac ataaagttgt 30720

cctgccgaca tacccatggc agaaggagcg ttactgggta gaattggatc aacagaagca 30780

cgccgctaaa aatctacatc ctctactgga caggtgcatg aagctgcctc gtcataacga 30840

aacaattttt gagaaagaat ttagtctaga gacattgccc tttcttgctg actatcgcat 30900

ttatggttca gttgtgtcgc caggtgcaag ttatctatca atgatactaa gtattgccga 30960

gtcgtatgca aatggtcatt tgaatggagg gaatagtgca aagcaaacca cttatttact 31020

aaaggatgtc acattcccag tacctcttgt gatctctgat gaggcaaatt acatggtgca 31080

agttgcttgt tctctctctt gtgctgcgcc acacaatcgt ggcgacgaga cgcagtttga 31140

attgttcagt tttgctgaga atgtacctga aagtagcagt ataaatgctg attttcagac 31200

acccattatt catgcaaaag ggcaatttaa gcttgaagat acagcacctc ctaaagtgga 31260

gctagaagaa ctacaagcgg gttgtcccca agaaattgat ctcaaccttt tctatcaaac 31320

attcacagac aaaggttttg tttttggatc tcgttttcgc tggttagaac aaatctgggt 31380

gggcgatgga gaagcattgg cgcgtctgcg acaaccggaa agtattgaat cgtttaaagg 31440

atatgtgatt catcccggtt tgttggatgc ctgtacacaa gtcccatttg caatttcgtc 31500

tgacgatgaa aataggcaat cagaaacgac aatgcccttt gcgctgaatg aattacgttg 31560

ttatcagcct gcaaacggac aaatgtggtg ggttcatgca acagaaaaag atagatatac 31620

atgggatgtt tctctgtttg atgagagcgg gcaagttatt gcggaattta taggtttaga 31680

agttcgtgct gctatgcccg aaggcttact aagggcagac ttttggcata actggctcta 31740

tacagtgaat tggcgatcgc aacctctaca aatcccagag gtgctggata ttaataagac 31800

aggtgcagaa acatggcttc tttttgcaca accagaggga ataggagcgg acttagccga 31860

atatttgcag agccaaggaa agcactgtgt ttttgtagtg cctgggagtg agtatacagt 31920

gaccgagcaa cacattggac gcactggaca tcttgatgtg acgaaactga caaaaattgt 31980

cacgatcaat cctgcttctc ctcatgacta taaatatttt ttagaaactc tgacggacat 32040

tagattacct tgtgaacata tactctattt atggaatcgt tatgatttaa caaatacttc 32100

taatcatcgg acagaattga ctgtaccaga tatagtctta aacttatgta ctagtcttac 32160

ttatttggta caagccctta gccacatggg tttttccccg aaattatggc taattacaca 32220

aaatagtcaa gcggttggta gtgacttagc gaatttagaa atcgaacaat ccccattatg 32280

ggcattgggt cgaagcatcc gcgccgaaca ccctgaattt gattgccgtt gtttagattt 32340

tgacacgctc tcaaatatcg caccactctt gttgaaagag atgcaagcta tagactatga 32400

atctcaaatt gcttaccgac aaggaacgcg ctatgttgca cgactaattc gtaatcaatc 32460

agaatgtcac gcaccgattc aaacaggaat ccgtcctgat ggcagctatt tgattacagg 32520

tggattaggc ggtctaggat tgcaggtagc actcgccctt gcggacgctg gagcaagaca 32580

cttgatcctc aatagtcgcc gtggtacggt ctccaaagaa gcccagttaa ttattgaccg 32640

actacgccaa gaggatgtta gggttgattt gattgcggca gatgtctctg atgcggcaga 32700

tagcgaacga ctcttagtag aaagtcagcg caagacctct cttcgaggga ttgtccatgt 32760

tgcgggagtc ttggatgatg gcatcctgct ccaacaaaat caagagcgtt ttgaaaaagt 32820

gatggcggct aaggtacgcg gagcttggca tctggaccaa cagagccaaa ccctcgattt 32880

agatttcttt gttgcgttct catctgttgc gtcgctcata gaagaaccag gacaagccaa 32940

ttacgccgca gcgaatgcgt ttttggattc attaatgtat tatcgtcaca taaagggatc 33000

taatagcttg agtatcaact gggggggcttg ggcagaagtc ggcatggcag ccaatttatc 33060

atgggaacaa cggggaatcg cggcaatttc tccaaagcaa gggaggcata ttctcgtcca 33120

acttattcaa aaacttaatc agcatacaat cccccaagtt gctgtacaac cgaccaattg 33180

ggctgaatat ctatcccatg atggcgtgaa tatgccattc tatgaatatt ttacacacca 33240

cttgcgtaac gaaaaagaag ccaaattgcg gcaaacagca ggcagcacct cagaggaagt 33300

cagtctgcgg caacagcttc aaacactctc agagaaagac cgggatgccc ttttgatgga 33360

acatcttcaa aaaactgcga tcagagttct cggtttggca tctaatcaaa aaattgatcc 33420

ctatcaggga ttgatgaata tgggactaga ctctttgatg gcggttgaat ttcggaatca 33480

cttgatacgt agtttagaac gccctctgcc agccactctg ctctttaatt gcccaacact 33540

tgattcattg catgattacc tagtcgcaaa aatgtttgat gatgcccctc agaaggcaga 33600

gcaaatggca caaccaacaa cactgacagc acacagcata tcaatagaat ccaaaataga 33660

tgataacgaa agcgtggatg acattgcaca aatgctggca caagcactca atatcgcctt 33720

tgagtagcaa tgggcagccc ttaacctttc aaggtgacta atcaatagac ctcttgcaca 33780

attgtttctg tggtacaata agtggtttta ggttttatgt atatttgggt gttgttgcga 33840

tagctacgct cgccgaaggc atcacaaatt caaagatagg cgtgtgattc taacttttag 33900

cttaacgggt gacaaggcgg ctaaagagct tgtttcataa gggatagagc ctgaaagccc 33960

cgttgaaaaa agaggcgttt atgaggcttg agattgatta aattcagagc taaatcagcc 34020

cataattcca taccataaat ccatagttgt ccgtagagac caaagctaaa atcactttga 34080

cgtgggtact tgtcctgatg ttgttgaatc ccacattcag catgagtaaa tatactcaaa 34140

atatttttcc cagcaggtta agtgttctaa tcctaagtct gatatcttat ttttgataag 34200

ggacttaccg cgtaatagtt aaatttttgt atagcctaat tttacttggt ttaaggctct 34260

tttttgctct tttggtgaat tattcaggat aatcaaagat gagtcagccc aattatggca 34320

ttttgatgaa aaatgcgttg aacgaaataa atagcctacg atcgcaacta gctgcggtag 34380

aagcccaaaa aaatgagtct attgccattg ttggtatgag ttgccgtttt ccaggcggtg 34440

caactactcc agagcgtttt tgggtattac tgcgcgaggg tatatcagcc attacagaaa 34500

tccctgctga tcgctgggat gttgataaat attatgatgc tgaccccaca tcgtccggta 34560

aaatgcatac tcgttacggc ggttttctga atgaagttga tacatttgag ccatcattct 34620

ttaatattgc tgcccgtgaa gccgttagca tggatccaca gcaacgcttg ctacttgaag 34680

tcagttggga agctctggaa tccggtaata ttgttcctgc aactcttttt gatagttcca 34740

ctggtgtatt tatcggtatt ggtggtagca actacaaatc tttaatgatc gaaaacagga 34800

gtcggatcgg gaaaaccgat ttgtatgagt taagtggcac tgatgtgagt gttgctgccg 34860

gcaggatatc ctatgtcctg ggtttgatgg gtcccagttt tgtgattgat acagcttgtt 34920

catcttcttt ggtctcagtt catcaagcct gtcagagtct gcgtcagaga gaatgtgatc 34980

tagcactagc tggtggagtc ggtttactca ttgatccaga tgagatgatt ggtctttctc 35040

aaggggggat gctggcacct gatggtagtt gtaaaacatt tgatgccaat gcaaatggct 35100

atgtgcgagg cgaaggttgt gggatgattg ttctaaaacg tctctcggat gcaacagccg 35160

atggggataa tattcttgcc atcattcgtg ggtctatggt taatcatgat ggtcatagca 35220

gtggtttaac tgctccaaga ggccccgcac aagtctctgt cattaagcaa gccttagata 35280

gagcaggtat tgcaccggat gccgtaagtt atttagaagc ccatggtaca ggcacacccc 35340

ttggtgatcc tatcgagatg gattcattga acgaagtgtt tggtcggaga acagaaccac 35400

tttgggtcgg ctcagttaag acaaatattg gtcatttaga agccgcgtcc ggtattgcag 35460

ggctgattaa ggttgtcttg atgctaaaaa acaagcagat tcctcctcac ttgcatttca 35520

agacaccaaa tccatatatt gattggaaaa atctcccggt cgaaattccg accacccttc 35580

atgcttggga tgacaagaca ttgaaggaca gaaagcgaat tgcaggggtt agttctttta 35640

gtttcagtgg tactaacgcc cacattgtat tatctgaagc cccatctagc gaactaatta 35700

gtaatcatgc ggcagtggaa agaccatggc acttgttaac ccttagtgct aagaatgagg 35760

aagcgttggc taacttggtt gggctttatc agtcatttat ttctactact gatgcaagtc 35820

ttgccgatat atgctacact gctaatacgg cacgaaccca tttttctcat cgccttgctc 35880

tatcggctac ttcacacatc caaatagagg ctcttttagc cgcttataag gaagggtcgg 35940

tgagtttgag catcaatcaa ggttgtgtcc tttccaacag tcgtgcgccg aaggtcgctt 36000

ttctctttac aggtcaaggt tcgcaatatg tgcaaatggc tggagaactt tatgagaccc 36060

agcctacttt ccgtaattgc ttagatcgct gtgccgaaat cttgcaatcc atcttttcat 36120

cgagaaacag cccttgggga aacccactgc tttcggtatt atatccaaac catgagtcaa 36180

aggaaattga ccagacggct tatacccaac ctgccctttt tgctgtagaa tatgccctag 36240

cacagatgtg gcggtcgtgg ggaatcgagc cagatatcgt aatgggtcat agcataggtg 36300

aatatgtggc agcttgtgtg gcggggatct tttctctgga ggatggtctc aaacttgctg 36360

ccgaaagagg ccgtttgatg caggcgctac cacaaaatgg cgagatggtt gctatatcgg 36420

cctcccttga ggaagttaag ccggctattc aatctgacca gcgagttgtg atagcggcgg 36480

taaatggacc acgaagtgtc gtcatttcgg gcgatcgcca agctgtgcaa gtcttcacca 36540

acaccctaga agatcaagga atccggtgca agagactgtc tgtttcacac gctttccact 36600

ctccattgat gaaaccaatg gagcaggagt tcgcacaggt ggccagggaa atcaactata 36660

gtcctccaaa aatagctctt gtcagtaatc taaccggcga cttgatttca cctgagtctt 36720

ccctggagga aggagtgatc gcttcccctg gttactgggt aaatcattta tgcaatcctg 36780

tcttgttcgc tgatggtatt gcaactatgc aagcgcagga tgtccaagtc ttccttgaag 36840

ttggaccaaa accgacctta tcaggactag tgcaacaata ttttgacgag gttgcccata 36900

gcgatcgccc tgtcaccatt cccaccttgc gccccaagca acccaactgg cagacactat 36960

tggagagttt gggacaactg tatgcgcttg gtgtccaggt aaattgggcg ggctttgata 37020

gagattacac cagacgcaaa gtaagcctac ccacctatgc ttggaagcgt caacgttatt 37080

ggctagagaa acagtccgct ccacgtttag aaacaacaca agttcgtccc gcaactgcca 37140

ttgtagagca tcttgaacaa ggcaatgtgc cgaaaatcgt ggacttgtta gcggcgacgg 37200

atgtactttc aggcgaagca cggaaattgc tacccagcat cattgaacta ttggttgcaa 37260

aacatcgtga ggaagcgaca cagaagccca tctgcgattg gctttatgaa gtggtttggc 37320

aaccccagtt gctgacccta tctaccttac ctgctgtgga aacagagggt agacaatggc 37380

tcatcttcgc cgatgctagt ggacacggtg aagcacttgc ggctcaatta cgtcagcaag 37440

gggatataat tacgcttgtc tatgctggtc taaaatatca ctcggctaat aataaacaaa 37500

ataccggggg ggacatccca tattttcaga ttgatccgat ccaaagggag gattatgaaa 37560

ggttgtttgc tgctttgcct ccactgtatg gtattgttca tctttggagt ttagatatac 37620

ttagcttgga caaagtatct aacctaattg aaaatgtaca attaggtagt ggcacgctat 37680

taaatttaat acagacagtc ttgcaacttg aaacgcccac ccctagcttg tggctcgtga 37740

caaagaacgc gcaagctgtg cgtaaaaacg atagcctagt cggagtgctt cagtcaccct 37800

tatggggtat gggtaaggtg atagccttag aacaccctga actcaactgt gtatcaatcg 37860

accttgatgg tgaagggctt ccagatgaac aagccaagtt tctggcggct gaactccgcg 37920

ccgcctccga gttcagacat accaccattc cccacgaaag tcaagttgct tggcgtaata 37980

ggactcgcta tgtgtcacgg ttcaaaggtt atcagaagca tcccgcgacc tcatcaaaaa 38040

tgcctattcg accagatgcc acttatttga tcacgggcgg ctttggtggt ttgggcttgc 38100

ttgtggctcg ttggatggtt gaacaggggg ctacccatct atttctgatg ggacgcagcc 38160

aacccaaacc agccgcccaa aaacaactgc aagagatagc cgcgctgggt gcaacagtga 38220

cggtggtgca agccgatgtt ggcatccgct cccaagtagc caatgtgttg gcacagattg 38280

ataaggcata tcctttggct ggtattattc atactgccgg tgtattagac gacggaatct 38340

tattgcagca aaattgggcg cgttttagca aggtgttcgc ccccaaacta gagggagctt 38400

ggcatctaca tacactgact gaagagatgc cgcttgattt ctttatttgt ttttcctcaa 38460

cagcaggatt gctgggcagt ggtggacaag ctaactatgc tgctgccaat gccttttag 38520

atgcctttgc ccatcatcgg cgaatacaag gcttgccagc tctctcgatt aactgggacg 38580

cttggtctca agtgggaatg acggtacgtc tccaacaagc ttcttcacaa agcaccacag 38640

ttgggcaaga tattagcact ttggaaattt caccagaaca gggattgcaa atctttgcct 38700

atcttctgca acaaccatcc gcccaaatag cggccatttc taccgatggg cttcgcaaga 38760

tgtacgacac aagctcggcc ttttttgctt tacttgatct tgacaggtct tcctccacta 38820

cccaggagca atctacactt tctcatgaag ttggccttac cttactcgaa caattgcagc 38880

aagctcggcc aaaagagcga gagaaaatgt tactgcgcca tctacagacc caagttgctg 38940

cggtcttgcg tagtcccgaa ctgcccgcag ttcatcaacc cttcactgac ttggggatgg 39000

attcgttgat gtcacttgaa ttgatgcggc gtttggaaga aagtctgggg attcagatgc 39060

ctgcaacgct tgcattcgat tatcctatgg tagaccgttt ggctaagttt atactgactc 39120

aaatatgtat aaattctgag ccagatacct cagcagttct cacaccagat ggaaatgggg 39180

aggaaaaaga cagtaataag gacagaagta ccagcacttc cgttgactca aatattactt 39240

ccatggcaga agatttattc gcactcgaat ccttactaaa taaaataaaa agagatcaat 39300

aatagagctg ttgggaaata aaagcatatt tccggatgac agaacttccc ccatcccgat 39360

tgaatttatg ctgcatctaa atagaagttc catagccctg cactgaccaa catcaattga 39420

tcatcaaaat cggtcacacg attcctatat gtgggataaa atttgcagta cagcaggata 39480

taaaatagtt tttcctctat acttctgagt gtaggcttgc gtccgccccc gggcgcacgt 39540

ttgcggtttg ctaaggagtt gaacacggtg cgttcatagg tatcagcaaa ctgagataac 39600

agctcgttga atgcttggcg gttaagtcca gtcattgctc gtagcagtcg ctcttgattc 39660

aggatgcggt ctaagttcaa cattaatgtc accctacttg tctgcttgat tattatccct 39720

tattttccaa caactctatt atagcttatc ttattttgga gtttaactac atgaaaatcg 39780

ctgtaaagac tcctactgag tgaaagtgaa cttctttccc acgtattcga gtagctgttg 39840

taagctggcc tcgatggaaa gttccgaagt ttccaccagt aaatctggtg ttctcggtgg 39900

ttcgtaggga gcgctaattc ccgtaaaaga ctcaatttct ccacggcgtg cttttgcata 39960

gagacccttg gggtcacgtt gttcacaaat ttccatcgga gttgcaatat atacttcatg 40020

aaacagatct ccggacagaa tacggatttg ctcccggtct ttcctgtaag gtgaaatgaa 40080

agcagtaatc actaaacaac ccgaatccgc aaaaagtttg gccacctcgc caatacgacg 40140

aatattttcc gcacgatcag cagcagaaaa tcccaagtca gcacataatc catgacggat 40200

attgtcacca tcaaggacaa aagtatacca acctttctgg aacaaaatcc gctctaattc 40260

tagagccaat gttgttttac ctgatcctga taatccagtg aaccatagaa ttccatttcg 40320

gtgaccattc tttaaacaac gatcaaatgg ggacacaaga tgttttgtat gttgaatatt 40380

gcttgatttc atatctatga taaatatgat aaaagtgatt ggccaaacag aactgctcac 40440

ccaataatat agttaaaggt tatttttca aaaactcctt ctaaattata gctcacaatt 40500

atgcctaaat actttaatac tgctggaccc tgtaaatccg aaatccacta tatgctctct 40560

cccacagctc gactaccgga tttgaaagca ctaattgacg gagaaaacta ctttataatt 40620

cacgcgccgc gacaagtcgg caaaactaca gctatgatag ccttagcacg agaattgact 40680

gatagtggaa aatataccgc agttattctt tccgttgaag tgggatcagt attctcccat 40740

aatccccagc aagcggagca ggttatttta gaagaatgga aacaggcaat caaattttat 40800

ttacccaaag aactacaacc atcctattgg ccagagcgtg aaacagactc aggaataggc 40860

aaaactttaa gtgagtggtc cgcacaatct ccaagacctc ttgtaatctt tttacatgaa 40920

atcgattccc taacagatga agctttaatc ctaattttaa gacaattacg ctcaggtttt 40980

ccccgtcgtc ctcggggatt tccccattcg gtggggttaa ttggtatgcg ggatgtgcgg 41040

gactataagg ttaaatctgg tggaagtgaa cgactgaata cgtcaagtcc tttcaatatc 41100

aaagcggaat ccttgacttt aagtaatttc actctgtcag aggtggaaga actttactta 41160

caacatacgc aagctacagg acaaattttt accccggaag caattaaaca agcattttat 41220

ttaaccgatg ggcaaccatg gttagtaaac gccctagctc gtcaagccac tcaggtgtta 41280

gtgaaagata ttactcaacc cattaccgct gaagtaatta accaagccaa agaagttctg 41340

attcagcgcc aggataccca tttggatagt ttggcagagc gcttacggga agatcgggtc 41400

aaagccatta ttcaacctat gttagctgga tcggacttac cagatacccc agaggatgat 41460

cgccgtttct tgctagattt aggcttggta aagcgcagtc ccttgggagg actaaccatt 41520

gccaatccca tttaccagga ggtgattcct cgtgttttgt cccagggtag tcaggatagt 41580

ctaccccaga ttcaacctac ttggttaaat actgataata ctttaaatcc tgacaaactc 41640

ttaaatgctt tcctagagtt ttggcgacaa catggggaac cattactcaa aagtgcgcct 41700

tatcatgaaa ttgctcccca tttagttttg atggcgtttt tacatcgggt agtgaatggt 41760

ggtggcactt tagaacggga atatgccgtt ggttctggaa gaatggatat ttgtttacgc 41820

tatggcaagg tagtgatggg catagagtta aaggtttggg ggggaaaatc ggatccgtta 41880

acgaagggtt tgacccaatt ggataaatat ctgggtgggt taggattaga tagaggttgg 41940

ttagtaattt ttgatcaccg tccgggatta ccacccatgg gtgagaggat tagtatggaa 42000

caggccatta gtccagaggg aagaaccatt acagtgattc gtagctagag cgttagatat 42060

cagatgattg aacctcaatt attgtgcaac gccacatttt ctttccaaag atgtatgtta 42120

aactctagta aactctaatt aggtcgagaa agagat 42156

<210> 81
<211> 5631
<212> DNA
<213> Cylindrospermopsis raciborskii AWT205

<400> 81
atgcggtcta agttcaacat taatgtcacc ctacttgtct gcttgattat tatcccttat 60

tttccaacaa ctctaatgaa agtacctata acagcaaacg aagatgcagc tacattactt 120

cagcgtgttg gactgtccct aaaggaagca caccaacaac ttgaggcaat gcaacgccga 180

gcgcacgaac cgatcgcaat tgtggggctg gggctgcggt ttccgggagc tgattcacca 240

cagacattct ggaaactact tcagaatggt gttgatatgg tcaccgaaat ccctagcgat 300

cgctgggcag ttgatgaata ctatgatccc caacctgggt gtccaggcaa aatgtatatt 360

cgtgaagccg cttttgttga tgcagtggat aaattcgatg cctcgttttt tgatatttcg 420

ccacgtgaag cggccaatat agatccccag catagaatgt tgctggaggt agcttgggag 480

gcactcgaaa gggctggcat tgctcccagc caattgatgg atagccaaac gggggtattt 540

gtcgggatga gcgaaaatga ctattatgct cacctagaaa atacagggga tcatcataat 600

gtctatgcgg caacgggcaa tagcaattac tatgctccgg ggcgtttatc ctatctattg 660

gggcttcaag gacctaacat ggtcgttgat agtgcctgtt cctcctcctt agtggctgta 720

catcttgcct gtaatagttt gcggatggga gaatgtgatc tggcactggc tggtggcgtt 780

cagcttatgt taatcccaga ccctatgatt gggactgccc agttaaatgc ctttgcgacc 840

gatggtcgta gtaaaacatt tgacgctgcc gccgatggct atggacgcgg cgaaggttgt 900

ggcatgattg tacttaaaag aataagtgac gcgatcgtgg cagacgatcc aattttagcc 960

gtaatccggg gtagtgcagt caatcatggc gggcgtagca gtggtttaac tgcccctaat 1020

aagctgtctc aagaagcctt actgcgtcag gcactacaaa acgccaaggt tcagccggaa 1080

gcagtcagtt atatcgaagc ccatggcaca gggacacaac tgggcgaccc gattgaggtg 1140

ggagcattaa cgaccgtctt tggatcttct cgttcagaac ccttgtggat tggctctgtc 1200

aaaactaata tcggacacct agaaccagcc gctggtattg cggggttaat aaaagtcatt 1260

ttatcattac aagaaaaaca gattcctccc agtctccatt ttcaaaaccc taatcccttc 1320

attgattggg aatcttcgcc agttcaagtg ccgacacagt gtgtaccctg gactgggaaa 1380

gagcgcgtcg ctggagttag ctcgtttggt atgagcggta caaactgtca tctagttgtc 1440

gcagaagcac ctgtccgcca aaacgaaaaa tctgaaaatg caccggagcg tccttgtcac 1500

attctgaccc tttcagccaa aaccgaagcg gcactcaacg cattggtagc ccgttacatg 1560

gcatttctca gggaagcgcc cgccatatcc ctagctgatc tttgttatag tgccaatgtc 1620

gggcgtaatc tttttgccca tcgcttaagt tttatctccg agaacatcgc gcagttatca 1680

gaacaattag aacactgccc acagcaggct acaatgccaa cgcaacataa tgtgatacta 1740

gataatcaac tcagccctca aatcgctttt ctgtttactg gacaaggttc gcagtacatc 1800

aacatggggc gtgagcttta cgaaactcag cccaccttcc gtcggattat ggacgaatgt 1860

gacgacattc tgcatccatt gttgggtgaa tcaattctga acatactcta cacttcccct 1920

agcaaactta atcaaaccgt ttatacccaa cctgcccttt ttgcttttga atatgcccta 1980

gcaaaactat ggatatcatg gggtattgag cctgatgtcg tactgggtca cagcgtgggt 2040

gaatatgtag ccgcttgtct ggcgggtgtc tttagtttag aagatgggtt aaaactcatt 2100

gcatctcgtg gatgtttgat gcaagcctta ccgccgggga aaatgcttag tatcagaagc 2160

aatgagatcg gagtgaaagc gctcatcgcg ccttatagtg cagaagtatc aattgcagca 2220

atcaatggac agcaaagcgt ggtgatctcc ggcaaagctg aaattataga taatttagca 2280

gcagagtttg catcggaagg catcaaaaca cacctaatta cagtctccca cgctttccac 2340

tcgccaatga tgacccccat gctgaaagca ttccgagacg ttgccagcac catcagctat 2400

aggtcaccca gtttatcact gatttctaac ggtacagggc aattggcaac aaaggaggtt 2460

gctacacctg attattgggt gcgtcatgtc cattctaccg tccgttttgc cgatggtatt 2520

gccacattgg cagaacagaa tactgacatc ctcctagaag taggacccaa accaatattg 2580

ttgggtatgg caaagcagat ttatagtgaa aacggttcag ctagtcatcc gctcatgcta 2640

cccagtttgc gtgaagatgg caacgattgg cagcagatgc tttctacttg tggacaactt 2700

gtagttaatg gagtcaagat tgactgggcg ggttttgaca aggattattc acgacacaaa 2760

atattgttgc ccacctatcc gtttcagaga gaacgatatt ggattgaaag ctccgtcaaa 2820

aagccccaaa aacaggagct gcgcccaatg ttggataaga tgatccggct accatcagag 2880

aacaaagtgg tgtttgaaac cgagtttggc gtgcgacaga tgcctcatat ctccgatcat 2940

cagatatacg gtgaagtcat tgtaccgggg gcagtattag cttccttaat cttcaatgca 3000

gcgcaggttt tatacccaga ctatcagcat gaattaactg atattgcttt ttatcagcca 3060

attatctttc atgacgacga tacggtgatc gtgcaggcga ttttcagccc tgataagtca 3120

caggagaatc aaagccatca aacatttcca cccatgagct tccagattat tagcttcatg 3180

ccggatggtc ccttagagaa caaaccgaaa gtccatgtca cagggtgtct gagaatgttg 3240

cgcgatgccc aaccgccaac actctccccg accgaaatac gtcagcgctg tccacatacc 3300

gtaaatggtc atgactggta caatagctta gtcaaacaaa aatttgaaat gggtccttcc 3360

tttaggtggg tacagcaact ttggcatggg gaaaatgaag cattgacccg tcttcacata 3420

ccagatgtgg tcggctctgt atcaggacat caacttcacg gcatattgct cgatggttca 3480

ctttcaacca ccgctgtcat ggagtacgag tacggagact ccgcgaccag agttcctttg 3540

tcatttgctt ctctgcaact gtacaaaccc gtcacgggaa cagagtggtg gtgctacgcg 3600

aggaagattg gggaattcaa atatgacttc cagattatga atgaaatcgg ggaaaccttg 3660

gtgaaagcaa ttggctttgt acttcgtgaa gcctctcccg aaaaattcct cagaacaaca 3720

tacgtacaca actggcttgt agacattgaa tggcaagctc aatcaacttc cctagtccct 3780

tctgatggca ctatctctgg cagttgtttg gttttatcag atcagcatgg aacaggggct 3840

gcattggcac aaaggctaga caatgctgga gtgccagtga ccatgatcta tgctgatctg 3900

atactggaca attacgaatt aatattccgt actttgccag atttacaaca agtcgtctat 3960

ttatgggggt tggatcaaaa agaggattgt caccccatga agcaagcaga ggataactgt 4020

acatcggtgc tatatcttgt gcaagcatta ctcaatacct actcaacccc gccatccctg 4080

cttattgtca cctgtgatgc acaagcggtg gttgaacaag atcgagtaaa tggcttcgcc 4140

caatcgtctt tgttgggact tgccaaagtt atcatgctag aacacccaga attgtcctgt 4200

gtttacatgg atgtggaagc cggatattta cagcaagatg tggcgaacac gatatttaca 4260

cagctaaaaa gaggccatct atcaaaggac ggagaagaga gtcagttggc ttggcgcaat 4320

ggacaagcat acgtagcacg tcttagtcaa tataaaccca aatccgaaca actggttgag 4380

atccgcagcg atcgcagcta tttgatcact ggtggacggg gcggtgtcgg cttacaaatc 4440

gcacggtggt tagtggaaaa gggggctaaa catctcgttt tgttggggcg cagtcagacc 4500

agttccgaag tcagtctggt gttggatgag ctagaatcag ccggggcgca aatcattgtg 4560

gctcaagctg atattagcga tgagaaggta ttagcgcaga ttctgaccaa tctaaccgta 4620

cctctgtgtg gtgtaatcca cgccgcagga gtgcttgatg atgcgagtct actccaacaa 4680

actccagcca agctcaaaaa agttctattg ccaaaagcag agggggcttg gattctgcat 4740

aatttgaccc tggagcagcg actagacttc tttgttctct tttcttctgc cagttctcta 4800

ttaggtgcgc cagggcaggc caactattca gcagccaatg ctttcctaga tggtttagct 4860

gcctatcggc gagggcgagg actcccctgt ttgtctatct gctgggggggc atgggatcaa 4920

gtcggtatgg ctgcacgaca agggctactg gacaagttac cgcaaagagg tgaagaggcc 4980

atcccgttac agaaaggctt agacctcttc ggcgaattac tgaacgagcc agccgctcaa 5040

attggtgtga tcccaattca atggactcgc ttcttggatc atcaaaaagg taatttgcct 5100

ttttatgaga agttttctaa gtctagccgg aaagcgcaga gttacgattc gatggcagtc 5160

agtcacacag aagatattca gaggaaactg aagcaagctg ctgtgcaaga tcgaccaaaa 5220

ttattagaag tgcatcttcg ctctcaagtc gctcaactgt taggaataaa cgtggcagag 5280

ctaccaaatg aagaaggaat tggttttgtt acattaggtc ttgactcgct cacctctatt 5340

gaactgcgta acagtttaca acgcacatta gattgttcat tacctgtcac ctttgctttt 5400

gactacccaa ctatagaaat agcggttaag tacctaacac aagttgtaat tgcaccgatg 5460

gaaagcacag catcgcagca aacagactct ttatcagcaa tgttcacaga tacttcgtcc 5520

atcgggagaa ttcttgacaa cgaaacagat gtgttagaca gcgaaatgca aagtgatgaa 5580

gatgaatctt tgtctacact tatacaaaaa ttatcaacac atttggatta g 5631

<210> 82
<211> 1876
<212> PRT
<213> Cylindrospermopsis raciborskii AWT205

<400> 82

Met Arg Ser Lys Phe Asn Ile Asn Val Thr Leu Leu Val Cys Leu Ile
1 5 10 15

Ile Ile Pro Tyr Phe Pro Thr Thr Leu Met Lys Val Pro Ile Thr Ala
20 25 30

Asn Glu Asp Ala Ala Thr Leu Leu Gln Arg Val Gly Leu Ser Leu Lys
35 40 45

Glu Ala His Gln Gln Leu Glu Ala Met Gln Arg Arg Ala His Glu Pro
50 55 60

Ile Ala Ile Val Gly Leu Gly Leu Arg Phe Pro Gly Ala Asp Ser Pro
65 70 75 80

Gln Thr Phe Trp Lys Leu Leu Gln Asn Gly Val Asp Met Val Thr Glu
85 90 95

Ile Pro Ser Asp Arg Trp Ala Val Asp Glu Tyr Tyr Asp Pro Gln Pro
100 105 110

Gly Cys Pro Gly Lys Met Tyr Ile Arg Glu Ala Ala Phe Val Asp Ala
115 120 125

Val Asp Lys Phe Asp Ala Ser Phe Phe Asp Ile Ser Pro Arg Glu Ala
130 135 140

Ala Asn Ile Asp Pro Gln His Arg Met Leu Leu Glu Val Ala Trp Glu
145 150 155 160

Ala Leu Glu Arg Ala Gly Ile Ala Pro Ser Gln Leu Met Asp Ser Gln
165 170 175

Thr Gly Val Phe Val Gly Met Ser Glu Asn Asp Tyr Tyr Ala His Leu
180 185 190

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

Asn Tyr Tyr Ala Pro Gly Arg Leu Ser Tyr Leu Leu Gly Leu Gln Gly
210 215 220

Pro Asn Met Val Val Asp Ser Ala Cys Ser Ser Ser Leu Val Ala Val
225 230 235 240

His Leu Ala Cys Asn Ser Leu Arg Met Gly Glu Cys Asp Leu Ala Leu
245 250 255

Ala Gly Gly Val Gln Leu Met Leu Ile Pro Asp Pro Met Ile Gly Thr
260 265 270

Ala Gln Leu Asn Ala Phe Ala Thr Asp Gly Arg Ser Lys Thr Phe Asp
275 280 285

Ala Ala Ala Asp Gly Tyr Gly Arg Gly Glu Gly Cys Gly Met Ile Val
290 295 300

Leu Lys Arg Ile Ser Asp Ala Ile Val Ala Asp Asp Pro Ile Leu Ala
305 310 315 320

Val Ile Arg Gly Ser Ala Val Asn His Gly Gly Arg Ser Ser Gly Leu
325 330 335

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

Gln Asn Ala Lys Val Gln Pro Glu Ala Val Ser Tyr Ile Glu Ala His
355 360 365

Gly Thr Gly Thr Gln Leu Gly Asp Pro Ile Glu Val Gly Ala Leu Thr
370 375 380

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

Lys Thr Asn Ile Gly His Leu Glu Pro Ala Ala Gly Ile Ala Gly Leu
405 410 415

Ile Lys Val Ile Leu Ser Leu Gln Glu Lys Gln Ile Pro Pro Ser Leu
420 425 430

His Phe Gln Asn Pro Asn Pro Phe Ile Asp Trp Glu Ser Ser Pro Val
435 440 445

Gln Val Pro Thr Gln Cys Val Pro Trp Thr Gly Lys Glu Arg Val Ala
450 455 460

Gly Val Ser Ser Phe Gly Met Ser Gly Thr Asn Cys His Leu Val Val
465 470 475 480

Ala Glu Ala Pro Val Arg Gln Asn Glu Lys Ser Glu Asn Ala Pro Glu
485 490 495

Arg Pro Cys His Ile Leu Thr Leu Ser Ala Lys Thr Glu Ala Ala Leu
500 505 510

Asn Ala Leu Val Ala Arg Tyr Met Ala Phe Leu Arg Glu Ala Pro Ala
515 520 525

Ile Ser Leu Ala Asp Leu Cys Tyr Ser Ala Asn Val Gly Arg Asn Leu
530 535 540

Phe Ala His Arg Leu Ser Phe Ile Ser Glu Asn Ile Ala Gln Leu Ser
545 550 555 560

Glu Gln Leu Glu His Cys Pro Gln Gln Ala Thr Met Pro Thr Gln His
565 570 575

Asn Val Ile Leu Asp Asn Gln Leu Ser Pro Gln Ile Ala Phe Leu Phe
580 585 590

Thr Gly Gln Gly Ser Gln Tyr Ile Asn Met Gly Arg Glu Leu Tyr Glu
595 600 605

Thr Gln Pro Thr Phe Arg Arg Ile Met Asp Glu Cys Asp Asp Ile Leu
610 615 620

His Pro Leu Leu Gly Glu Ser Ile Leu Asn Ile Leu Tyr Thr Ser Pro
625 630 635 640

Ser Lys Leu Asn Gln Thr Val Tyr Thr Gln Pro Ala Leu Phe Ala Phe
645 650 655

Glu Tyr Ala Leu Ala Lys Leu Trp Ile Ser Trp Gly Ile Glu Pro Asp
660 665 670

Val Val Leu Gly His Ser Val Gly Glu Tyr Val Ala Ala Cys Leu Ala
675 680 685

Gly Val Phe Ser Leu Glu Asp Gly Leu Lys Leu Ile Ala Ser Arg Gly
690 695 700

Cys Leu Met Gln Ala Leu Pro Pro Gly Lys Met Leu Ser Ile Arg Ser
705 710 715 720

Asn Glu Ile Gly Val Lys Ala Leu Ile Ala Pro Tyr Ser Ala Glu Val
725 730 735

Ser Ile Ala Ala Ile Asn Gly Gln Gln Ser Val Val Ile Ser Gly Lys
740 745 750

Ala Glu Ile Ile Asp Asn Leu Ala Ala Glu Phe Ala Ser Glu Gly Ile
755 760 765

Lys Thr His Leu Ile Thr Val Ser His Ala Phe His Ser Pro Met Met
770 775 780

Thr Pro Met Leu Lys Ala Phe Arg Asp Val Ala Ser Thr Ile Ser Tyr
785 790 795 800

Arg Ser Pro Ser Leu Ser Leu Ile Ser Asn Gly Thr Gly Gln Leu Ala
805 810 815

Thr Lys Glu Val Ala Thr Pro Asp Tyr Trp Val Arg His Val His Ser
820 825 830

Thr Val Arg Phe Ala Asp Gly Ile Ala Thr Leu Ala Glu Gln Asn Thr
835 840 845

Asp Ile Leu Leu Glu Val Gly Pro Lys Pro Ile Leu Leu Gly Met Ala
850 855 860

Lys Gln Ile Tyr Ser Glu Asn Gly Ser Ala Ser His Pro Leu Met Leu
865 870 875 880

Pro Ser Leu Arg Glu Asp Gly Asn Asp Trp Gln Gln Met Leu Ser Thr
885 890 895

Cys Gly Gln Leu Val Val Asn Gly Val Lys Ile Asp Trp Ala Gly Phe
900 905 910

Asp Lys Asp Tyr Ser Arg His Lys Ile Leu Leu Pro Thr Tyr Pro Phe
915 920 925

Gln Arg Glu Arg Tyr Trp Ile Glu Ser Ser Val Lys Lys Pro Gln Lys
930 935 940

Gln Glu Leu Arg Pro Met Leu Asp Lys Met Ile Arg Leu Pro Ser Glu
945 950 955 960

Asn Lys Val Val Phe Glu Thr Glu Phe Gly Val Arg Gln Met Pro His
965 970 975

Ile Ser Asp His Gln Ile Tyr Gly Glu Val Ile Val Pro Gly Ala Val
980 985 990

Leu Ala Ser Leu Ile Phe Asn Ala Ala Gln Val Leu Tyr Pro Asp Tyr
995 1000 1005

Gln His Glu Leu Thr Asp Ile Ala Phe Tyr Gln Pro Ile Ile Phe
1010 1015 1020

His Asp Asp Asp Thr Val Ile Val Gln Ala Ile Phe Ser Pro Asp
1025 1030 1035

Lys Ser Gln Glu Asn Gln Ser His Gln Thr Phe Pro Pro Met Ser
1040 1045 1050

Phe Gln Ile Ile Ser Phe Met Pro Asp Gly Pro Leu Glu Asn Lys
1055 1060 1065

Pro Lys Val His Val Thr Gly Cys Leu Arg Met Leu Arg Asp Ala
1070 1075 1080

Gln Pro Pro Thr Leu Ser Pro Thr Glu Ile Arg Gln Arg Cys Pro
1085 1090 1095

His Thr Val Asn Gly His Asp Trp Tyr Asn Ser Leu Val Lys Gln
1100 1105 1110

Lys Phe Glu Met Gly Pro Ser Phe Arg Trp Val Gln Gln Leu Trp
1115 1120 1125

His Gly Glu Asn Glu Ala Leu Thr Arg Leu His Ile Pro Asp Val
1130 1135 1140

Val Gly Ser Val Ser Gly His Gln Leu His Gly Ile Leu Leu Asp
1145 1150 1155

Gly Ser Leu Ser Thr Thr Ala Val Met Glu Tyr Glu Tyr Gly Asp
1160 1165 1170

Ser Ala Thr Arg Val Pro Leu Ser Phe Ala Ser Leu Gln Leu Tyr
1175 1180 1185

Lys Pro Val Thr Gly Thr Glu Trp Trp Cys Tyr Ala Arg Lys Ile
1190 1195 1200

Gly Glu Phe Lys Tyr Asp Phe Gln Ile Met Asn Glu Ile Gly Glu
1205 1210 1215

Thr Leu Val Lys Ala Ile Gly Phe Val Leu Arg Glu Ala Ser Pro
1220 1225 1230

Glu Lys Phe Leu Arg Thr Thr Tyr Val His Asn Trp Leu Val Asp
1235 1240 1245

Ile Glu Trp Gln Ala Gln Ser Thr Ser Leu Val Pro Ser Asp Gly
1250 1255 1260

Thr Ile Ser Gly Ser Cys Leu Val Leu Ser Asp Gln His Gly Thr
1265 1270 1275

Gly Ala Ala Leu Ala Gln Arg Leu Asp Asn Ala Gly Val Pro Val
1280 1285 1290

Thr Met Ile Tyr Ala Asp Leu Ile Leu Asp Asn Tyr Glu Leu Ile
1295 1300 1305

Phe Arg Thr Leu Pro Asp Leu Gln Gln Val Val Tyr Leu Trp Gly
1310 1315 1320

Leu Asp Gln Lys Glu Asp Cys His Pro Met Lys Gln Ala Glu Asp
1325 1330 1335

Asn Cys Thr Ser Val Leu Tyr Leu Val Gln Ala Leu Leu Asn Thr
1340 1345 1350

Tyr Ser Thr Pro Pro Ser Leu Leu Ile Val Thr Cys Asp Ala Gln
1355 1360 1365

Ala Val Val Glu Gln Asp Arg Val Asn Gly Phe Ala Gln Ser Ser
1370 1375 1380

Leu Leu Gly Leu Ala Lys Val Ile Met Leu Glu His Pro Glu Leu
1385 1390 1395

Ser Cys Val Tyr Met Asp Val Glu Ala Gly Tyr Leu Gln Gln Asp
1400 1405 1410

Val Ala Asn Thr Ile Phe Thr Gln Leu Lys Arg Gly His Leu Ser
1415 1420 1425

Lys Asp Gly Glu Glu Ser Gln Leu Ala Trp Arg Asn Gly Gln Ala
1430 1435 1440

Tyr Val Ala Arg Leu Ser Gln Tyr Lys Pro Lys Ser Glu Gln Leu
1445 1450 1455

Val Glu Ile Arg Ser Asp Arg Ser Tyr Leu Ile Thr Gly Gly Arg
1460 1465 1470

Gly Gly Val Gly Leu Gln Ile Ala Arg Trp Leu Val Glu Lys Gly
1475 1480 1485

Ala Lys His Leu Val Leu Leu Gly Arg Ser Gln Thr Ser Ser Glu
1490 1495 1500

Val Ser Leu Val Leu Asp Glu Leu Glu Ser Ala Gly Ala Gln Ile
1505 1510 1515

Ile Val Ala Gln Ala Asp Ile Ser Asp Glu Lys Val Leu Ala Gln
1520 1525 1530

Ile Leu Thr Asn Leu Thr Val Pro Leu Cys Gly Val Ile His Ala
1535 1540 1545

Ala Gly Val Leu Asp Asp Ala Ser Leu Leu Gln Gln Thr Pro Ala
1550 1555 1560

Lys Leu Lys Lys Val Leu Leu Pro Lys Ala Glu Gly Ala Trp Ile
1565 1570 1575

Leu His Asn Leu Thr Leu Glu Gln Arg Leu Asp Phe Phe Val Leu
1580 1585 1590

Phe Ser Ser Ala Ser Ser Leu Leu Gly Ala Pro Gly Gln Ala Asn
1595 1600 1605

Tyr Ser Ala Ala Asn Ala Phe Leu Asp Gly Leu Ala Ala Tyr Arg
1610 1615 1620

Arg Gly Arg Gly Leu Pro Cys Leu Ser Ile Cys Trp Gly Ala Trp
1625 1630 1635

Asp Gln Val Gly Met Ala Ala Arg Gln Gly Leu Leu Asp Lys Leu
1640 1645 1650

Pro Gln Arg Gly Glu Glu Ala Ile Pro Leu Gln Lys Gly Leu Asp
1655 1660 1665

Leu Phe Gly Glu Leu Leu Asn Glu Pro Ala Ala Gln Ile Gly Val
1670 1675 1680

Ile Pro Ile Gln Trp Thr Arg Phe Leu Asp His Gln Lys Gly Asn
1685 1690 1695

Leu Pro Phe Tyr Glu Lys Phe Ser Lys Ser Ser Arg Lys Ala Gln
1700 1705 1710

Ser Tyr Asp Ser Met Ala Val Ser His Thr Glu Asp Ile Gln Arg
1715 1720 1725

Lys Leu Lys Gln Ala Ala Val Gln Asp Arg Pro Lys Leu Leu Glu
1730 1735 1740

Val His Leu Arg Ser Gln Val Ala Gln Leu Leu Gly Ile Asn Val
1745 1750 1755

Ala Glu Leu Pro Asn Glu Glu Gly Ile Gly Phe Val Thr Leu Gly
1760 1765 1770

Leu Asp Ser Leu Thr Ser Ile Glu Leu Arg Asn Ser Leu Gln Arg
1775 1780 1785

Thr Leu Asp Cys Ser Leu Pro Val Thr Phe Ala Phe Asp Tyr Pro
1790 1795 1800

Thr Ile Glu Ile Ala Val Lys Tyr Leu Thr Gln Val Val Ile Ala
1805 1810 1815

Pro Met Glu Ser Thr Ala Ser Gln Gln Thr Asp Ser Leu Ser Ala
1820 1825 1830

Met Phe Thr Asp Thr Ser Ser Ile Gly Arg Ile Leu Asp Asn Glu
1835 1840 1845

Thr Asp Val Leu Asp Ser Glu Met Gln Ser Asp Glu Asp Glu Ser
1850 1855 1860

Leu Ser Thr Leu Ile Gln Lys Leu Ser Thr His Leu Asp
1865 1870 1875

<210> 83
<211> 4074
<212> DNA
<213> Cylindrospermopsis raciborskii AWT205

<400> 83
atgaacgctt tgtcagaaaa tcaggtaact tctatagtca agaaggcatt gaacaaaata 60

gaggagttac aagccgaact tgaccgttta aaatacgcgc aacgggaacc aatcgccatc 120

attggaatgg gctgtcgctt tcctggtgca gacacacctg aagctttttg gaaattattg 180

cacaatgggg ttgatgctat ccaagagatt ccaaaaagcc gttgggatat tgacgactat 240

tatgatccca caccagcaac acccggcaaa atgtatacac gttttggtgg ttttctcgac 300

caaatagcag ccttcgaccc tgagttcttt cgcatttcta ctcgtgaggc aatcagctta 360

gaccctcaac agagattgct tctggaagtg agttgggaag ccttagaacg ggctgggctg 420

acaggcaata aactgactac acaaacaggt gtctttgttg gcatcagtga aagtgattat 480

cgtgatttga ttatgcgtaa tggttctgac ctagatgtat attctggttc aggtaactgc 540

catagtacag ccagcgggcg tttatcttat tatttgggac ttactggacc caatttgtcc 600

cttgataccg cctgttcgtc ctctttggtt tgtgtggcat tggctgtcaa gagcctacgt 660

caacaggagt gtgatttggc attggcgggt ggtgtacaga tacaagtgat accagatggc 720

tttatcaaag cctgtcaatc ccgtatgttg tcgcctgatg gacggtgcaa aacatttgat 780

ttccaggcag atggttatgc ccgtgctgag gggtgtggga tggtagttct caaacgccta 840

tccgatgcaa ttgctgacaa tgataatatc ctggccttga ttcgtggtgc cgcagtcaat 900

catgatggct acacgagtgg attaaccgtt cccagtggtc cctcacaacg ggcggtgatc 960

caacaggcat tagcggatgc tggaatacac ccggatcaaa ttagctatat tgaggcacat 1020

ggcacaggta catccttagg cgatcctatt gaaatgggtg cgattgggca agtctttggt 1080

caacgctcac agatgctttt cgtcggttcg gtcaagacga atattggtca tactgaggct 1140

gctgctggta ttgctggtct catcaaggtt gtactctcaa tgcagcacgg tgaaatccca 1200

gcaaacttac acttcgacca gccaagtcct tatattaact gggatcaatt accagtcagt 1260

atcccaacag aaacaatacc ttggtctact agcgatcgct ttgcaggagt cagtagcttt 1320

ggctttagtg gcacaaactc tcatatcgta ctagaggcag ccccaaacat agagcaacct 1380

actgatgata ttaatcaaac gccgcatatt ttgaccttag ctgcaaaaac acccgcagcc 1440

ctgcaagaac tggctcggcg ttatgcgact cagatagaga cctctcccga tgttcctctg 1500

gcggacattt gtttcacagc acacataggg cgtaaacatt ttaaacatag gtttgcggta 1560

gtcacggaat ctaaagagca actgcgtttg caattggatg catttgcaca atcaggggggt 1620

gtggggcgag aagtcaaatc gctaccaaag atagcctttc tttttacagg tcaaggctca 1680

cagtatgtgg gaatgggtcg tcaactttac gaaaaccaac ctaccttccg aaaagcactc 1740

gcccattgtg atgacatctt gcgtgctggt gcatatttcg accgatcact actttcgatt 1800

ctctacccag agggaaaatc agaagccatt caccaaaccg cttatactca gcccgcgctt 1860

tttgctcttg agtatgcgat cgctcagttg tggcactcct ggggtatcaa accagatatc 1920

gtgatggggc atagtgtagg tgaatacgtc gccgcttgtg tggcgggcat attttcttta 1980

gaggatgggc tgaaactaat tgctactcgt ggtcgtctga tgcaatccct acctcaagac 2040

ggaacgatgg tttcttcttt ggcaagtgaa gctcgtatcc aggaagctat tacaccttac 2100

cgagatgatg tgtcaatcgc agcgataaat gggacagaaa gcgtggttat ctctggcaaa 2160

cgcacctctg tgatggcaat tgctgaacaa ctcgccaccg ttggcatcaa gacacgccaa 2220

ctgacggttt cccatgcctt ccattcacca cttatgacac ccatcttgga tgagttccgc 2280

caggtggcag ccagtatcac ctatcaccag cccaagttgc tacttgtctc caacgtctcc 2340

gggaaagtgg ccggccctga aatcaccaga ccagattact gggtacgcca tgtccgtgag 2400

gcagtgcgct ttgccgatgg agtgaggacg ctgaatgaac aaggtgtcaa tatctttctg 2460

gaaatcggtt ctaccgctac cctgttgggc atggcactgc gagtaaatga ggaagattca 2520

aatgcctcaa aaggaacttc gtcttgctac ctgcccagtt tacgggaaag ccagaaggat 2580

tgtcagcaga tgttcactag tctgggtgag ttgtacgtac atggatatga tattgattgg 2640

ggtgcattta atcggggata tcaaggacgc aaggtgatat tgccaaccta tccgtttcag 2700

cgacaacgtt attggcttcc cgaccctaag ttggcacaaa gttccgattt agataccttt 2760

caagctcaga gcagcgcatc atcacaaaat cctagcgctg tgtccacttt actgatggaa 2820

tatttgcaag caggtgatgt ccaatcttta gttgggcttt tggatgatga acggaaactc 2880

tctgctgctg aacgaattgc actacccagt attttggagt ttttggtaga ggaacaacag 2940

cgacaaataa gctcaaccac aactcctcaa acagttttac aaaaaataag tcaaacttcc 3000

catgaggaca gatatgaaat attgaagaac ctgatcaaat ctgaaatcga aacgattatc 3060

aaaagtgttc cctccgatga acaaatgttt tctgacttag gaattgattc cttgatggcg 3120

atcgaactgc gtaataagct ccgttctgct atagggttgg aactgccagt ggcaatagta 3180

tttgaccatc ccacgattaa gcagttaact aacttcgtac tggacagaat tgtgccgcag 3240

gcagaccaaa aggacgttcc caccgaatcc ttgtttgctt ctaaacagga gatatcagtt 3300

gaggagcagt cttttgcaat taccaagctg ggcttatccc ctgcttccca ctccctgcat 3360

cttcctccat ggacggttag acctgcggta atggcagatg taacaaaact aagccaactt 3420

gaaagagagg cctatggctg gatcggagaa ggagcgatcg ccccgcccca tctcattgcc 3480

gatcgcatca atttactcaa cagtggtgat atgccttggt tctgggtaat ggagcgatca 3540

ggagagttgg gcgcgtggca ggtgctacaa ccgacatctg ttgatccata tacttatgga 3600

agttgggatg aagtaactga ccaaggtaaa ctgcaagcaa ccttcgaccc aagtggacgc 3660

aatgtgtata ttgtcgcggg tgggtctagc aacctcccca cggtagccag ccacctcatg 3720

acgcttcaga ctttattgat gctgcgggaa actggtcgtg acacaatctt tgtctgtctg 3780

gcaatgccag gttatgccaa ataccacagt caaacaggaa aatcgccgga agagtatatt 3840

gcgctgactg acgaggatgg tatcccaatg gacgagttta ttgcactttc tgtctacgac 3900

tggcctgtta ccccatcgtt tcgtgttctg cgagacggtt atccacctga tcgagattct 3960

ggtggtcacg cagttagtac ggttttccag ctcaatgatt tcgatggagc gatcgaagaa 4020

acatatcgtc gtattatccg ccatgccgat gtccttggtc tcgaaagagg ctaa 4074

<210> 84
<211> 1357
<212> PRT
<213> Cylindrospermopsis raciborskii AWT205

<400> 84

Met Asn Ala Leu Ser Glu Asn Gln Val Thr Ser Ile Val Lys Lys Ala
1 5 10 15

Leu Asn Lys Ile Glu Glu Leu Gln Ala Glu Leu Asp Arg Leu Lys Tyr
20 25 30

Ala Gln Arg Glu Pro Ile Ala Ile Ile Gly Met Gly Cys Arg Phe Pro
35 40 45

Gly Ala Asp Thr Pro Glu Ala Phe Trp Lys Leu Leu His Asn Gly Val
50 55 60

Asp Ala Ile Gln Glu Ile Pro Lys Ser Arg Trp Asp Ile Asp Asp Tyr
65 70 75 80

Tyr Asp Pro Thr Pro Ala Thr Pro Gly Lys Met Tyr Thr Arg Phe Gly
85 90 95

Gly Phe Leu Asp Gln Ile Ala Ala Phe Asp Pro Glu Phe Phe Arg Ile
100 105 110

Ser Thr Arg Glu Ala Ile Ser Leu Asp Pro Gln Gln Arg Leu Leu Leu
115 120 125

Glu Val Ser Trp Glu Ala Leu Glu Arg Ala Gly Leu Thr Gly Asn Lys
130 135 140

Leu Thr Thr Gln Thr Gly Val Phe Val Gly Ile Ser Glu Ser Asp Tyr
145 150 155 160

Arg Asp Leu Ile Met Arg Asn Gly Ser Asp Leu Asp Val Tyr Ser Gly
165 170 175

Ser Gly Asn Cys His Ser Thr Ala Ser Gly Arg Leu Ser Tyr Tyr Leu
180 185 190

Gly Leu Thr Gly Pro Asn Leu Ser Leu Asp Thr Ala Cys Ser Ser Ser
195 200 205

Leu Val Cys Val Ala Leu Ala Val Lys Ser Leu Arg Gln Gln Glu Cys
210 215 220

Asp Leu Ala Leu Ala Gly Gly Val Gln Ile Gln Val Ile Pro Asp Gly
225 230 235 240

Phe Ile Lys Ala Cys Gln Ser Arg Met Leu Ser Pro Asp Gly Arg Cys
245 250 255

Lys Thr Phe Asp Phe Gln Ala Asp Gly Tyr Ala Arg Ala Glu Gly Cys
260 265 270

Gly Met Val Val Leu Lys Arg Leu Ser Asp Ala Ile Ala Asp Asn Asp
275 280 285

Asn Ile Leu Ala Leu Ile Arg Gly Ala Ala Val Asn His Asp Gly Tyr
290 295 300

Thr Ser Gly Leu Thr Val Pro Ser Gly Pro Ser Gln Arg Ala Val Ile
305 310 315 320

Gln Gln Ala Leu Ala Asp Ala Gly Ile His Pro Asp Gln Ile Ser Tyr
325 330 335

Ile Glu Ala His Gly Thr Gly Thr Ser Leu Gly Asp Pro Ile Glu Met
340 345 350

Gly Ala Ile Gly Gln Val Phe Gly Gln Arg Ser Gln Met Leu Phe Val
355 360 365

Gly Ser Val Lys Thr Asn Ile Gly His Thr Glu Ala Ala Ala Gly Ile
370 375 380

Ala Gly Leu Ile Lys Val Val Leu Ser Met Gln His Gly Glu Ile Pro
385 390 395 400

Ala Asn Leu His Phe Asp Gln Pro Ser Pro Tyr Ile Asn Trp Asp Gln
405 410 415

Leu Pro Val Ser Ile Pro Thr Glu Thr Ile Pro Trp Ser Thr Ser Asp
420 425 430

Arg Phe Ala Gly Val Ser Ser Phe Gly Phe Ser Gly Thr Asn Ser His
435 440 445

Ile Val Leu Glu Ala Ala Pro Asn Ile Glu Gln Pro Thr Asp Asp Ile
450 455 460

Asn Gln Thr Pro His Ile Leu Thr Leu Ala Ala Lys Thr Pro Ala Ala
465 470 475 480

Leu Gln Glu Leu Ala Arg Arg Tyr Ala Thr Gln Ile Glu Thr Ser Pro
485 490 495

Asp Val Pro Leu Ala Asp Ile Cys Phe Thr Ala His Ile Gly Arg Lys
500 505 510

His Phe Lys His Arg Phe Ala Val Val Thr Glu Ser Lys Glu Gln Leu
515 520 525

Arg Leu Gln Leu Asp Ala Phe Ala Gln Ser Gly Gly Val Gly Arg Glu
530 535 540

Val Lys Ser Leu Pro Lys Ile Ala Phe Leu Phe Thr Gly Gln Gly Ser
545 550 555 560

Gln Tyr Val Gly Met Gly Arg Gln Leu Tyr Glu Asn Gln Pro Thr Phe
565 570 575

Arg Lys Ala Leu Ala His Cys Asp Asp Ile Leu Arg Ala Gly Ala Tyr
580 585 590

Phe Asp Arg Ser Leu Leu Ser Ile Leu Tyr Pro Glu Gly Lys Ser Glu
595 600 605

Ala Ile His Gln Thr Ala Tyr Thr Gln Pro Ala Leu Phe Ala Leu Glu
610 615 620

Tyr Ala Ile Ala Gln Leu Trp His Ser Trp Gly Ile Lys Pro Asp Ile
625 630 635 640

Val Met Gly His Ser Val Gly Glu Tyr Val Ala Ala Cys Val Ala Gly
645 650 655

Ile Phe Ser Leu Glu Asp Gly Leu Lys Leu Ile Ala Thr Arg Gly Arg
660 665 670

Leu Met Gln Ser Leu Pro Gln Asp Gly Thr Met Val Ser Ser Leu Ala
675 680 685

Ser Glu Ala Arg Ile Gln Glu Ala Ile Thr Pro Tyr Arg Asp Asp Val
690 695 700

Ser Ile Ala Ala Ile Asn Gly Thr Glu Ser Val Val Ile Ser Gly Lys
705 710 715 720

Arg Thr Ser Val Met Ala Ile Ala Glu Gln Leu Ala Thr Val Gly Ile
725 730 735

Lys Thr Arg Gln Leu Thr Val Ser His Ala Phe His Ser Pro Leu Met
740 745 750

Thr Pro Ile Leu Asp Glu Phe Arg Gln Val Ala Ala Ser Ile Thr Tyr
755 760 765

His Gln Pro Lys Leu Leu Leu Val Ser Asn Val Ser Gly Lys Val Ala
770 775 780

Gly Pro Glu Ile Thr Arg Pro Asp Tyr Trp Val Arg His Val Arg Glu
785 790 795 800

Ala Val Arg Phe Ala Asp Gly Val Arg Thr Leu Asn Glu Gln Gly Val
805 810 815

Asn Ile Phe Leu Glu Ile Gly Ser Thr Ala Thr Leu Leu Gly Met Ala
820 825 830

Leu Arg Val Asn Glu Glu Asp Ser Asn Ala Ser Lys Gly Thr Ser Ser
835 840 845

Cys Tyr Leu Pro Ser Leu Arg Glu Ser Gln Lys Asp Cys Gln Gln Met
850 855 860

Phe Thr Ser Leu Gly Glu Leu Tyr Val His Gly Tyr Asp Ile Asp Trp
865 870 875 880

Gly Ala Phe Asn Arg Gly Tyr Gln Gly Arg Lys Val Ile Leu Pro Thr
885 890 895

Tyr Pro Phe Gln Arg Gln Arg Tyr Trp Leu Pro Asp Pro Lys Leu Ala
900 905 910

Gln Ser Ser Asp Leu Asp Thr Phe Gln Ala Gln Ser Ser Ala Ser Ser
915 920 925

Gln Asn Pro Ser Ala Val Ser Thr Leu Leu Met Glu Tyr Leu Gln Ala
930 935 940

Gly Asp Val Gln Ser Leu Val Gly Leu Leu Asp Asp Glu Arg Lys Leu
945 950 955 960

Ser Ala Ala Glu Arg Ile Ala Leu Pro Ser Ile Leu Glu Phe Leu Val
965 970 975

Glu Glu Gln Gln Arg Gln Ile Ser Ser Thr Thr Thr Pro Gln Thr Val
980 985 990

Leu Gln Lys Ile Ser Gln Thr Ser His Glu Asp Arg Tyr Glu Ile Leu
995 1000 1005

Lys Asn Leu Ile Lys Ser Glu Ile Glu Thr Ile Ile Lys Ser Val
1010 1015 1020

Pro Ser Asp Glu Gln Met Phe Ser Asp Leu Gly Ile Asp Ser Leu
1025 1030 1035

Met Ala Ile Glu Leu Arg Asn Lys Leu Arg Ser Ala Ile Gly Leu
1040 1045 1050

Glu Leu Pro Val Ala Ile Val Phe Asp His Pro Thr Ile Lys Gln
1055 1060 1065

Leu Thr Asn Phe Val Leu Asp Arg Ile Val Pro Gln Ala Asp Gln
1070 1075 1080

Lys Asp Val Pro Thr Glu Ser Leu Phe Ala Ser Lys Gln Glu Ile
1085 1090 1095

Ser Val Glu Glu Gln Ser Phe Ala Ile Thr Lys Leu Gly Leu Ser
1100 1105 1110

Pro Ala Ser His Ser Leu His Leu Pro Pro Trp Thr Val Arg Pro
1115 1120 1125

Ala Val Met Ala Asp Val Thr Lys Leu Ser Gln Leu Glu Arg Glu
1130 1135 1140

Ala Tyr Gly Trp Ile Gly Glu Gly Ala Ile Ala Pro Pro His Leu
1145 1150 1155

Ile Ala Asp Arg Ile Asn Leu Leu Asn Ser Gly Asp Met Pro Trp
1160 1165 1170

Phe Trp Val Met Glu Arg Ser Gly Glu Leu Gly Ala Trp Gln Val
1175 1180 1185

Leu Gln Pro Thr Ser Val Asp Pro Tyr Thr Tyr Gly Ser Trp Asp
1190 1195 1200

Glu Val Thr Asp Gln Gly Lys Leu Gln Ala Thr Phe Asp Pro Ser
1205 1210 1215

Gly Arg Asn Val Tyr Ile Val Ala Gly Gly Ser Ser Asn Leu Pro
1220 1225 1230

Thr Val Ala Ser His Leu Met Thr Leu Gln Thr Leu Leu Met Leu
1235 1240 1245

Arg Glu Thr Gly Arg Asp Thr Ile Phe Val Cys Leu Ala Met Pro
1250 1255 1260

Gly Tyr Ala Lys Tyr His Ser Gln Thr Gly Lys Ser Pro Glu Glu
1265 1270 1275

Tyr Ile Ala Leu Thr Asp Glu Asp Gly Ile Pro Met Asp Glu Phe
1280 1285 1290

Ile Ala Leu Ser Val Tyr Asp Trp Pro Val Thr Pro Ser Phe Arg
1295 1300 1305

Val Leu Arg Asp Gly Tyr Pro Pro Asp Arg Asp Ser Gly Gly His
1310 1315 1320

Ala Val Ser Thr Val Phe Gln Leu Asn Asp Phe Asp Gly Ala Ile
1325 1330 1335

Glu Glu Thr Tyr Arg Arg Ile Ile Arg His Ala Asp Val Leu Gly
1340 1345 1350

Leu Glu Arg Gly
1355

<210> 85
<211> 1437
<212> DNA
<213> cylindrospermopsis raciborskii awt205

<400> 85
atgaataaaa aacaggtaga cacattgtta atacacgctc atctttttac catgcagggc 60

aatggcctgg gatatattgc cgatggggca attgcggttc agggtagcca gatcgtagca 120

gtggattcga cagaggcttt gctgagtcat tttgaaggaa ataaaacaat taatgcggta 180

aattgtgcag tgttgcctgg actaattgat gctcatatac atacgacttg tgctattctg 240

cgtggagtgg cacaggatgt aaccaattgg ctaatggacg cgacaattcc ttatgcactt 300

cagatgacac ccgcagtaaa tatagccgga acgcgcttga gtgtactcga agggctgaaa 360

gcaggaacaa ccacattcgg cgattctgag actccttacc cgctctgggg agagtttttc 420

gatgaaattg gggtacgtgc tattctatcc cctgccttta acgcctttcc actagaatgg 480

tcggcatgga aggagggaga cctctatccc ttcgatatga aggcaggacg acgtggtatg 540

gaagaggctg tggattttgc ttgtgcatgg aatggagccg cagagggacg tatcaccact 600

atgttgggac tacaggcggc ggatatgcta ccactggaga tcctacacgc agctaaagag 660

attgcccaac gggaaggctt aatgctgcat attcatgtgg cccagggaga tcgagaaaca 720

aaacaaattg tcaaacgata tggtaagcgt ccgatcgcat ttctagctga aattggctac 780

ttggacgaac agttgctggc agttcacctc accgatgcca cagatgaaga agtgatacaa 840

gtagccaaaa gtggtgctgg catggcactc tgttcgggcg ctattggcat cattgacggt 900

cttgttccgc ccgctcatgt ttttcgacaa gcaggcggtt ccgttgcact cggttctgat 960

caagcctgtg gcaacaactg ttgtaacatc ttcaatgaaa tgaagctgac cgccttattc 1020

aacaaaataa aatatcatga tccaaccatt atgccggctt gggaagtcct gcgtatggct 1080

accatcgaag gagcgcaggc gattggttta gatcacaaga ttggctctct tcaagtgggc 1140

aaagaagccg acctgatctt aatagacctc agttccccta acctctcgcc caccctgctc 1200

aaccctattc gtaaccttgt acctaacttg gtgtatgctg cttcaggaca tgaagttaaa 1260

agcgtcatgg tggcgggaaa acttttagtg gaagactacc aagtcctcac ggtagatgag 1320

tccgctattc tcgctgaagc gcaagtacaa gctcaacaac tctgccaacg tgtgaccgct 1380

gaccccattc acaaaaagat ggtgttaatg gaagcgatgg ctaagggtaa attatag 1437

<210> 86
<211> 478
<212> PRT
<213> Cylindrospermopsis raciborskii AWT205

<400> 86

Met Asn Lys Lys Gln Val Asp Thr Leu Leu Ile His Ala His Leu Phe
1 5 10 15

Thr Met Gln Gly Asn Gly Leu Gly Tyr Ile Ala Asp Gly Ala Ile Ala
20 25 30

Val Gln Gly Ser Gln Ile Val Ala Val Asp Ser Thr Glu Ala Leu Leu
35 40 45

Ser His Phe Glu Gly Asn Lys Thr Ile Asn Ala Val Asn Cys Ala Val
50 55 60

Leu Pro Gly Leu Ile Asp Ala His Ile His Thr Thr Cys Ala Ile Leu
65 70 75 80

Arg Gly Val Ala Gln Asp Val Thr Asn Trp Leu Met Asp Ala Thr Ile
85 90 95

Pro Tyr Ala Leu Gln Met Thr Pro Ala Val Asn Ile Ala Gly Thr Arg
100 105 110

Leu Ser Val Leu Glu Gly Leu Lys Ala Gly Thr Thr Thr Phe Gly Asp
115 120 125

Ser Glu Thr Pro Tyr Pro Leu Trp Gly Glu Phe Phe Asp Glu Ile Gly
130 135 140

Val Arg Ala Ile Leu Ser Pro Ala Phe Asn Ala Phe Pro Leu Glu Trp
145 150 155 160

Ser Ala Trp Lys Glu Gly Asp Leu Tyr Pro Phe Asp Met Lys Ala Gly
165 170 175

Arg Arg Gly Met Glu Glu Ala Val Asp Phe Ala Cys Ala Trp Asn Gly
180 185 190

Ala Ala Glu Gly Arg Ile Thr Thr Met Leu Gly Leu Gln Ala Ala Asp
195 200 205

Met Leu Pro Leu Glu Ile Leu His Ala Ala Lys Glu Ile Ala Gln Arg
210 215 220

Glu Gly Leu Met Leu His Ile His Val Ala Gln Gly Asp Arg Glu Thr
225 230 235 240

Lys Gln Ile Val Lys Arg Tyr Gly Lys Arg Pro Ile Ala Phe Leu Ala
245 250 255

Glu Ile Gly Tyr Leu Asp Glu Gln Leu Leu Ala Val His Leu Thr Asp
260 265 270

Ala Thr Asp Glu Glu Val Ile Gln Val Ala Lys Ser Gly Ala Gly Met
275 280 285

Ala Leu Cys Ser Gly Ala Ile Gly Ile Ile Asp Gly Leu Val Pro Pro
290 295 300

Ala His Val Phe Arg Gln Ala Gly Gly Ser Val Ala Leu Gly Ser Asp
305 310 315 320

Gln Ala Cys Gly Asn Asn Cys Cys Asn Ile Phe Asn Glu Met Lys Leu
325 330 335

Thr Ala Leu Phe Asn Lys Ile Lys Tyr His Asp Pro Thr Ile Met Pro
340 345 350

Ala Trp Glu Val Leu Arg Met Ala Thr Ile Glu Gly Ala Gln Ala Ile
355 360 365

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

Leu Ile Leu Ile Asp Leu Ser Ser Pro Asn Leu Ser Pro Thr Leu Leu
385 390 395 400

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

His Glu Val Lys Ser Val Met Val Ala Gly Lys Leu Leu Val Glu Asp
420 425 430

Tyr Gln Val Leu Thr Val Asp Glu Ser Ala Ile Leu Ala Glu Ala Gln
435 440 445

Val Gln Ala Gln Gln Leu Cys Gln Arg Val Thr Ala Asp Pro Ile His
450 455 460

Lys Lys Met Val Leu Met Glu Ala Met Ala Lys Gly Lys Leu
465 470 475

<210> 87
<211> 831
<212> DNA
<213> Cylindrospermopsis raciborskii AWT205

<400> 87
atgaccatat atgaaaataa gttgagtagt tatcaaaaaa atcaagatgc cataatatct 60

gcaaaagaac tcgaagaatg gcatttaatt ggacttctag accattcaat agatgcggta 120

atagtaccga attattttct tgagcaagag tgtatgacaa tttcagagag aataaaaaag 180

agtaaatatt ttagcgctta tcccggtcat ccatcagtaa gtagcttggg acaagagttg 240

tatgaatgcg aaagtgagct tgaattagca aagtatcaag aagacgcacc cacattgatt 300

aaagaaatgc ggaggctggt acatccgtac ataagtccaa ttgatagact tagggttgaa 360

gttgatgata tttggagtta tggctgtaat ttagcaaaac ttggtgataa aaaactgttt 420

gcgggtatcg ttagagagtt taaagaagat aaccctggcg caccacattg tgacgtaatg 480

gcatggggtt ttctcgaata ttataaagat aaaccaaata tcataaatca aatcgcagca 540

aatgtatatt taaaaacgtc tgcatcagga ggagaaatag tgctttggga tgaatggcca 600

actcaaagcg aatatatagc atacaaaaca gatgatccag ctagtttcgg tcttgatagc 660

aaaaagatcg cacaaccaaa acttgagatc caaccgaacc agggagattt aattctattc 720

aattccatga gaattcatgc ggtgaaaaag atagaaactg gtgtacgtat gacatgggga 780

tgtttgattg gatactctgg aactgataaa ccgcttgtta tttggactta a 831

<210> 88
<211> 276
<212> PRT
<213> Cylindrospermopsis raciborskii AWT205

<400> 88

Met Thr Ile Tyr Glu Asn Lys Leu Ser Ser Tyr Gln Lys Asn Gln Asp
1 5 10 15

Ala Ile Ile Ser Ala Lys Glu Leu Glu Glu Trp His Leu Ile Gly Leu
20 25 30

Leu Asp His Ser Ile Asp Ala Val Ile Val Pro Asn Tyr Phe Leu Glu
35 40 45

Gln Glu Cys Met Thr Ile Ser Glu Arg Ile Lys Lys Ser Lys Tyr Phe
50 55 60

Ser Ala Tyr Pro Gly His Pro Ser Val Ser Ser Leu Gly Gln Glu Leu
65 70 75 80

Tyr Glu Cys Glu Ser Glu Leu Glu Leu Ala Lys Tyr Gln Glu Asp Ala
85 90 95

Pro Thr Leu Ile Lys Glu Met Arg Arg Leu Val His Pro Tyr Ile Ser
100 105 110

Pro Ile Asp Arg Leu Arg Val Glu Val Asp Asp Ile Trp Ser Tyr Gly
115 120 125

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

Arg Glu Phe Lys Glu Asp Asn Pro Gly Ala Pro His Cys Asp Val Met
145 150 155 160

Ala Trp Gly Phe Leu Glu Tyr Tyr Lys Asp Lys Pro Asn Ile Ile Asn
165 170 175

Gln Ile Ala Ala Asn Val Tyr Leu Lys Thr Ser Ala Ser Gly Gly Glu
180 185 190

Ile Val Leu Trp Asp Glu Trp Pro Thr Gln Ser Glu Tyr Ile Ala Tyr
195 200 205

Lys Thr Asp Asp Pro Ala Ser Phe Gly Leu Asp Ser Lys Lys Ile Ala
210 215 220

Gln Pro Lys Leu Glu Ile Gln Pro Asn Gln Gly Asp Leu Ile Leu Phe
225 230 235 240

Asn Ser Met Arg Ile His Ala Val Lys Lys Ile Glu Thr Gly Val Arg
245 250 255

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

Val Ile Trp Thr
275

<210> 89
<211> 1398
<212> DNA
<213> Cylindrospermopsis raciborskii AWT205

<400> 89
ttaatgtagc gtttccattt gagtcaaggc acgagaagct tctaaagctg gaatagatac 60

actatcattc tcaactacac tctcaaatgt cctaggtaac tgtgccccaa acatcagcat 120

tccaatggcg ttgaacaaaa agaaagccaa ccacaagata tggttactct caaatttaac 180

agcagctaca tccgcaggta aaaatcctac accaaacgcg attaagttaa cattgcggag 240

agtatgccct tgagccaaac ccaagaagta cccacatagt atgcaacata ctgaattgca 300

tactaggaca agtaccaacc agggaataaa aatatcaata ttctcaataa tttctgcgtg 360

gttggttaac aacccaaaaa catcatcggg aaatagccaa cacgctccgc cgaaaaccag 420

actcactagc agagccattc ccacagaaac ttttgccaga ggtgctaact gttctgtggc 480

tcctttccct ttaaaatttc ctgccagagt ttctgtacag aatcccaatc cttcaacaat 540

gtagatgctc aaagcccata tctgtaagag caaggcattt tgagcgtaga taattgtccc 600

catttgtgcc ccttcgtagt taaacgttaa gttggtaaac atacaaacta aattgctgac 660

aaagatgttt ccattgagag ttaaggtgga gcgtatagct tttatgtccc aaatttttcc 720

agctaattct tttacctctt gccacgggat ttctttgcag acaaaaaaca atcccaccaa 780

tagggtgaga tattgacttg cagcagaagc tactcctgcc cccatgctcg accagtctaa 840

gtggataata aacaagtagt cgagtgcgat attggcagca ttgcccacaa ccgacaacaa 900

cacaactaag ccatttttt cccgtcccag aaaccagcca agcaggacaa agttgagcaa 960

aatggcaggc gctccccaac tctgggtgtt aaaatacgct tgagctgaag acttcacctc 1020

tgggccgaca tctagtatag aaaaccccaa caccctaac gggtactgta acagtatgat 1080

cgccacccc agcaccagag caattaaacc attaagcagt cccgccaaca gtacgccctc 1140

tcggtcatct cgtccgactg cttgtgctgt taacgcagtg gtacccattc gtaaaaacga 1200

taaaacaaag tagagaaagt taagcaggtt tccagcaagg gctactccag ctaggtagtg 1260

gatttccgag agatgaccta agaacatgat actgactaaa ttactcagtg gtactataat 1320

attcgatagg acgttggtaa aagctagtcg gaagtagcgg ggtataaagt catactggct 1380

tggaaatgtc aggctcat 1398

<210> 90
<211> 465
<212> PRT
<213> Cylindrospermopsis raciborskii AWT205

<400> 90

Met Ser Leu Thr Phe Pro Ser Gln Tyr Asp Phe Ile Pro Arg Tyr Phe
1 5 10 15

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

Asn Leu Val Ser Ile Met Phe Leu Gly His Leu Ser Glu Ile His Tyr
35 40 45

Leu Ala Gly Val Ala Leu Ala Gly Asn Leu Leu Asn Phe Leu Tyr Phe
50 55 60

Val Leu Ser Phe Leu Arg Met Gly Thr Thr Ala Leu Thr Ala Gln Ala
65 70 75 80

Val Gly Arg Asp Asp Arg Glu Gly Val Leu Leu Ala Gly Leu Leu Asn
85 90 95

Gly Leu Ile Ala Leu Val Leu Gly Val Ala Ile Ile Leu Leu Gln Tyr
100 105 110

Pro Leu Gly Val Leu Gly Phe Ser Ile Leu Asp Val Gly Pro Glu Val
115 120 125

Lys Ser Ser Ala Gln Ala Tyr Phe Asn Thr Gln Ser Trp Gly Ala Pro
130 135 140

Ala Ile Leu Leu Asn Phe Val Leu Leu Gly Trp Phe Leu Gly Arg Glu
145 150 155 160

Lys Asn Gly Leu Val Val Leu Leu Ser Val Val Gly Asn Ala Ala Asn
165 170 175

Ile Ala Leu Asp Tyr Leu Phe Ile Ile His Leu Asp Trp Ser Ser Met
180 185 190

Gly Ala Gly Val Ala Ser Ala Ala Ser Gln Tyr Leu Thr Leu Leu Val
195 200 205

Gly Leu Phe Phe Val Cys Lys Glu Ile Pro Trp Gln Glu Val Lys Glu
210 215 220

Leu Ala Gly Lys Ile Trp Asp Ile Lys Ala Ile Arg Ser Thr Leu Thr
225 230 235 240

Leu Asn Gly Asn Ile Phe Val Ser Asn Leu Val Cys Met Phe Thr Asn
245 250 255

Leu Thr Phe Asn Tyr Glu Gly Ala Gln Met Gly Thr Ile Ile Tyr Ala
260 265 270

Gln Asn Ala Leu Leu Leu Gln Ile Trp Ala Leu Ser Ile Tyr Ile Val
275 280 285

Glu Gly Leu Gly Phe Cys Thr Glu Thr Leu Ala Gly Asn Phe Lys Gly
290 295 300

Lys Gly Ala Thr Glu Gln Leu Ala Pro Leu Ala Lys Val Ser Val Gly
305 310 315 320

Met Ala Leu Leu Val Ser Leu Val Phe Gly Gly Ala Cys Trp Leu Phe
325 330 335

Pro Asp Asp Val Phe Gly Leu Leu Thr Asn His Ala Glu Ile Ile Glu
340 345 350

Asn Ile Asp Ile Phe Ile Pro Trp Leu Val Leu Val Leu Val Cys Asn
355 360 365

Ser Val Cys Cys Ile Leu Cys Gly Tyr Phe Leu Gly Leu Ala Gln Gly
370 375 380

His Thr Leu Arg Asn Val Asn Leu Ile Ala Phe Gly Val Gly Phe Leu
385 390 395 400

Pro Ala Asp Val Ala Ala Val Lys Phe Glu Ser Asn His Ile Leu Trp
405 410 415

Leu Ala Phe Phe Leu Phe Asn Ala Ile Gly Met Leu Met Phe Gly Ala
420 425 430

Gln Leu Pro Arg Thr Phe Glu Ser Val Val Glu Asn Asp Ser Val Ser
435 440 445

Ile Pro Ala Leu Glu Ala Ser Arg Ala Leu Thr Gln Met Glu Thr Leu
450 455 460

His
465

<210> 91
<211> 750
<212> DNA
<213> Cylindrospermopsis raciborskii AWT205

<400> 91
atgttgaact tagaccgcat cctgaatcaa gagcgactgc tacgagaaat gactggactt 60

aaccgccaag cattcaacga gctgttatct cagtttgctg atacctatga acgcaccgtg 120

ttcaactcct tagcaaaccg caaacgtgcg cccgggggcg gacgcaagcc tacactcaga 180

agtatagagg aaaaactatt ttatatcctg ctgtactgca aatgttatcc gacgtttgac 240

ttgctgagtg tgttgttcaa ctttgaccgc tcctgtgctc atgattgggt acatcgacta 300

ctgtctgtgc tagaaaccac tttaggagaa aagcaagttt tgccagcacg caaactcagg 360

agcatggagg aattcaccaa aaggtttcca gatgtgaagg aggtgattgt ggatggtacg 420

gagcgtccag tccagcgtcc tcaaaaccga gaacgccaaa aagagtatta ctctggcaag 480

aaaaagcggc atacatgcaa gcagattaca gtcagcacaa gggagaaacg agtgattatt 540

cggacggaaa ccagagcagg taaagtgcat gacaaacggc tactccatga atcagagata 600

gtgcaataca ttcctgatga agtagcaata gagggagatt tgggttttca tgggttggag 660

aaagaatttg tcaatgtcca tttaccacac aagaaaccga aaggtatcga agcaaggagg 720

catggcggcg ggatgggtca gtttttataa 750

<210> 92
<211> 249
<212> PRT
<213> Cylindrospermopsis raciborskii AWT205

<400> 92

Met Leu Asn Leu Asp Arg Ile Leu Asn Gln Glu Arg Leu Leu Arg Glu
1 5 10 15

Met Thr Gly Leu Asn Arg Gln Ala Phe Asn Glu Leu Leu Ser Gln Phe
20 25 30

Ala Asp Thr Tyr Glu Arg Thr Val Phe Asn Ser Leu Ala Asn Arg Lys
35 40 45

Arg Ala Pro Gly Gly Gly Arg Lys Pro Thr Leu Arg Ser Ile Glu Glu
50 55 60

Lys Leu Phe Tyr Ile Leu Leu Tyr Cys Lys Cys Tyr Pro Thr Phe Asp
65 70 75 80

Leu Leu Ser Val Leu Phe Asn Phe Asp Arg Ser Cys Ala His Asp Trp
85 90 95

Val His Arg Leu Leu Ser Val Leu Glu Thr Thr Leu Gly Glu Lys Gln
100 105 110

Val Leu Pro Ala Arg Lys Leu Arg Ser Met Glu Glu Phe Thr Lys Arg
115 120 125

Phe Pro Asp Val Lys Glu Val Ile Val Asp Gly Thr Glu Arg Pro Val
130 135 140

Gln Arg Pro Gln Asn Arg Glu Arg Gln Lys Glu Tyr Tyr Ser Gly Lys
145 150 155 160

Lys Lys Arg His Thr Cys Lys Gln Ile Thr Val Ser Thr Arg Glu Lys
165 170 175

Arg Val Ile Ile Arg Thr Glu Thr Arg Ala Gly Lys Val His Asp Lys
180 185 190

Arg Leu Leu His Glu Ser Glu Ile Val Gln Tyr Ile Pro Asp Glu Val
195 200 205

Ala Ile Glu Gly Asp Leu Gly Phe His Gly Leu Glu Lys Glu Phe Val
210 215 220

Asn Val His Leu Pro His Lys Lys Pro Lys Gly Ile Glu Ala Arg Arg
225 230 235 240

His Gly Gly Gly Met Gly Gln Phe Leu
245

<210> 93
<211> 1431
<212> DNA
<213> Cylindrospermopsis raciborskii AWT205

<400> 93
atgaatctta taacaacaaa aaaacaggta gatacattag tgatacacgc tcatcttttt 60

accatgcagg gaaatggtgt gggatatatt gcagatgggg cacttgcggt tgagggtagc 120

cgtattgtag cagttgattc gacggaggcg ttgctgagtc attttgaggg cagaaaggtt 180

attgagtccg cgaattgtgc cgtcttgcct gggctgatta atgctcacgt agacacaagt 240

ttggtgctga tgcgtggggc ggcgcaagat gtaactaatt ggctaatgga cgcgaccatg 300

ccttattttg ctcacatgac acccgtggcg agtatggctg caacacgctt aagggtggta 360

gaagagttga aagcaggcac aacaacattc tgtgacaata aaattattag ccccctgtgg 420

ggcgaatttt tcgatgaaat tggtgtacgg gctagtttag ctcctatgtt cgatgcactc 480

ccactggaga tgccaccgct tcaagacggg gagctttatc ccttcgatat caaggcggga 540

cggcgggcga tggcagaggc tgtggatttt gcctgtgggt ggaatggggc agcagagggg 600

cgtatcacta ccatgttagg aatgtattcg ccagatatga tgccgcttga gatgctacgc 660

gcagccaaag agattgctca acgggaaggc ttaatgctgc attttcatgt agcgcaggga 720

gatcgggaaa cagagcaaat cgttaaacga tatggtaagc gtccgatcgc atttctagct 780

gagattggct acttggacga acagttgctg gcagttcacc tcaccgatgc caccgatgaa 840

gaggtgatac aagtagccaa aagtggcgct ggcatggtac tctgttcggg aatgattggc 900

actattgacg gtatcgtgcc gcccgctcat gtgtttcggc aagcaggcgg acccgttgcg 960

ctaggcagca gctacaataa tattttccat gagatgaagc tgaccgcctt attcaacaaa 1020

ataaaatatc acgatccaac cattatgccg gcttgggaag tcctgcgtat ggctaccatc 1080

gaaggagcgc gggcgattgg tttagatcac aagattggct ctcttgaagt tggcaaagaa 1140

gccgacctga tcttaataga cctcagcacc cctaacctct cacccactct gcttaacccc 1200

attcgtaacc ttgtacctaa tttcgtgtac gctgcttcag gacatgaagt taaaagtgtc 1260

atggtggcgg gaaaactgtt attggaagac taccaagtcc tcacagtaga tgagtctgct 1320

atcattgctg aagcacaatt gcaagcccaa cagatttctc aatgcgtagc atctgaccct 1380

atccacaaaa aaatggtgct gatggcggcg atggcaaggg gccaattgta g 1431

<210> 94
<211> 476
<212> PRT
<213> Cylindrospermopsis raciborskii AWT205

<400> 94

Met Asn Leu Ile Thr Thr Lys Lys Gln Val Asp Thr Leu Val Ile His
1 5 10 15

Ala His Leu Phe Thr Met Gln Gly Asn Gly Val Gly Tyr Ile Ala Asp
20 25 30

Gly Ala Leu Ala Val Glu Gly Ser Arg Ile Val Ala Val Asp Ser Thr
35 40 45

Glu Ala Leu Leu Ser His Phe Glu Gly Arg Lys Val Ile Glu Ser Ala
50 55 60

Asn Cys Ala Val Leu Pro Gly Leu Ile Asn Ala His Val Asp Thr Ser
65 70 75 80

Leu Val Leu Met Arg Gly Ala Ala Gln Asp Val Thr Asn Trp Leu Met
85 90 95

Asp Ala Thr Met Pro Tyr Phe Ala His Met Thr Pro Val Ala Ser Met
100 105 110

Ala Ala Thr Arg Leu Arg Val Val Glu Glu Leu Lys Ala Gly Thr Thr
115 120 125

Thr Phe Cys Asp Asn Lys Ile Ile Ser Pro Leu Trp Gly Glu Phe Phe
130 135 140

Asp Glu Ile Gly Val Arg Ala Ser Leu Ala Pro Met Phe Asp Ala Leu
145 150 155 160

Pro Leu Glu Met Pro Pro Leu Gln Asp Gly Glu Leu Tyr Pro Phe Asp
165 170 175

Ile Lys Ala Gly Arg Arg Ala Met Ala Glu Ala Val Asp Phe Ala Cys
180 185 190

Gly Trp Asn Gly Ala Ala Glu Gly Arg Ile Thr Thr Met Leu Gly Met
195 200 205

Tyr Ser Pro Asp Met Met Pro Leu Glu Met Leu Arg Ala Ala Lys Glu
210 215 220

Ile Ala Gln Arg Glu Gly Leu Met Leu His Phe His Val Ala Gln Gly
225 230 235 240

Asp Arg Glu Thr Glu Gln Ile Val Lys Arg Tyr Gly Lys Arg Pro Ile
245 250 255

Ala Phe Leu Ala Glu Ile Gly Tyr Leu Asp Glu Gln Leu Leu Ala Val
260 265 270

His Leu Thr Asp Ala Thr Asp Glu Glu Val Ile Gln Val Ala Lys Ser
275 280 285

Gly Ala Gly Met Val Leu Cys Ser Gly Met Ile Gly Thr Ile Asp Gly
290 295 300

Ile Val Pro Pro Ala His Val Phe Arg Gln Ala Gly Gly Pro Val Ala
305 310 315 320

Leu Gly Ser Ser Tyr Asn Asn Ile Phe His Glu Met Lys Leu Thr Ala
325 330 335

Leu Phe Asn Lys Ile Lys Tyr His Asp Pro Thr Ile Met Pro Ala Trp
340 345 350

Glu Val Leu Arg Met Ala Thr Ile Glu Gly Ala Arg Ala Ile Gly Leu
355 360 365

Asp His Lys Ile Gly Ser Leu Glu Val Gly Lys Glu Ala Asp Leu Ile
370 375 380

Leu Ile Asp Leu Ser Thr Pro Asn Leu Ser Pro Thr Leu Leu Asn Pro
385 390 395 400

Ile Arg Asn Leu Val Pro Asn Phe Val Tyr Ala Ala Ser Gly His Glu
405 410 415

Val Lys Ser Val Met Val Ala Gly Lys Leu Leu Leu Glu Asp Tyr Gln
420 425 430

Val Leu Thr Val Asp Glu Ser Ala Ile Ile Ala Glu Ala Gln Leu Gln
435 440 445

Ala Gln Gln Ile Ser Gln Cys Val Ala Ser Asp Pro Ile His Lys Lys
450 455 460

Met Val Leu Met Ala Ala Met Ala Arg Gly Gln Leu
465 470 475

<210> 95
<211> 780
<212> DNA
<213> Cylindrospermopsis raciborskii AWT205

<400> 95
atgcaagaaa aacgaatcgc aatgtggtct gtgccacgaa gtttgggtac agtgctgcta 60

caagcctggt cgagtcggcc agataccgta gtctttgatg aacttctctc ctttccctat 120

ctctttatca aagggaaaga tatgggcttt acttggacag accttgattc tagccaaatg 180

ccccacgcag attggcgatc cgtcatcgat ctgttaaagg ctcccctgcc tgaagggaaa 240

tcaatcatcg atctgttaaa ggctcccctg cctgaaggga aatcaatttg ctatcagaag 300

catcaagcgt atcatttaat cgaagagacc atggggattg agtggatatt gcccttcagc 360

aactgctttc tgattcgcca acccaaagaa atgctcttat cttttcgtaa gattgtgcca 420

cattttacct ttgaagaaac aggctggatc gaattaaaac ggctgtttga ctatgtacat 480

caaacgagcg gagtaatccc gcctgtcata gatgcacacg acttgctgaa cgatccgcgg 540

agaatgctct ccaagctttg tcaggttgta ggggttgagt ttaccgagac aatgctcagt 600

tggcccccca tggaggtcga gttgaacgaa aaactagccc cttggtacag caccgtagca 660

agttctacgc attttcactc gtatcagaat aaaaatgagt cgttgccgct atatcttgtc 720

gatatttgta aacgctgcga tgaaatatat caggaattat atcaatttcg actttattag 780

<210> 96
<211> 259
<212> PRT
<213> Cylindrospermopsis raciborskii AWT205

<400> 96

Met Gln Glu Lys Arg Ile Ala Met Trp Ser Val Pro Arg Ser Leu Gly
1 5 10 15

Thr Val Leu Leu Gln Ala Trp Ser Ser Arg Pro Asp Thr Val Val Phe
20 25 30

Asp Glu Leu Leu Ser Phe Pro Tyr Leu Phe Ile Lys Gly Lys Asp Met
35 40 45

Gly Phe Thr Trp Thr Asp Leu Asp Ser Ser Gln Met Pro His Ala Asp
50 55 60

Trp Arg Ser Val Ile Asp Leu Leu Lys Ala Pro Leu Pro Glu Gly Lys
65 70 75 80

Ser Ile Ile Asp Leu Leu Lys Ala Pro Leu Pro Glu Gly Lys Ser Ile
85 90 95

Cys Tyr Gln Lys His Gln Ala Tyr His Leu Ile Glu Glu Thr Met Gly
100 105 110

Ile Glu Trp Ile Leu Pro Phe Ser Asn Cys Phe Leu Ile Arg Gln Pro
115 120 125

Lys Glu Met Leu Leu Ser Phe Arg Lys Ile Val Pro His Phe Thr Phe
130 135 140

Glu Glu Thr Gly Trp Ile Glu Leu Lys Arg Leu Phe Asp Tyr Val His
145 150 155 160

Gln Thr Ser Gly Val Ile Pro Pro Val Ile Asp Ala His Asp Leu Leu
165 170 175

Asn Asp Pro Arg Arg Met Leu Ser Lys Leu Cys Gln Val Val Gly Val
180 185 190

Glu Phe Thr Glu Thr Met Leu Ser Trp Pro Pro Met Glu Val Glu Leu
195 200 205

Asn Glu Lys Leu Ala Pro Trp Tyr Ser Thr Val Ala Ser Ser Thr His
210 215 220

Phe His Ser Tyr Gln Asn Lys Asn Glu Ser Leu Pro Leu Tyr Leu Val
225 230 235 240

Asp Ile Cys Lys Arg Cys Asp Glu Ile Tyr Gln Glu Leu Tyr Gln Phe
245 250 255

Arg Leu Tyr

<210> 97
<211> 1176
<212> DNA
<213> Cylindrospermopsis raciborskii AWT205

<400> 97
atgcaaacaa gaattgtaaa tagctggaat gagtgggatg aactaaagga gatggttgtc 60

gggattgcag atggtgctta ttttgaacca actgagccag gtaaccgccc tgctttacgc 120

gataagaaca ttgccaaaat gttctctttt cccaggggtc cgaaaaagca agaggtaaca 180

gagaaagcta atgaggagtt gaatgggctg gtagcgcttc tagaatcaca gggcgtaact 240

gtacgccgcc cagagaaaca taactttggc ctgtctgtga agacaccatt ctttgaggta 300

gagaatcaat attgtgcggt ctgcccacgt gatgttatga tcacctttgg gaacgaaatt 360

ctcgaagcaa ctatgtcacg gcggtcacgc ttctttgagt atttacccta tcgcaaacta 420

gtctatgaat attggcataa agatccagat atgatctgga atgctgcgcc taaaccgact 480

atgcaaaatg ccatgtaccg cgaagatttc tgggagtgtc cgatggaaga tcgatttgag 540

agtatgcatg attttgagtt ctgcgtcacc caggatgagg tgatttttga cgcagcagac 600

tgtagccgct ttggccgtga tatttttgtg caggagtcaa tgacgactaa tcgtgcaggg 660

attcgctggc tcaaacggca tttagagccg cgtcgcttcc gcgtgcatga tattcacttc 720

ccactagata ttttcccatc ccacattgat tgtacttttg tccccttagc acctggggtt 780

gtgttagtga atccagatcg ccccatcaaa gagggtgaag agaaactctt catggataac 840

ggttggcaat tcatcgaagc acccctcccc acttccaccg acgatgagat gcctatgttc 900

tgccagtcca gtaagtggtt ggcgatgaat gtgttaagca tttcccccaa gaaggtcatc 960

tgtgaagagc aagagcatcc gcttcatgag ttgctagata aacacggctt tgaggtctat 1020

ccaattccct ttcgcaatgt ctttgagttt ggcggttcgc tccattgtgc cacctgggat 1080

atccatcgca cgggaacctg tgaggattac ttccctaaac taaactatac gccggtaact 1140

gcatcaacca atggcgtttc tcgcttcatc atttag 1176

<210> 98
<211> 391
<212> PRT
<213> Cylindrospermopsis raciborskii AWT205

<400> 98

Met Gln Thr Arg Ile Val Asn Ser Trp Asn Glu Trp Asp Glu Leu Lys
1 5 10 15

Glu Met Val Val Gly Ile Ala Asp Gly Ala Tyr Phe Glu Pro Thr Glu
20 25 30

Pro Gly Asn Arg Pro Ala Leu Arg Asp Lys Asn Ile Ala Lys Met Phe
35 40 45

Ser Phe Pro Arg Gly Pro Lys Lys Gln Glu Val Thr Glu Lys Ala Asn
50 55 60

Glu Glu Leu Asn Gly Leu Val Ala Leu Leu Glu Ser Gln Gly Val Thr
65 70 75 80

Val Arg Arg Pro Glu Lys His Asn Phe Gly Leu Ser Val Lys Thr Pro
85 90 95

Phe Phe Glu Val Glu Asn Gln Tyr Cys Ala Val Cys Pro Arg Asp Val
100 105 110

Met Ile Thr Phe Gly Asn Glu Ile Leu Glu Ala Thr Met Ser Arg Arg
115 120 125

Ser Arg Phe Phe Glu Tyr Leu Pro Tyr Arg Lys Leu Val Tyr Glu Tyr
130 135 140

Trp His Lys Asp Pro Asp Met Ile Trp Asn Ala Ala Pro Lys Pro Thr
145 150 155 160

Met Gln Asn Ala Met Tyr Arg Glu Asp Phe Trp Glu Cys Pro Met Glu
165 170 175

Asp Arg Phe Glu Ser Met His Asp Phe Glu Phe Cys Val Thr Gln Asp
180 185 190

Glu Val Ile Phe Asp Ala Ala Asp Cys Ser Arg Phe Gly Arg Asp Ile
195 200 205

Phe Val Gln Glu Ser Met Thr Thr Asn Arg Ala Gly Ile Arg Trp Leu
210 215 220

Lys Arg His Leu Glu Pro Arg Arg Phe Arg Val His Asp Ile His Phe
225 230 235 240

Pro Leu Asp Ile Phe Pro Ser His Ile Asp Cys Thr Phe Val Pro Leu
245 250 255

Ala Pro Gly Val Val Leu Val Asn Pro Asp Arg Pro Ile Lys Glu Gly
260 265 270

Glu Glu Lys Leu Phe Met Asp Asn Gly Trp Gln Phe Ile Glu Ala Pro
275 280 285

Leu Pro Thr Ser Thr Asp Asp Glu Met Pro Met Phe Cys Gln Ser Ser
290 295 300

Lys Trp Leu Ala Met Asn Val Leu Ser Ile Ser Pro Lys Lys Val Ile
305 310 315 320

Cys Glu Glu Gln Glu His Pro Leu His Glu Leu Leu Asp Lys His Gly
325 330 335

Phe Glu Val Tyr Pro Ile Pro Phe Arg Asn Val Phe Glu Phe Gly Gly
340 345 350

Ser Leu His Cys Ala Thr Trp Asp Ile His Arg Thr Gly Thr Cys Glu
355 360 365

Asp Tyr Phe Pro Lys Leu Asn Tyr Thr Pro Val Thr Ala Ser Thr Asn
370 375 380

Gly Val Ser Arg Phe Ile Ile
385 390

<210> 99
<211> 8754
<212> DNA
<213> Cylindrospermopsis raciborskii AWT205

<400> 99
atgcaaaaga gagaaagccc acagatacta tttgatggga atggaacaca atctgagttt 60

ccagatagtt gcattcacca cttgttcgag gatcaagccg caaagcgacc ggatgcgatc 120

gctctcattg acggtgagca atcccttacc tacggggaac taaatgtacg cgctaaccac 180

ctagcccagc atctcttgtc cctaggctgt caacccgatg acctcctcgc catctgcatc 240

gagcgttcgg cagaactctt tattggtttg ttgggtatcc taaaagccgg atgtgcttat 300

gtgcctttgg atgtaggcta tcctggcgat cgcatagagt atatgttgcg ggactcggat 360

gcgcgtattt tactaacctc aacggatgtc gctaagaaac ttgccttaac catacctgca 420

ttgcaagagt gccaaaccgt ctatttagat caagagatat ttgagtatga ttttcatttt 480

ttagcgatag ctaaactatt acataaccaa tacttgagat tattacattt ttatttttat 540

accttgattc agcaatgcca ggcaacttcg gtttcccaag ggattcagac acaggttctc 600

cccaataatc tcgcttactg catttacacc tctggctcta ccggaaatcc caaagggatc 660

ttgatggaac atcgctcact ggtgaatatg ctttggtggc atcagcaaac gcggccttcg 720

gttcagggtg ttaggacgct gcaattttgt gcagtcagct ttgactttc ctgccatgaa 780

atttttcta ccctctgtct tggcgggata ttggtcttgg tgccagaggc agtgcgccaa 840

aatccctttg cattggctga gttcatcagt caacagaaaa ttgaaaaatt gtttcttccc 900

gttatagcat tactacagtt ggccgaagct gtaaatggga ataaaagcac ctccctcgcg 960

ctttgcgaag ttatcactac cggggagcag atgcagatca cacctgctgt cgccaacctc 1020

tttcagaaaa ccggggcgat gttgcataat cactacgggg caacagaatt tcaagatgcc 1080

accactcata ccctcaaggg caatccagag ggctggccaa cactggtgcc agtgggtcgt 1140

ccactgcaca atgttcaagt gtatattctg gatgaggcac agcaacctgt acctcttggt 1200

ggagagggtg aattctgtat tggtggtatt ggactggctc gtggctatca caatttgcct 1260

gacctaacga atgaaaaatt tattcccaat ccatttgggg ctaatgagaa cgctaaaaaa 1320

ctctaccgca caggggactt ggcacgctac ctacccgacg gcacgattga gcatttagga 1380

cggatagacc accaggttaa gatccgaggt ttccgcgtgg aattggggga aattgagtcc 1440

gtgctggcaa gtcaccaagc tgtgcgtgaa tgtgccgttg tggcacggga gattgcaggt 1500

catacacagt tggtagggta tatcatagca aaggatacac ttaatctcag tttcgacaaa 1560

cttgaaccta tcctgcgtca atattcggaa gcggtgctgc cagaatacat gatacccact 1620

cggttcatca atatcagtaa tatgccgttg actcccagtg gtaaacttga ccgcagggca 1680

ttacctgatc ccaaaggcga tcgccctgca ttgtctaccc cacttgtcaa gcctcgtacc 1740

cagacagaga aacgtttagc agagatttgg ggcagttatc ttgctgtaga tattgtggga 1800

acccacgaca atttctttga tctaggcggt acgtcactgc tattgactca agcgcacaaa 1860

ttcctgtgcg agacctttaa tattaatttg tccgctgtct cactctttca atatcccaca 1920

attcagacat tggcacaata tattgattgc caaggagaca caacctcaag cgatacagca 1980

tccaggcaca agaaagtacg taaaaagcag tccggtgaca gcaacgatat tgccatcatc 2040

agtgtggcag gtcgctttcc gggtgctgaa acgattgagc agttctggca taatctctgt 2100

aatggtgttg aatccatcac ccttttttagt gatgatgagc tagagcagac tttgcctgag 2160

ttatttaata atcccgctta tgtcaaagca ggtgcggtgc tagaaggcgt tgaattattt 2220

gatgctacct tttttggcta cagccccaaa gaagctgcgg tgacagaccc tcagcaacgg 2280

attttgctag agtgtgcctg ggaagcattt gaacgggctg gctacaaccc cgaaacctat 2340

ccagaaccag ttggtgttta tgctggttca agcctgagta cctatctgct taacaatatt 2400

ggctctgctt taggcataat taccgagcaa ccctttattg aaacggatat ggagcagttt 2460

caggctaaaa ttggcaatga ccggagctat cttgctacac gcatctctta caagctgaat 2520

ctcaagggtc caagcgtcaa tgtgcagacc gcctgctcaa cctcgttagt tgcggttcac 2580

atggcctgtc agagtctcat tagtggagag tgtcaaatgg ctttagccgg tggtatttct 2640

gtggttgtac cacagaaggg gggctatctc tacgaagaag gcatggttcg ttcccaggat 2700

ggtcattgtc gcgcctttga tgccgaagcc caagggacta tatttggcaa tggcggcggc 2760

ttggttttgc ttaaacggtt gcaggatgca ctggacgata acgacaacat tatggcagtc 2820

atcaaagcca cagccatcaa caacgacggt gcgctcaaga tgggctacac agcaccgagc 2880

gtggatgggc aagctgatgt aattagcgag gcgattgcta tcgctgacat agatgcaagc 2940

accattggct atgtagaagc tcatggcaca gccacccaat tgggtgatcc gattgaagta 3000

gcagggttag caagggcatt tcagcgtagt acggacagcg tccttggtaa acaacaatgc 3060

gctattggat cagttaaaac taatattggc cacttagatg aggcggcagg cattgccgga 3120

ctgataaagg ctgctctagc tctacaatat ggacagattc caccgagctt gcactatgcc 3180

aatcctaatc cacggattga ttttgacgca accccatttt ttgtcaacac agaactacgc 3240

gaatggtcaa ggaatggtta tcctcggcgg gcgggggtga gttcttttgg tgtgggtgga 3300

actaacagcc atattgtgct ggaggagtcg cctgtaaagc aacccacatt gttctcttct 3360

ttgccagaac gcagtcatca tctgctgacg ctttctgccc atacacaaga ggctttgcat 3420

gagttggtgc aacgctacat ccaacataac gagacacacc ttgatattaa cttaggcgac 3480

ctctgtttca cagccaatac gggacgcaag cattttgagc atcgcctagc ggttgtagcc 3540

gaatcaatcc ctggcttaca ggcacaactg gaaactgcac agactgcgat ttcagcacag 3600

aaaaaaaatg ccccgccgac gatcgcattc ctgtttacag gtcaaggctc acaatacatt 3660

aacatggggc gcaccctcta cgatactgaa tcaacattcc gtgcagccct tgaccgatgt 3720

gaaaccattc tccaaaattt agggatcgag tccattctct ccgttatttt tggttcatct 3780

gagcatggac tctcattaga tgacacagcc tatacccagc ccgcactctt tgccatcgaa 3840

tacgcgctct atcaattatg gaagtcgtgg ggcatccagc cctcagtggt gataggtcat 3900

agtgtaggtg aatatgtgtc cgcttgtgtg gcgggagtct ttagcttaga ggatgggttg 3960

aaactgattg cagaacgagg acgactgata caggcacttc ctcgtgatgg gagcatggtt 4020

tccgtgatgg caagcgagaa gcgtattgca gatatcattt taccttatgg gggacaggta 4080

gggatcgccg cgattaatgg cccacaaagt gttgtaattt ctgggcaaca gcaagcgatt 4140

gatgctattt gtgccatctt ggaaactgag ggcatcaaaa gcaagaagct aaacgtctcc 4200

catgccttcc actcgccgct agtggaagca atgttagact ctttcttgca ggttgcacaa 4260

gaggtcactt actcgcaacc tcaaatcaag cttatctcta atgtaacggg aacattggca 4320

agccatgaat cttgtcccga tgaacttccg atcaccaccg cagagtattg ggtacgtcat 4380

gtgcgacagc ccgtccggtt tgcggcggga atggagagcc ttgagggtca aggggtaaac 4440

gtatttatag aaatcggtcc taaacctgtt cttttaggca tgggacgcga ctgcttgcct 4500

gaacaagagg gactttggtt gcctagtttg cgcccaaaac aggatgattg gcaacaggtg 4560

ttaagtagtt tgcgtgatct atacttagca ggtgtaaccg tagattggag cagtttcgat 4620

caggggtatg ctcgtcgccg tgtgccacta ccgacttatc cttggcagcg agagcggcat 4680

tgggtagagc caattattcg tcaacggcaa tcagtattac aagccacaaa taccaccaag 4740

ctaactcgta acgccagcgt ggcgcagcat cctctgcttg gtcaacggct gcatttgtcg 4800

cggactcaag agatttactt tcaaaccttc atccactccg acttcccaat atgggttgct 4860

gatcataaag tatttggaaa tgtcatcatt ccgggtgtcg cctattttga gatggcactg 4920

gcagcaggga aggcacttaa accagacagt atattttggc tcgaagatgt atccatcgcc 4980

caagcactga ttattcccga tgaagggcaa actgtgcaaa tagtattaag cccacaggaa 5040

gagtcagctt attttttga aatcctctct ttagaaaaag aaaactcttg ggtgcttcat 5100

gcctctggta agctagtcgc ccaagagcaa gtgctagaaa ccgagccaat tgacttgatt 5160

gcgttacagg cacattgttc cgaagaagtg tcagtagatg tgctatatca ggaagaaatg 5220

gcgcgccggc tggatatggg tccaatgatg cgtggggtga agcagctttg gcgttatccg 5280

ctctcctttg ccaaaagtca tgatgcgatc gcactcgcca aggtcagctt gccagaaatc 5340

ttgcttcatg agtccaatgc ctaccaattc catcctgtaa tcttggatgc ggggctgcaa 5400

atgataacgg tctcttatcc tgaagcaaac caaggccaga cttatgtacc tgttggtata 5460

gagggtctac aagtctatgg tcgtcccagt tcagaacttt ggtgtcgcgc ccaatatcgg 5520

cctcctttgg atacagatca aaggcagggt attgatttgc tgccaaagaa attgattgca 5580

gacttgcatc tatttgatac ccagggtcgt gtggttgcca tcatgtttgg tgtgcaatct 5640

gtccttgtgg gacgggaagc aatgttgcga tcgcaagata cttggcgaaa ttggctttat 5700

caagtcctgt ggaaacctca agcctgtttt ggacttttac cgaattacct gccaacccca 5760

gataagattc ggaaacgcct ggaaacaaag ttagcgacat tgatcatcga agctaatttg 5820

gcgacttatg cgatcgccta tacccaactg gaaaggttaa gtctagctta cgttgtggcg 5880

gctttccgac aaatgggctg gctgtttcaa cccggtgagc gtttttccac cgcccagaag 5940

gtatcagcgt taggaatcgt tgatcaacat cggcaactat tcgctcgttt gctcgacatt 6000

ctagccgaag cagacatact ccgcagcgaa aacttgatga cgatatggga agtcatttca 6060

tacccggaaa cgattgatat acaggtactt cttgacgacc tcgaagccaa agaagcagaa 6120

gccgaagtca cactggtttc ccgttgcagt gcaaaattgg ccgaagtatt acaaggaaaa 6180

tgtgacccca tacagttgct ctttcccgca ggggacacaa caacgttaag caaactctat 6240

cgtgaagccc cagttttggg tgttactaat actctagtcc aagaagcgct tctttccgcc 6300

ctggagcagt tgccgccgga acgtggttgg cgaattttag agattggtgc tggaacaggt 6360

ggaaccacag cctacttgtt accgcatctg cctggggatc agacaaaata tgtctttacc 6420

gatattagtg ccttttttct tgccaaagcg gaagagcgtt ttaaagatta cccgtttgta 6480

cgttatcagg tattagatat cgaacaagca ccacaggcgc aaggatttga accccaaata 6540

tacgatttaa tcgtagcagc ggatgtcttg catgctacta gtgacctgcg tcaaactctt 6600

gtacatatcc ggcaattatt agcgccgggc gggatgttga tcctgatgga agacagcgaa 6660

cccgcacgct gggctgattt aacctttggc ttaacagaag gctggtggaa gtttacagac 6720

catgacttac gccccaacca tccgctattg tctcctgagc agtggcaaat cttgttgtca 6780

gaaatgggat ttagtcaaac aaccgcctta tggccaaaaa tagatagccc ccataaattg 6840

ccacgggagg cggtgattgt ggcgcgtaat gaaccagcca tcagaaaacc ccgaagatgg 6900

ctgatcttgg ctgacgagga gattggtgga ctactagcca aacagctacg tgaagaagga 6960

gaagattgta tactcctctt gccaggggaa aagtacacag agagagattc acaaacgttt 7020

acaatcaatc ctggagatat tgaagagtgg caacagttat tgaaccgagt accgaacata 7080

caagaaattg tacattgttg gagtatggtt tccactgact tagatagagc cactattttc 7140

agttgcagca gtacgctgca tttagttcaa gcattagcaa actatccaaa aaaccctcgc 7200

ttgtcacttg tcaccctagg cgcacaagcc gttaacgaac atcatgttca aaatgtagtt 7260

ggagcagccc tctggggcat gggaaaggta attgcactcg aacacccaga gctacaagta 7320

gcacaaatgg atttagaccc gaatgggaag gttaaggcgc aagtagaagt gcttagggat 7380

gaacttctcg ccagaaaaga ccctgcatca gcaatgtctg tgcctgatct gcaaacacga 7440

cctcatgaaa agcaaatagc ctttcgtgag caaacacgtt atgtggcaag actttcgccc 7500

ttagaccgcc ccaatcctgg agagaaaggc acacaagagg ctcttacctt ccgtgatgat 7560

ggcagctatc tgattgctgg tggtttaggc ggactggggt tagtggtggc tcgttttctg 7620

gttacaaatg gggctaaata ccttgtgcta gtcggacgac gtggtgcgag ggaggaacag 7680

caagctcaat taagcgaact agagcaactc ggagcttccg tgaaagtttt acaagccgat 7740

attgctgatg cagaacaact agcccaagca ctttcagcag taacctaccc accattacgg 7800

ggtgttattc atgcggcagg tacattgaac gatgggattc tacagcagca aagttggcaa 7860

gcctttaaag aagtgatgaa tcccaaggta gcaggtgcgt ggaacctaca tatactgaca 7920

aaaaatcagc ctttagactt ctttgtcctg ttctcctccg ccacctcttt gttaggtaac 7980

gctggacaag ccaatcacgc cgccgcaaat gctttccttg atgggttagc ctcctatcgt 8040

cgtcacttag gactaccgag cctctcgatt aattgggggа catggagcga agtgggaatt 8100

gcggctcgac ttgaactaga taagttgtcc agcaaacagg gagagggaac cattacgcta 8160

ggacagggct tacaaattct tgagcagttg ctcaaagacg agaatggggt gtatcaagtg 8220

ggtgtcatgc ctatcaactg gacacaattc ttagcaaggc aattgactcc gcagccgttc 8280

ttcagcgatg ccatgaagag tattgacacc tctgtaggta aactaacctt gcaggagcgg 8340

gactcttgcc cccaaggtta cgggcataat attcgagagc aattagagaa cgctccgccc 8400

aaagagggtc tgactctctt gcaggctcat gttcgggagc aggtttccca agttttgggg 8460

atagacacga agacattatt ggcagaacaa gacgtgggtt tctttaccct ggggatggat 8520

tcgctgacct ctgtcgagtt aagaaacagg ttacaagcca gtttgggctg ctctctttct 8580

tccactttgg cttttgacta tccaacacaa caggctcttg tgaattatct tgccaatgaa 8640

ttgctgggaa cccctgagca gctacaagag cctgaatctg atgaagaaga tcagatatcg 8700

tcaatggatg acatcgtgca gttgctgtcc gcgaaactag agatggaaat ttaa 8754

<210> 100
<211> 2917
<212> PRT
<213> Cylindrospermopsis raciborskii AWT205

<400> 100

Met Gln Lys Arg Glu Ser Pro Gln Ile Leu Phe Asp Gly Asn Gly Thr
1 5 10 15

Gln Ser Glu Phe Pro Asp Ser Cys Ile His His Leu Phe Glu Asp Gln
20 25 30

Ala Ala Lys Arg Pro Asp Ala Ile Ala Leu Ile Asp Gly Glu Gln Ser
35 40 45

Leu Thr Tyr Gly Glu Leu Asn Val Arg Ala Asn His Leu Ala Gln His
50 55 60

Leu Leu Ser Leu Gly Cys Gln Pro Asp Asp Leu Leu Ala Ile Cys Ile
65 70 75 80

Glu Arg Ser Ala Glu Leu Phe Ile Gly Leu Leu Gly Ile Leu Lys Ala
85 90 95

Gly Cys Ala Tyr Val Pro Leu Asp Val Gly Tyr Pro Gly Asp Arg Ile
100 105 110

Glu Tyr Met Leu Arg Asp Ser Asp Ala Arg Ile Leu Leu Thr Ser Thr
115 120 125

Asp Val Ala Lys Lys Leu Ala Leu Thr Ile Pro Ala Leu Gln Glu Cys
130 135 140

Gln Thr Val Tyr Leu Asp Gln Glu Ile Phe Glu Tyr Asp Phe His Phe
145 150 155 160

Leu Ala Ile Ala Lys Leu Leu His Asn Gln Tyr Leu Arg Leu Leu His
165 170 175

Phe Tyr Phe Tyr Thr Leu Ile Gln Gln Cys Gln Ala Thr Ser Val Ser
180 185 190

Gln Gly Ile Gln Thr Gln Val Leu Pro Asn Asn Leu Ala Tyr Cys Ile
195 200 205

Tyr Thr Ser Gly Ser Thr Gly Asn Pro Lys Gly Ile Leu Met Glu His
210 215 220

Arg Ser Leu Val Asn Met Leu Trp Trp His Gln Gln Thr Arg Pro Ser
225 230 235 240

Val Gln Gly Val Arg Thr Leu Gln Phe Cys Ala Val Ser Phe Asp Phe
245 250 255

Ser Cys His Glu Ile Phe Ser Thr Leu Cys Leu Gly Gly Ile Leu Val
260 265 270

Leu Val Pro Glu Ala Val Arg Gln Asn Pro Phe Ala Leu Ala Glu Phe
275 280 285

Ile Ser Gln Gln Lys Ile Glu Lys Leu Phe Leu Pro Val Ile Ala Leu
290 295 300

Leu Gln Leu Ala Glu Ala Val Asn Gly Asn Lys Ser Thr Ser Leu Ala
305 310 315 320

Leu Cys Glu Val Ile Thr Thr Gly Glu Gln Met Gln Ile Thr Pro Ala
325 330 335

Val Ala Asn Leu Phe Gln Lys Thr Gly Ala Met Leu His Asn His Tyr
340 345 350

Gly Ala Thr Glu Phe Gln Asp Ala Thr Thr His Thr Leu Lys Gly Asn
355 360 365

Pro Glu Gly Trp Pro Thr Leu Val Pro Val Gly Arg Pro Leu His Asn
370 375 380

Val Gln Val Tyr Ile Leu Asp Glu Ala Gln Gln Pro Val Pro Leu Gly
385 390 395 400

Gly Glu Gly Glu Phe Cys Ile Gly Gly Ile Gly Leu Ala Arg Gly Tyr
405 410 415

His Asn Leu Pro Asp Leu Thr Asn Glu Lys Phe Ile Pro Asn Pro Phe
420 425 430

Gly Ala Asn Glu Asn Ala Lys Lys Leu Tyr Arg Thr Gly Asp Leu Ala
435 440 445

Arg Tyr Leu Pro Asp Gly Thr Ile Glu His Leu Gly Arg Ile Asp His
450 455 460

Gln Val Lys Ile Arg Gly Phe Arg Val Glu Leu Gly Glu Ile Glu Ser
465 470 475 480

Val Leu Ala Ser His Gln Ala Val Arg Glu Cys Ala Val Val Ala Arg
485 490 495

Glu Ile Ala Gly His Thr Gln Leu Val Gly Tyr Ile Ile Ala Lys Asp
500 505 510

Thr Leu Asn Leu Ser Phe Asp Lys Leu Glu Pro Ile Leu Arg Gln Tyr
515 520 525

Ser Glu Ala Val Leu Pro Glu Tyr Met Ile Pro Thr Arg Phe Ile Asn
530 535 540

Ile Ser Asn Met Pro Leu Thr Pro Ser Gly Lys Leu Asp Arg Arg Ala
545 550 555 560

Leu Pro Asp Pro Lys Gly Asp Arg Pro Ala Leu Ser Thr Pro Leu Val
565 570 575

Lys Pro Arg Thr Gln Thr Glu Lys Arg Leu Ala Glu Ile Trp Gly Ser
580 585 590

Tyr Leu Ala Val Asp Ile Val Gly Thr His Asp Asn Phe Phe Asp Leu
595 600 605

Gly Gly Thr Ser Leu Leu Leu Thr Gln Ala His Lys Phe Leu Cys Glu
610 615 620

Thr Phe Asn Ile Asn Leu Ser Ala Val Ser Leu Phe Gln Tyr Pro Thr
625 630 635 640

Ile Gln Thr Leu Ala Gln Tyr Ile Asp Cys Gln Gly Asp Thr Thr Ser
645 650 655

Ser Asp Thr Ala Ser Arg His Lys Lys Val Arg Lys Lys Gln Ser Gly
660 665 670

Asp Ser Asn Asp Ile Ala Ile Ile Ser Val Ala Gly Arg Phe Pro Gly
675 680 685

Ala Glu Thr Ile Glu Gln Phe Trp His Asn Leu Cys Asn Gly Val Glu
690 695 700

Ser Ile Thr Leu Phe Ser Asp Asp Glu Leu Glu Gln Thr Leu Pro Glu
705 710 715 720

Leu Phe Asn Asn Pro Ala Tyr Val Lys Ala Gly Ala Val Leu Glu Gly
725 730 735

Val Glu Leu Phe Asp Ala Thr Phe Phe Gly Tyr Ser Pro Lys Glu Ala
740 745 750

Ala Val Thr Asp Pro Gln Gln Arg Ile Leu Leu Glu Cys Ala Trp Glu
755 760 765

Ala Phe Glu Arg Ala Gly Tyr Asn Pro Glu Thr Tyr Pro Glu Pro Val
770 775 780

Gly Val Tyr Ala Gly Ser Ser Leu Ser Thr Tyr Leu Leu Asn Asn Ile
785 790 795 800

Gly Ser Ala Leu Gly Ile Ile Thr Glu Gln Pro Phe Ile Glu Thr Asp
805 810 815

Met Glu Gln Phe Gln Ala Lys Ile Gly Asn Asp Arg Ser Tyr Leu Ala
820 825 830

Thr Arg Ile Ser Tyr Lys Leu Asn Leu Lys Gly Pro Ser Val Asn Val
835 840 845

Gln Thr Ala Cys Ser Thr Ser Leu Val Ala Val His Met Ala Cys Gln
850 855 860

Ser Leu Ile Ser Gly Glu Cys Gln Met Ala Leu Ala Gly Gly Ile Ser
865 870 875 880

Val Val Val Pro Gln Lys Gly Gly Tyr Leu Tyr Glu Glu Gly Met Val
885 890 895

Arg Ser Gln Asp Gly His Cys Arg Ala Phe Asp Ala Glu Ala Gln Gly
900 905 910

Thr Ile Phe Gly Asn Gly Gly Gly Leu Val Leu Leu Lys Arg Leu Gln
915 920 925

Asp Ala Leu Asp Asp Asn Asp Asn Ile Met Ala Val Ile Lys Ala Thr
930 935 940

Ala Ile Asn Asn Asp Gly Ala Leu Lys Met Gly Tyr Thr Ala Pro Ser
945 950 955 960

Val Asp Gly Gln Ala Asp Val Ile Ser Glu Ala Ile Ala Ile Ala Asp
965 970 975

Ile Asp Ala Ser Thr Ile Gly Tyr Val Glu Ala His Gly Thr Ala Thr
980 985 990

Gln Leu Gly Asp Pro Ile Glu Val Ala Gly Leu Ala Arg Ala Phe Gln
995 1000 1005

Arg Ser Thr Asp Ser Val Leu Gly Lys Gln Gln Cys Ala Ile Gly
1010 1015 1020

Ser Val Lys Thr Asn Ile Gly His Leu Asp Glu Ala Ala Gly Ile
1025 1030 1035

Ala Gly Leu Ile Lys Ala Ala Leu Ala Leu Gln Tyr Gly Gln Ile
1040 1045 1050

Pro Pro Ser Leu His Tyr Ala Asn Pro Asn Pro Arg Ile Asp Phe
1055 1060 1065

Asp Ala Thr Pro Phe Phe Val Asn Thr Glu Leu Arg Glu Trp Ser
1070 1075 1080

Arg Asn Gly Tyr Pro Arg Arg Ala Gly Val Ser Ser Phe Gly Val
1085 1090 1095

Gly Gly Thr Asn Ser His Ile Val Leu Glu Glu Ser Pro Val Lys
1100 1105 1110

Gln Pro Thr Leu Phe Ser Ser Leu Pro Glu Arg Ser His His Leu
1115 1120 1125

Leu Thr Leu Ser Ala His Thr Gln Glu Ala Leu His Glu Leu Val
1130 1135 1140

Gln Arg Tyr Ile Gln His Asn Glu Thr His Leu Asp Ile Asn Leu
1145 1150 1155

Gly Asp Leu Cys Phe Thr Ala Asn Thr Gly Arg Lys His Phe Glu
1160 1165 1170

His Arg Leu Ala Val Val Ala Glu Ser Ile Pro Gly Leu Gln Ala
1175 1180 1185

Gln Leu Glu Thr Ala Gln Thr Ala Ile Ser Ala Gln Lys Lys Asn
1190 1195 1200

Ala Pro Pro Thr Ile Ala Phe Leu Phe Thr Gly Gln Gly Ser Gln
1205 1210 1215

Tyr Ile Asn Met Gly Arg Thr Leu Tyr Asp Thr Glu Ser Thr Phe
1220 1225 1230

Arg Ala Ala Leu Asp Arg Cys Glu Thr Ile Leu Gln Asn Leu Gly
1235 1240 1245

Ile Glu Ser Ile Leu Ser Val Ile Phe Gly Ser Ser Glu His Gly
1250 1255 1260

Leu Ser Leu Asp Asp Thr Ala Tyr Thr Gln Pro Ala Leu Phe Ala
1265 1270 1275

Ile Glu Tyr Ala Leu Tyr Gln Leu Trp Lys Ser Trp Gly Ile Gln
1280 1285 1290

Pro Ser Val Val Ile Gly His Ser Val Gly Glu Tyr Val Ser Ala
1295 1300 1305

Cys Val Ala Gly Val Phe Ser Leu Glu Asp Gly Leu Lys Leu Ile
1310 1315 1320

Ala Glu Arg Gly Arg Leu Ile Gln Ala Leu Pro Arg Asp Gly Ser
1325 1330 1335

Met Val Ser Val Met Ala Ser Glu Lys Arg Ile Ala Asp Ile Ile
1340 1345 1350

Leu Pro Tyr Gly Gly Gln Val Gly Ile Ala Ala Ile Asn Gly Pro
1355 1360 1365

Gln Ser Val Val Ile Ser Gly Gln Gln Gln Ala Ile Asp Ala Ile
1370 1375 1380

Cys Ala Ile Leu Glu Thr Glu Gly Ile Lys Ser Lys Lys Leu Asn
1385 1390 1395

Val Ser His Ala Phe His Ser Pro Leu Val Glu Ala Met Leu Asp
1400 1405 1410

Ser Phe Leu Gln Val Ala Gln Glu Val Thr Tyr Ser Gln Pro Gln
1415 1420 1425

Ile Lys Leu Ile Ser Asn Val Thr Gly Thr Leu Ala Ser His Glu
1430 1435 1440

Ser Cys Pro Asp Glu Leu Pro Ile Thr Thr Ala Glu Tyr Trp Val
1445 1450 1455

Arg His Val Arg Gln Pro Val Arg Phe Ala Ala Gly Met Glu Ser
1460 1465 1470

Leu Glu Gly Gln Gly Val Asn Val Phe Ile Glu Ile Gly Pro Lys
1475 1480 1485

Pro Val Leu Leu Gly Met Gly Arg Asp Cys Leu Pro Glu Gln Glu
1490 1495 1500

Gly Leu Trp Leu Pro Ser Leu Arg Pro Lys Gln Asp Asp Trp Gln
1505 1510 1515

Gln Val Leu Ser Ser Leu Arg Asp Leu Tyr Leu Ala Gly Val Thr
1520 1525 1530

Val Asp Trp Ser Ser Phe Asp Gln Gly Tyr Ala Arg Arg Arg Val
1535 1540 1545

Pro Leu Pro Thr Tyr Pro Trp Gln Arg Glu Arg His Trp Val Glu
1550 1555 1560

Pro Ile Ile Arg Gln Arg Gln Ser Val Leu Gln Ala Thr Asn Thr
1565 1570 1575

Thr Lys Leu Thr Arg Asn Ala Ser Val Ala Gln His Pro Leu Leu
1580 1585 1590

Gly Gln Arg Leu His Leu Ser Arg Thr Gln Glu Ile Tyr Phe Gln
1595 1600 1605

Thr Phe Ile His Ser Asp Phe Pro Ile Trp Val Ala Asp His Lys
1610 1615 1620

Val Phe Gly Asn Val Ile Ile Pro Gly Val Ala Tyr Phe Glu Met
1625 1630 1635

Ala Leu Ala Ala Gly Lys Ala Leu Lys Pro Asp Ser Ile Phe Trp
1640 1645 1650

Leu Glu Asp Val Ser Ile Ala Gln Ala Leu Ile Ile Pro Asp Glu
1655 1660 1665

Gly Gln Thr Val Gln Ile Val Leu Ser Pro Gln Glu Glu Ser Ala
1670 1675 1680

Tyr Phe Phe Glu Ile Leu Ser Leu Glu Lys Glu Asn Ser Trp Val
1685 1690 1695

Leu His Ala Ser Gly Lys Leu Val Ala Gln Glu Gln Val Leu Glu
1700 1705 1710

Thr Glu Pro Ile Asp Leu Ile Ala Leu Gln Ala His Cys Ser Glu
1715 1720 1725

Glu Val Ser Val Asp Val Leu Tyr Gln Glu Glu Met Ala Arg Arg
1730 1735 1740

Leu Asp Met Gly Pro Met Met Arg Gly Val Lys Gln Leu Trp Arg
1745 1750 1755

Tyr Pro Leu Ser Phe Ala Lys Ser His Asp Ala Ile Ala Leu Ala
1760 1765 1770

Lys Val Ser Leu Pro Glu Ile Leu Leu His Glu Ser Asn Ala Tyr
1775 1780 1785

Gln Phe His Pro Val Ile Leu Asp Ala Gly Leu Gln Met Ile Thr
1790 1795 1800

Val Ser Tyr Pro Glu Ala Asn Gln Gly Gln Thr Tyr Val Pro Val
1805 1810 1815

Gly Ile Glu Gly Leu Gln Val Tyr Gly Arg Pro Ser Ser Glu Leu
1820 1825 1830

Trp Cys Arg Ala Gln Tyr Arg Pro Pro Leu Asp Thr Asp Gln Arg
1835 1840 1845

Gln Gly Ile Asp Leu Leu Pro Lys Lys Leu Ile Ala Asp Leu His
1850 1855 1860

Leu Phe Asp Thr Gln Gly Arg Val Val Ala Ile Met Phe Gly Val
1865 1870 1875

Gln Ser Val Leu Val Gly Arg Glu Ala Met Leu Arg Ser Gln Asp
1880 1885 1890

Thr Trp Arg Asn Trp Leu Tyr Gln Val Leu Trp Lys Pro Gln Ala
1895 1900 1905

Cys Phe Gly Leu Leu Pro Asn Tyr Leu Pro Thr Pro Asp Lys Ile
1910 1915 1920

Arg Lys Arg Leu Glu Thr Lys Leu Ala Thr Leu Ile Ile Glu Ala
1925 1930 1935

Asn Leu Ala Thr Tyr Ala Ile Ala Tyr Thr Gln Leu Glu Arg Leu
1940 1945 1950

Ser Leu Ala Tyr Val Val Ala Ala Phe Arg Gln Met Gly Trp Leu
1955 1960 1965

Phe Gln Pro Gly Glu Arg Phe Ser Thr Ala Gln Lys Val Ser Ala
1970 1975 1980

Leu Gly Ile Val Asp Gln His Arg Gln Leu Phe Ala Arg Leu Leu
1985 1990 1995

Asp Ile Leu Ala Glu Ala Asp Ile Leu Arg Ser Glu Asn Leu Met
2000 2005 2010

Thr Ile Trp Glu Val Ile Ser Tyr Pro Glu Thr Ile Asp Ile Gln
2015 2020 2025

Val Leu Leu Asp Asp Leu Glu Ala Lys Glu Ala Glu Ala Glu Val
2030 2035 2040

Thr Leu Val Ser Arg Cys Ser Ala Lys Leu Ala Glu Val Leu Gln
2045 2050 2055

Gly Lys Cys Asp Pro Ile Gln Leu Leu Phe Pro Ala Gly Asp Thr
2060 2065 2070

Thr Thr Leu Ser Lys Leu Tyr Arg Glu Ala Pro Val Leu Gly Val
2075 2080 2085

Thr Asn Thr Leu Val Gln Glu Ala Leu Leu Ser Ala Leu Glu Gln
2090 2095 2100

Leu Pro Pro Glu Arg Gly Trp Arg Ile Leu Glu Ile Gly Ala Gly
2105 2110 2115

Thr Gly Gly Thr Thr Ala Tyr Leu Leu Pro His Leu Pro Gly Asp
2120 2125 2130

Gln Thr Lys Tyr Val Phe Thr Asp Ile Ser Ala Phe Phe Leu Ala
2135 2140 2145

Lys Ala Glu Glu Arg Phe Lys Asp Tyr Pro Phe Val Arg Tyr Gln
2150 2155 2160

Val Leu Asp Ile Glu Gln Ala Pro Gln Ala Gln Gly Phe Glu Pro
2165 2170 2175

Gln Ile Tyr Asp Leu Ile Val Ala Ala Asp Val Leu His Ala Thr
2180 2185 2190

Ser Asp Leu Arg Gln Thr Leu Val His Ile Arg Gln Leu Leu Ala
2195 2200 2205

Pro Gly Gly Met Leu Ile Leu Met Glu Asp Ser Glu Pro Ala Arg
2210 2215 2220

Trp Ala Asp Leu Thr Phe Gly Leu Thr Glu Gly Trp Trp Lys Phe
2225 2230 2235

Thr Asp His Asp Leu Arg Pro Asn His Pro Leu Leu Ser Pro Glu
2240 2245 2250

Gln Trp Gln Ile Leu Leu Ser Glu Met Gly Phe Ser Gln Thr Thr
2255 2260 2265

Ala Leu Trp Pro Lys Ile Asp Ser Pro His Lys Leu Pro Arg Glu
2270 2275 2280

Ala Val Ile Val Ala Arg Asn Glu Pro Ala Ile Arg Lys Pro Arg
2285 2290 2295

Arg Trp Leu Ile Leu Ala Asp Glu Glu Ile Gly Gly Leu Leu Ala
2300 2305 2310

Lys Gln Leu Arg Glu Glu Gly Glu Asp Cys Ile Leu Leu Leu Pro
2315 2320 2325

Gly Glu Lys Tyr Thr Glu Arg Asp Ser Gln Thr Phe Thr Ile Asn
2330 2335 2340

Pro Gly Asp Ile Glu Glu Trp Gln Gln Leu Leu Asn Arg Val Pro
2345 2350 2355

Asn Ile Gln Glu Ile Val His Cys Trp Ser Met Val Ser Thr Asp
2360 2365 2370

Leu Asp Arg Ala Thr Ile Phe Ser Cys Ser Ser Thr Leu His Leu
2375 2380 2385

Val Gln Ala Leu Ala Asn Tyr Pro Lys Asn Pro Arg Leu Ser Leu
2390 2395 2400

Val Thr Leu Gly Ala Gln Ala Val Asn Glu His His Val Gln Asn
2405 2410 2415

Val Val Gly Ala Ala Leu Trp Gly Met Gly Lys Val Ile Ala Leu
2420 2425 2430

Glu His Pro Glu Leu Gln Val Ala Gln Met Asp Leu Asp Pro Asn
2435 2440 2445

Gly Lys Val Lys Ala Gln Val Glu Val Leu Arg Asp Glu Leu Leu
2450 2455 2460

Ala Arg Lys Asp Pro Ala Ser Ala Met Ser Val Pro Asp Leu Gln
2465 2470 2475

Thr Arg Pro His Glu Lys Gln Ile Ala Phe Arg Glu Gln Thr Arg
2480 2485 2490

Tyr Val Ala Arg Leu Ser Pro Leu Asp Arg Pro Asn Pro Gly Glu
2495 2500 2505

Lys Gly Thr Gln Glu Ala Leu Thr Phe Arg Asp Asp Gly Ser Tyr
2510 2515 2520

Leu Ile Ala Gly Gly Leu Gly Gly Leu Gly Leu Val Val Ala Arg
2525 2530 2535

Phe Leu Val Thr Asn Gly Ala Lys Tyr Leu Val Leu Val Gly Arg
2540 2545 2550

Arg Gly Ala Arg Glu Glu Gln Gln Ala Gln Leu Ser Glu Leu Glu
2555 2560 2565

Gln Leu Gly Ala Ser Val Lys Val Leu Gln Ala Asp Ile Ala Asp
2570 2575 2580

Ala Glu Gln Leu Ala Gln Ala Leu Ser Ala Val Thr Tyr Pro Pro
2585 2590 2595

Leu Arg Gly Val Ile His Ala Ala Gly Thr Leu Asn Asp Gly Ile
2600 2605 2610

Leu Gln Gln Gln Ser Trp Gln Ala Phe Lys Glu Val Met Asn Pro
2615 2620 2625

Lys Val Ala Gly Ala Trp Asn Leu His Ile Leu Thr Lys Asn Gln
2630 2635 2640

Pro Leu Asp Phe Phe Val Leu Phe Ser Ser Ala Thr Ser Leu Leu
2645 2650 2655

Gly Asn Ala Gly Gln Ala Asn His Ala Ala Ala Asn Ala Phe Leu
2660 2665 2670

Asp Gly Leu Ala Ser Tyr Arg Arg His Leu Gly Leu Pro Ser Leu
2675 2680 2685

Ser Ile Asn Trp Gly Thr Trp Ser Glu Val Gly Ile Ala Ala Arg
2690 2695 2700

Leu Glu Leu Asp Lys Leu Ser Ser Lys Gln Gly Glu Gly Thr Ile
2705 2710 2715

Thr Leu Gly Gln Gly Leu Gln Ile Leu Glu Gln Leu Leu Lys Asp
2720 2725 2730

Glu Asn Gly Val Tyr Gln Val Gly Val Met Pro Ile Asn Trp Thr
2735 2740 2745

Gln Phe Leu Ala Arg Gln Leu Thr Pro Gln Pro Phe Phe Ser Asp
2750 2755 2760

Ala Met Lys Ser Ile Asp Thr Ser Val Gly Lys Leu Thr Leu Gln
2765 2770 2775

Glu Arg Asp Ser Cys Pro Gln Gly Tyr Gly His Asn Ile Arg Glu
2780 2785 2790

Gln Leu Glu Asn Ala Pro Pro Lys Glu Gly Leu Thr Leu Leu Gln
2795 2800 2805

Ala His Val Arg Glu Gln Val Ser Gln Val Leu Gly Ile Asp Thr
2810 2815 2820

Lys Thr Leu Leu Ala Glu Gln Asp Val Gly Phe Phe Thr Leu Gly
2825 2830 2835

Met Asp Ser Leu Thr Ser Val Glu Leu Arg Asn Arg Leu Gln Ala
2840 2845 2850

Ser Leu Gly Cys Ser Leu Ser Ser Thr Leu Ala Phe Asp Tyr Pro
2855 2860 2865

Thr Gln Gln Ala Leu Val Asn Tyr Leu Ala Asn Glu Leu Leu Gly
2870 2875 2880

Thr Pro Glu Gln Leu Gln Glu Pro Glu Ser Asp Glu Glu Asp Gln
2885 2890 2895

Ile Ser Ser Met Asp Asp Ile Val Gln Leu Leu Ser Ala Lys Leu
2900 2905 2910

Glu Met Glu Ile
2915

<210> 101
<211> 5667
<212> DNA
<213> Cylindrospermopsis raciborskii AWT205

<400> 101
atggatgaaa aactaagaac atacgaacga ttaatcaagc aatcctatca caagatagag 60

gctctggaag ctgaagttaa caggttgaag caaacccaat gtgaacctat cgccatcgtc 120

ggcatgggct gtcgttttcc tggtgcgaat agtccagaag cgttttggca gttgttgtgt 180

gatggggttg atgctattcg tgagatacca aaaaatcgat gggttgttga tgcctacata 240

gatgaaaatt tggaccgcgc agacaagaca tcaatgcgat ttggcgggtt tgtcgagcaa 300

cttgagaagt ttgatgccca attctttggc atatcaccgc gagaagcggt ttctcttgac 360

cctcagcaac gtttgttatt agaagtaagt tgggaagcac tggaaaatgc agcggtgata 420

ccaccttcgg caacgggcgt attcgtcggt attagtaacc ttgattatcg tgaaacgctc 480

ttgaagcaag gagcaattgg tacttatttt gcttcgggta atgcccatag cacagccagt 540

ggtcgcttgt cttactttct cggtctgaca ggcccctgtc tctcgataga tacagcttgt 600

tcttcgtcgt tggtcgctgt acatcagtca ctgataagtc tgcgtcagcg agaatgtgac 660

ttagcgttgg ttgggggagt ccatcggctg atagccccag aggaaagtgt ctcgttagca 720

aaagcccata tgttatctcc cgatggtcgt tgcaaagtct ttgatgcgtc ggcaaacggg 780

tatgtccgag ccgaaggatg tggcatgata gtcctcaaac gattatcgga cgcgcaagct 840

gatggggata aaatcttggc gttgattcgc gggtcagcca taaatcaaga cggtcgcacg 900

agtggcttga ccgttccaaa tggtccccaa caagccgacg tgattcgcca agccctcgcc 960

aatagtggca taagaccaga acaagttaac tatgtagaag ctcatggcac agggacttcc 1020

ctaggagacc cgattgaggt cggcgcgttg ggaacgatct ttaatcaacg ctcccaacct 1080

ttaattattg gttcagttaa aacaaatatt gggcatctag aagcagcagc agggattgct 1140

ggactgatta aagtcgtcct tgccatgcag catggagaaa ttccacctaa tttacacttt 1200

caccagccca atcctcgcat taactgggat aaattgccaa tcaggatccc cacagaacga 1260

acagcttggc ctactggcga tcgcatcgca gggataagtt ctttcggctt tagtggcact 1320

aattctcatg tcgtgttaga ggaagcccca aaaatagagc cgtctacttt agagattcat 1380

tcaaagcagt atgtttttac cttatcagca gcgacacctc aagcactaca agaacttact 1440

cagcgttatg taacttatct cactgaacac ttacaagaga gtctggcgga tatttgcttt 1500

acagccaaca cagggcgcaa acactttaga catcgctttg cagtagtagc agagtctaaa 1560

acccagttgc gccaacaatt ggaaacgttt gcccaatcgg gagaggggca ggggaagagg 1620

acatctctct caaaaatagc ttttctcttt acaggtcaag gctcacagta tgtggggatg 1680

gggcaagaac tttatgagag ccaacccacc ttccggcaaa ccattgaccg atgtgatgag 1740

attcttcgtt cactgttggg caaatcaatc ctctcaatac tctatcccag ccaacaaatg 1800

ggattggaaa cgccatccca aattgatgaa accgcctata ctcaacccac tctttttct 1860

cttgaatatg cactggcgca gttgtggcgc tcctggggta ttgagcctga tgtggtgatg 1920

gggcatagtg tgggagaata tgtggccgct tgtgtggcgg gtgtcttttc tttagaggat 1980

ggactcaaac taattgctga aagaggccgt ctgatgcaag aattgcctcc cgatggggcg 2040

atggtttcag ttatggccaa taaatcgcgc atagagcaag caattcaatc tgtcagccga 2100

gaggtttcta ttgcggccat caatggacct gagagtgtgg ttatctctgg taaaagggag 2160

atattacaac agattaccga acatctggtt gccgaaggca ttaagacacg ccaactgaag 2220

gtctctcatg cctttcactc accattgatg gagccaatat taggtcagtt ccgccgagtt 2280

gccaatacca tcacctatcg gccaccgcaa attaaccttg tctcaaatgt cacaggcgga 2340

caggtgtata aagaaatcgc tactcccgat tattgggtga gacatctgca agagactgtc 2400

cgttttgcgg atggggttaa ggtgttacat gaacagaatg tcaatttcat gctcgaaatt 2460

ggtcccaaac ccacactgct gggcatggtt gagttacaaa gttctgagaa tccattttct 2520

atgccaatga tgatgcccag tttgcgtcag aatcgtagcg actggcagca gatgttggag 2580

agcttgagtc aactctatgt tcatggtgtt gagattgact ggatcggttt taataaagac 2640

tatgtgcgac ataaagttgt cctgccgaca tacccatggc agaaggagcg ttactgggta 2700

gaattggatc aacagaagca cgccgctaaa aatctacatc ctctactgga caggtgcatg 2760

aagctgcctc gtcataacga aacaattttt gagaaagaat ttagtctaga gacattgccc 2820

tttcttgctg actatcgcat ttatggttca gttgtgtcgc caggtgcaag ttatctatca 2880

atgatactaa gtattgccga gtcgtatgca aatggtcatt tgaatggagg gaatagtgca 2940

aagcaaacca cttatttact aaaggatgtc acattcccag tacctcttgt gatctctgat 3000

gaggcaaatt acatggtgca agttgcttgt tctctctctt gtgctgcgcc acacaatcgt 3060

ggcgacgaga cgcagtttga attgttcagt tttgctgaga atgtacctga aagtagcagt 3120

ataaatgctg attttcagac acccattatt catgcaaaag ggcaatttaa gcttgaagat 3180

acagcacctc ctaaagtgga gctagaagaa ctacaagcgg gttgtcccca agaaattgat 3240

ctcaaccttt tctatcaaac attcacagac aaaggttttg tttttggatc tcgttttcgc 3300

tggttagaac aaatctgggt gggcgatgga gaagcattgg cgcgtctgcg acaaccggaa 3360

agtattgaat cgtttaaagg atatgtgatt catcccggtt tgttggatgc ctgtacacaa 3420

gtcccatttg caatttcgtc tgacgatgaa aataggcaat cagaaacgac aatgcccttt 3480

gcgctgaatg aattacgttg ttatcagcct gcaaacggac aaatgtggtg ggttcatgca 3540

acagaaaaag atagatatac atgggatgtt tctctgtttg atgagagcgg gcaagttatt 3600

gcggaattta taggtttaga agttcgtgct gctatgcccg aaggcttact aagggcagac 3660

ttttggcata actggctcta tacagtgaat tggcgatcgc aacctctaca aatcccagag 3720

gtgctggata ttaataagac aggtgcagaa acatggcttc tttttgcaca accagaggga 3780

ataggagcgg acttagccga atatttgcag agccaaggaa agcactgtgt ttttgtagtg 3840

cctgggagtg agtatacagt gaccgagcaa cacattggac gcactggaca tcttgatgtg 3900

acgaaactga caaaaattgt cacgatcaat cctgcttctc ctcatgacta taaatatttt 3960

ttagaaactc tgacggacat tagattacct tgtgaacata tactctattt atggaatcgt 4020

tatgatttaa caaatacttc taatcatcgg acagaattga ctgtaccaga tatagtctta 4080

aacttatgta ctagtcttac ttatttggta caagccctta gccacatggg tttttccccg 4140

aaattatggc taattacaca aaatagtcaa gcggttggta gtgacttagc gaatttagaa 4200

atcgaacaat ccccattatg ggcattgggt cgaagcatcc gcgccgaaca ccctgaattt 4260

gattgccgtt gtttagattt tgacacgctc tcaaatatcg caccactctt gttgaaagag 4320

atgcaagcta tagactatga atctcaaatt gcttaccgac aaggaacgcg ctatgttgca 4380

cgactaattc gtaatcaatc agaatgtcac gcaccgattc aaacaggaat ccgtcctgat 4440

ggcagctatt tgattacagg tggattaggc ggtctaggat tgcaggtagc actcgccctt 4500

gcggacgctg gagcaagaca cttgatcctc aatagtcgcc gtggtacggt ctccaaagaa 4560

gcccagttaa ttattgaccg actacgccaa gaggatgtta gggttgattt gattgcggca 4620

gatgtctctg atgcggcaga tagcgaacga ctcttagtag aaagtcagcg caagacctct 4680

cttcgaggga ttgtccatgt tgcgggagtc ttggatgatg gcatcctgct ccaacaaaat 4740

caagagcgtt ttgaaaaagt gatggcggct aaggtacgcg gagcttggca tctggaccaa 4800

cagagccaaa ccctcgattt agatttcttt gttgcgttct catctgttgc gtcgctcata 4860

gaagaaccag gacaagccaa ttacgccgca gcgaatgcgt ttttggattc attaatgtat 4920

tatcgtcaca taaagggatc taatagcttg agtatcaact ggggggcttg ggcagaagtc 4980

ggcatggcag ccaatttatc atgggaacaa cggggaatcg cggcaatttc tccaaagcaa 5040

gggaggcata ttctcgtcca acttattcaa aaacttaatc agcatacaat cccccaagtt 5100

gctgtacaac cgaccaattg ggctgaatat ctatcccatg atggcgtgaa tatgccattc 5160

tatgaatatt ttacacacca cttgcgtaac gaaaaagaag ccaaattgcg gcaaacagca 5220

ggcagcacct cagaggaagt cagtctgcgg caacagcttc aaacactctc agagaaagac 5280

cgggatgccc ttttgatgga acatcttcaa aaaactgcga tcagagttct cggtttggca 5340

tctaatcaaa aaattgatcc ctatcaggga ttgatgaata tgggactaga ctctttgatg 5400

gcggttgaat ttcggaatca cttgatacgt agtttagaac gccctctgcc agccactctg 5460

ctctttaatt gcccaacact tgattcattg catgattacc tagtcgcaaa aatgtttgat 5520

gatgcccctc agaaggcaga gcaaatggca caaccaacaa cactgacagc acacagcata 5580

tcaatagaat ccaaaataga tgataacgaa agcgtggatg acattgcaca aatgctggca 5640

caagcactca atatcgcctt tgagtag 5667

<210> 102
<211> 1888
<212> PRT
<213> Cylindrospermopsis raciborskii AWT205

<400> 102

Met Asp Glu Lys Leu Arg Thr Tyr Glu Arg Leu Ile Lys Gln Ser Tyr
1 5 10 15

His Lys Ile Glu Ala Leu Glu Ala Glu Val Asn Arg Leu Lys Gln Thr
20 25 30

Gln Cys Glu Pro Ile Ala Ile Val Gly Met Gly Cys Arg Phe Pro Gly
35 40 45

Ala Asn Ser Pro Glu Ala Phe Trp Gln Leu Leu Cys Asp Gly Val Asp
50 55 60

Ala Ile Arg Glu Ile Pro Lys Asn Arg Trp Val Val Asp Ala Tyr Ile
65 70 75 80

Asp Glu Asn Leu Asp Arg Ala Asp Lys Thr Ser Met Arg Phe Gly Gly
85 90 95

Phe Val Glu Gln Leu Glu Lys Phe Asp Ala Gln Phe Phe Gly Ile Ser
100 105 110

Pro Arg Glu Ala Val Ser Leu Asp Pro Gln Gln Arg Leu Leu Leu Glu
115 120 125

Val Ser Trp Glu Ala Leu Glu Asn Ala Ala Val Ile Pro Pro Ser Ala
130 135 140

Thr Gly Val Phe Val Gly Ile Ser Asn Leu Asp Tyr Arg Glu Thr Leu
145 150 155 160

Leu Lys Gln Gly Ala Ile Gly Thr Tyr Phe Ala Ser Gly Asn Ala His
165 170 175

Ser Thr Ala Ser Gly Arg Leu Ser Tyr Phe Leu Gly Leu Thr Gly Pro
180 185 190

Cys Leu Ser Ile Asp Thr Ala Cys Ser Ser Ser Leu Val Ala Val His
195 200 205

Gln Ser Leu Ile Ser Leu Arg Gln Arg Glu Cys Asp Leu Ala Leu Val
210 215 220

Gly Gly Val His Arg Leu Ile Ala Pro Glu Glu Ser Val Ser Leu Ala
225 230 235 240

Lys Ala His Met Leu Ser Pro Asp Gly Arg Cys Lys Val Phe Asp Ala
245 250 255

Ser Ala Asn Gly Tyr Val Arg Ala Glu Gly Cys Gly Met Ile Val Leu
260 265 270

Lys Arg Leu Ser Asp Ala Gln Ala Asp Gly Asp Lys Ile Leu Ala Leu
275 280 285

Ile Arg Gly Ser Ala Ile Asn Gln Asp Gly Arg Thr Ser Gly Leu Thr
290 295 300

Val Pro Asn Gly Pro Gln Gln Ala Asp Val Ile Arg Gln Ala Leu Ala
305 310 315 320

Asn Ser Gly Ile Arg Pro Glu Gln Val Asn Tyr Val Glu Ala His Gly
325 330 335

Thr Gly Thr Ser Leu Gly Asp Pro Ile Glu Val Gly Ala Leu Gly Thr
340 345 350

Ile Phe Asn Gln Arg Ser Gln Pro Leu Ile Ile Gly Ser Val Lys Thr
355 360 365

Asn Ile Gly His Leu Glu Ala Ala Ala Gly Ile Ala Gly Leu Ile Lys
370 375 380

Val Val Leu Ala Met Gln His Gly Glu Ile Pro Pro Asn Leu His Phe
385 390 395 400

His Gln Pro Asn Pro Arg Ile Asn Trp Asp Lys Leu Pro Ile Arg Ile
405 410 415

Pro Thr Glu Arg Thr Ala Trp Pro Thr Gly Asp Arg Ile Ala Gly Ile
420 425 430

Ser Ser Phe Gly Phe Ser Gly Thr Asn Ser His Val Val Leu Glu Glu
435 440 445

Ala Pro Lys Ile Glu Pro Ser Thr Leu Glu Ile His Ser Lys Gln Tyr
450 455 460

Val Phe Thr Leu Ser Ala Ala Thr Pro Gln Ala Leu Gln Glu Leu Thr
465 470 475 480

Gln Arg Tyr Val Thr Tyr Leu Thr Glu His Leu Gln Glu Ser Leu Ala
485 490 495

Asp Ile Cys Phe Thr Ala Asn Thr Gly Arg Lys His Phe Arg His Arg
500 505 510

Phe Ala Val Val Ala Glu Ser Lys Thr Gln Leu Arg Gln Gln Leu Glu
515 520 525

Thr Phe Ala Gln Ser Gly Glu Gly Gln Gly Lys Arg Thr Ser Leu Ser
530 535 540

Lys Ile Ala Phe Leu Phe Thr Gly Gln Gly Ser Gln Tyr Val Gly Met
545 550 555 560

Gly Gln Glu Leu Tyr Glu Ser Gln Pro Thr Phe Arg Gln Thr Ile Asp
565 570 575

Arg Cys Asp Glu Ile Leu Arg Ser Leu Leu Gly Lys Ser Ile Leu Ser
580 585 590

Ile Leu Tyr Pro Ser Gln Gln Met Gly Leu Glu Thr Pro Ser Gln Ile
595 600 605

Asp Glu Thr Ala Tyr Thr Gln Pro Thr Leu Phe Ser Leu Glu Tyr Ala
610 615 620

Leu Ala Gln Leu Trp Arg Ser Trp Gly Ile Glu Pro Asp Val Val Met
625 630 635 640

Gly His Ser Val Gly Glu Tyr Val Ala Ala Cys Val Ala Gly Val Phe
645 650 655

Ser Leu Glu Asp Gly Leu Lys Leu Ile Ala Glu Arg Gly Arg Leu Met
660 665 670

Gln Glu Leu Pro Pro Asp Gly Ala Met Val Ser Val Met Ala Asn Lys
675 680 685

Ser Arg Ile Glu Gln Ala Ile Gln Ser Val Ser Arg Glu Val Ser Ile
690 695 700

Ala Ala Ile Asn Gly Pro Glu Ser Val Val Ile Ser Gly Lys Arg Glu
705 710 715 720

Ile Leu Gln Gln Ile Thr Glu His Leu Val Ala Glu Gly Ile Lys Thr
725 730 735

Arg Gln Leu Lys Val Ser His Ala Phe His Ser Pro Leu Met Glu Pro
740 745 750

Ile Leu Gly Gln Phe Arg Arg Val Ala Asn Thr Ile Thr Tyr Arg Pro
755 760 765

Pro Gln Ile Asn Leu Val Ser Asn Val Thr Gly Gly Gln Val Tyr Lys
770 775 780

Glu Ile Ala Thr Pro Asp Tyr Trp Val Arg His Leu Gln Glu Thr Val
785 790 795 800

Arg Phe Ala Asp Gly Val Lys Val Leu His Glu Gln Asn Val Asn Phe
805 810 815

Met Leu Glu Ile Gly Pro Lys Pro Thr Leu Leu Gly Met Val Glu Leu
820 825 830

Gln Ser Ser Glu Asn Pro Phe Ser Met Pro Met Met Met Pro Ser Leu
835 840 845

Arg Gln Asn Arg Ser Asp Trp Gln Gln Met Leu Glu Ser Leu Ser Gln
850 855 860

Leu Tyr Val His Gly Val Glu Ile Asp Trp Ile Gly Phe Asn Lys Asp
865 870 875 880

Tyr Val Arg His Lys Val Val Leu Pro Thr Tyr Pro Trp Gln Lys Glu
885 890 895

Arg Tyr Trp Val Glu Leu Asp Gln Gln Lys His Ala Ala Lys Asn Leu
900 905 910

His Pro Leu Leu Asp Arg Cys Met Lys Leu Pro Arg His Asn Glu Thr
915 920 925

Ile Phe Glu Lys Glu Phe Ser Leu Glu Thr Leu Pro Phe Leu Ala Asp
930 935 940

Tyr Arg Ile Tyr Gly Ser Val Val Ser Pro Gly Ala Ser Tyr Leu Ser
945 950 955 960

Met Ile Leu Ser Ile Ala Glu Ser Tyr Ala Asn Gly His Leu Asn Gly
965 970 975

Gly Asn Ser Ala Lys Gln Thr Thr Tyr Leu Leu Lys Asp Val Thr Phe
980 985 990

Pro Val Pro Leu Val Ile Ser Asp Glu Ala Asn Tyr Met Val Gln Val
995 1000 1005

Ala Cys Ser Leu Ser Cys Ala Ala Pro His Asn Arg Gly Asp Glu
1010 1015 1020

Thr Gln Phe Glu Leu Phe Ser Phe Ala Glu Asn Val Pro Glu Ser
1025 1030 1035

Ser Ser Ile Asn Ala Asp Phe Gln Thr Pro Ile Ile His Ala Lys
1040 1045 1050

Gly Gln Phe Lys Leu Glu Asp Thr Ala Pro Pro Lys Val Glu Leu
1055 1060 1065

Glu Glu Leu Gln Ala Gly Cys Pro Gln Glu Ile Asp Leu Asn Leu
1070 1075 1080

Phe Tyr Gln Thr Phe Thr Asp Lys Gly Phe Val Phe Gly Ser Arg
1085 1090 1095

Phe Arg Trp Leu Glu Gln Ile Trp Val Gly Asp Gly Glu Ala Leu
1100 1105 1110

Ala Arg Leu Arg Gln Pro Glu Ser Ile Glu Ser Phe Lys Gly Tyr
1115 1120 1125

Val Ile His Pro Gly Leu Leu Asp Ala Cys Thr Gln Val Pro Phe
1130 1135 1140

Ala Ile Ser Ser Asp Asp Glu Asn Arg Gln Ser Glu Thr Thr Met
1145 1150 1155

Pro Phe Ala Leu Asn Glu Leu Arg Cys Tyr Gln Pro Ala Asn Gly
1160 1165 1170

Gln Met Trp Trp Val His Ala Thr Glu Lys Asp Arg Tyr Thr Trp
1175 1180 1185

Asp Val Ser Leu Phe Asp Glu Ser Gly Gln Val Ile Ala Glu Phe
1190 1195 1200

Ile Gly Leu Glu Val Arg Ala Ala Met Pro Glu Gly Leu Leu Arg
1205 1210 1215

Ala Asp Phe Trp His Asn Trp Leu Tyr Thr Val Asn Trp Arg Ser
1220 1225 1230

Gln Pro Leu Gln Ile Pro Glu Val Leu Asp Ile Asn Lys Thr Gly
1235 1240 1245

Ala Glu Thr Trp Leu Leu Phe Ala Gln Pro Glu Gly Ile Gly Ala
1250 1255 1260

Asp Leu Ala Glu Tyr Leu Gln Ser Gln Gly Lys His Cys Val Phe
1265 1270 1275

Val Val Pro Gly Ser Glu Tyr Thr Val Thr Glu Gln His Ile Gly
1280 1285 1290

Arg Thr Gly His Leu Asp Val Thr Lys Leu Thr Lys Ile Val Thr
1295 1300 1305

Ile Asn Pro Ala Ser Pro His Asp Tyr Lys Tyr Phe Leu Glu Thr
1310 1315 1320

Leu Thr Asp Ile Arg Leu Pro Cys Glu His Ile Leu Tyr Leu Trp
1325 1330 1335

Asn Arg Tyr Asp Leu Thr Asn Thr Ser Asn His Arg Thr Glu Leu
1340 1345 1350

Thr Val Pro Asp Ile Val Leu Asn Leu Cys Thr Ser Leu Thr Tyr
1355 1360 1365

Leu Val Gln Ala Leu Ser His Met Gly Phe Ser Pro Lys Leu Trp
1370 1375 1380

Leu Ile Thr Gln Asn Ser Gln Ala Val Gly Ser Asp Leu Ala Asn
1385 1390 1395

Leu Glu Ile Glu Gln Ser Pro Leu Trp Ala Leu Gly Arg Ser Ile
1400 1405 1410

Arg Ala Glu His Pro Glu Phe Asp Cys Arg Cys Leu Asp Phe Asp
1415 1420 1425

Thr Leu Ser Asn Ile Ala Pro Leu Leu Leu Lys Glu Met Gln Ala
1430 1435 1440

Ile Asp Tyr Glu Ser Gln Ile Ala Tyr Arg Gln Gly Thr Arg Tyr
1445 1450 1455

Val Ala Arg Leu Ile Arg Asn Gln Ser Glu Cys His Ala Pro Ile
1460 1465 1470

Gln Thr Gly Ile Arg Pro Asp Gly Ser Tyr Leu Ile Thr Gly Gly
1475 1480 1485

Leu Gly Gly Leu Gly Leu Gln Val Ala Leu Ala Leu Ala Asp Ala
1490 1495 1500

Gly Ala Arg His Leu Ile Leu Asn Ser Arg Arg Gly Thr Val Ser
1505 1510 1515

Lys Glu Ala Gln Leu Ile Ile Asp Arg Leu Arg Gln Glu Asp Val
1520 1525 1530

Arg Val Asp Leu Ile Ala Ala Asp Val Ser Asp Ala Ala Asp Ser
1535 1540 1545

Glu Arg Leu Leu Val Glu Ser Gln Arg Lys Thr Ser Leu Arg Gly
1550 1555 1560

Ile Val His Val Ala Gly Val Leu Asp Asp Gly Ile Leu Leu Gln
1565 1570 1575

Gln Asn Gln Glu Arg Phe Glu Lys Val Met Ala Ala Lys Val Arg
1580 1585 1590

Gly Ala Trp His Leu Asp Gln Gln Ser Gln Thr Leu Asp Leu Asp
1595 1600 1605

Phe Phe Val Ala Phe Ser Ser Val Ala Ser Leu Ile Glu Glu Pro
1610 1615 1620

Gly Gln Ala Asn Tyr Ala Ala Ala Asn Ala Phe Leu Asp Ser Leu
1625 1630 1635

Met Tyr Tyr Arg His Ile Lys Gly Ser Asn Ser Leu Ser Ile Asn
1640 1645 1650

Trp Gly Ala Trp Ala Glu Val Gly Met Ala Ala Asn Leu Ser Trp
1655 1660 1665

Glu Gln Arg Gly Ile Ala Ala Ile Ser Pro Lys Gln Gly Arg His
1670 1675 1680

Ile Leu Val Gln Leu Ile Gln Lys Leu Asn Gln His Thr Ile Pro
1685 1690 1695

Gln Val Ala Val Gln Pro Thr Asn Trp Ala Glu Tyr Leu Ser His
1700 1705 1710

Asp Gly Val Asn Met Pro Phe Tyr Glu Tyr Phe Thr His His Leu
1715 1720 1725

Arg Asn Glu Lys Glu Ala Lys Leu Arg Gln Thr Ala Gly Ser Thr
1730 1735 1740

Ser Glu Glu Val Ser Leu Arg Gln Gln Leu Gln Thr Leu Ser Glu
1745 1750 1755

Lys Asp Arg Asp Ala Leu Leu Met Glu His Leu Gln Lys Thr Ala
1760 1765 1770

Ile Arg Val Leu Gly Leu Ala Ser Asn Gln Lys Ile Asp Pro Tyr
1775 1780 1785

Gln Gly Leu Met Asn Met Gly Leu Asp Ser Leu Met Ala Val Glu
1790 1795 1800

Phe Arg Asn His Leu Ile Arg Ser Leu Glu Arg Pro Leu Pro Ala
1805 1810 1815

Thr Leu Leu Phe Asn Cys Pro Thr Leu Asp Ser Leu His Asp Tyr
1820 1825 1830

Leu Val Ala Lys Met Phe Asp Asp Ala Pro Gln Lys Ala Glu Gln
1835 1840 1845

Met Ala Gln Pro Thr Thr Leu Thr Ala His Ser Ile Ser Ile Glu
1850 1855 1860

Ser Lys Ile Asp Asp Asn Glu Ser Val Asp Asp Ile Ala Gln Met
1865 1870 1875

Leu Ala Gln Ala Leu Asn Ile Ala Phe Glu
1880 1885

<210> 103
<211> 5004
<212> DNA
<213> Cylindrospermopsis raciborskii AWT205

<400> 103
atgagtcagc ccaattatgg cattttgatg aaaaatgcgt tgaacgaaat aaatagccta 60

cgatcgcaac tagctgcggt agaagcccaa aaaaatgagt ctattgccat tgttggtatg 120

agttgccgtt ttccaggcgg tgcaactact ccagagcgtt tttgggtatt actgcgcgag 180

ggtatatcag ccattacaga aatccctgct gatcgctggg atgttgataa atattatgat 240

gctgacccca catcgtccgg taaaatgcat actcgttacg gcggttttct gaatgaagtt 300

gatacatttg agccatcatt ctttaatatt gctgcccgtg aagccgttag catggatcca 360

cagcaacgct tgctacttga agtcagttgg gaagctctgg aatccggtaa tattgttcct 420

gcaactcttt ttgatagttc cactggtgta tttatcggta ttggtggtag caactacaaa 480

tctttaatga tcgaaaacag gagtcggatc gggaaaaccg atttgtatga gttaagtggc 540

actgatgtga gtgttgctgc cggcaggata tcctatgtcc tgggtttgat gggtcccagt 600

tttgtgattg atacagcttg ttcatcttct ttggtctcag ttcatcaagc ctgtcagagt 660

ctgcgtcaga gagaatgtga tctagcacta gctggtggag tcggtttact cattgatcca 720

gatgagatga ttggtctttc tcaaggggg atgctggcac ctgatggtag ttgtaaaaca 780

tttgatgcca atgcaaatgg ctatgtgcga ggcgaaggtt gtgggatgat tgttctaaaa 840

cgtctctcgg atgcaacagc cgatggggat aatattcttg ccatcattcg tgggtctatg 900

gttaatcatg atggtcatag cagtggttta actgctccaa gaggccccgc acaagtctct 960

gtcattaagc aagccttaga tagagcaggt attgcaccgg atgccgtaag ttatttagaa 1020

gcccatggta caggcacacc ccttggtgat cctatcgaga tggattcatt gaacgaagtg 1080

tttggtcgga gaacagaacc actttgggtc ggctcagtta agacaaatat tggtcattta 1140

gaagccgcgt ccggtattgc agggctgatt aaggttgtct tgatgctaaa aaacaagcag 1200

attcctcctc acttgcattt caagacacca aatccatata ttgattggaa aaatctcccg 1260

gtcgaaattc cgaccaccct tcatgcttgg gatgacaaga cattgaagga cagaaagcga 1320

attgcagggg ttagttcttt tagtttcagt ggtactaacg cccacattgt attatctgaa 1380

gccccatcta gcgaactaat tagtaatcat gcggcagtgg aaagaccatg gcacttgtta 1440

acccttagtg ctaagaatga ggaagcgttg gctaacttgg ttgggcttta tcagtcattt 1500

atttctacta ctgatgcaag tcttgccgat atatgctaca ctgctaatac ggcacgaacc 1560

catttttctc atcgccttgc tctatcggct acttcacaca tccaaataga ggctctttta 1620

gccgcttata aggaagggtc ggtgagtttg agcatcaatc aaggttgtgt cctttccaac 1680

agtcgtgcgc cgaaggtcgc ttttctcttt acaggtcaag gttcgcaata tgtgcaaatg 1740

gctggagaac tttatgagac ccagcctact ttccgtaatt gcttagatcg ctgtgccgaa 1800

atcttgcaat ccatcttttc atcgagaaac agcccttggg gaaacccact gctttcggta 1860

ttatatccaa accatgagtc aaaggaaatt gaccagacgg cttataccca acctgccctt 1920

tttgctgtag aatatgccct agcacagatg tggcggtcgt ggggaatcga gccagatatc 1980

gtaatgggtc atagcatagg tgaatatgtg gcagcttgtg tggcggggat cttttctctg 2040

gaggatggtc tcaaacttgc tgccgaaaga ggccgtttga tgcaggcgct accacaaaat 2100

ggcgagatgg ttgctatatc ggcctccctt gaggaagtta agccggctat tcaatctgac 2160

cagcgagttg tgatagcggc ggtaaatgga ccacgaagtg tcgtcatttc gggcgatcgc 2220

caagctgtgc aagtcttcac caacacccta gaagatcaag gaatccggtg caagagactg 2280

tctgtttcac acgctttcca ctctccattg atgaaaccaa tggagcagga gttcgcacag 2340

gtggccaggg aaatcaacta tagtcctcca aaaatagctc ttgtcagtaa tctaaccggc 2400

gacttgattt cacctgagtc ttccctggag gaaggagtga tcgcttcccc tggttactgg 2460

gtaaatcatt tatgcaatcc tgtcttgttc gctgatggta ttgcaactat gcaagcgcag 2520

gatgtccaag tcttccttga agttggacca aaaccgacct tatcaggact agtgcaacaa 2580

tattttgacg aggttgccca tagcgatcgc cctgtcacca ttcccacctt gcgccccaag 2640

caacccaact ggcagacact attggagagt ttgggacaac tgtatgcgct tggtgtccag 2700

gtaaattggg cgggctttga tagagattac accagacgca aagtaagcct acccacctat 2760

gcttggaagc gtcaacgtta ttggctagag aaacagtccg ctccacgttt agaaacaaca 2820

caagttcgtc ccgcaactgc cattgtagag catcttgaac aaggcaatgt gccgaaaatc 2880

gtggacttgt tagcggcgac ggatgtactt tcaggcgaag cacggaaatt gctacccagc 2940

atcattgaac tattggttgc aaaacatcgt gaggaagcga cacagaagcc catctgcgat 3000

tggctttatg aagtggtttg gcaaccccag ttgctgaccc tatctacctt acctgctgtg 3060

gaaacagagg gtagacaatg gctcatcttc gccgatgcta gtggacacgg tgaagcactt 3120

gcggctcaat tacgtcagca aggggatata attacgcttg tctatgctgg tctaaaatat 3180

cactcggcta ataataaaca aaataccggg ggggacatcc catattttca gattgatccg 3240

atccaaaggg aggattatga aaggttgttt gctgctttgc ctccactgta tggtattgtt 3300

catctttgga gtttagatat acttagcttg gacaaagtat ctaacctaat tgaaaatgta 3360

caattaggta gtggcacgct attaaattta atacagacag tcttgcaact tgaaacgccc 3420

acccctagct tgtggctcgt gacaaagaac gcgcaagctg tgcgtaaaaa cgatagccta 3480

gtcggagtgc ttcagtcacc cttatggggt atgggtaagg tgatagcctt agaacaccct 3540

gaactcaact gtgtatcaat cgaccttgat ggtgaagggc ttccagatga acaagccaag 3600

tttctggcgg ctgaactccg cgccgcctcc gagttcagac ataccaccat tccccacgaa 3660

agtcaagttg cttggcgtaa taggactcgc tatgtgtcac ggttcaaagg ttatcagaag 3720

catcccgcga cctcatcaaa aatgcctatt cgaccagatg ccacttattt gatcacgggc 3780

ggctttggtg gtttgggctt gcttgtggct cgttggatgg ttgaacaggg ggctacccat 3840

ctatttctga tgggacgcag ccaacccaaa ccagccgccc aaaaacaact gcaagagata 3900

gccgcgctgg gtgcaacagt gacggtggtg caagccgatg ttggcatccg ctcccaagta 3960

gccaatgtgt tggcacagat tgataaggca tatcctttgg ctggtattat tcatactgcc 4020

ggtgtattag acgacggaat cttattgcag caaaattggg cgcgttttag caaggtgttc 4080

gcccccaaac tagagggagc ttggcatcta catacactga ctgaagagat gccgcttgat 4140

ttctttattt gtttttcctc aacagcagga ttgctgggca gtggtggaca agctaactat 4200

gctgctgcca atgccttttt agatgccttt gcccatcatc ggcgaataca aggcttgcca 4260

gctctctcga ttaactggga cgcttggtct caagtgggaa tgacggtacg tctccaacaa 4320

gcttcttcac aaagcaccac agttgggcaa gatattagca ctttggaaat ttcaccagaa 4380

cagggattgc aaatctttgc ctatcttctg caacaaccat ccgcccaaat agcggccatt 4440

tctaccgatg ggcttcgcaa gatgtacgac acaagctcgg ccttttttgc tttacttgat 4500

cttgacaggt cttcctccac tacccaggag caatctacac tttctcatga agttggcctt 4560

accttactcg aacaattgca gcaagctcgg ccaaaagagc gagagaaaat gttactgcgc 4620

catctacaga cccaagttgc tgcggtcttg cgtagtcccg aactgcccgc agttcatcaa 4680

cccttcactg acttggggat ggattcgttg atgtcacttg aattgatgcg gcgtttggaa 4740

gaaagtctgg ggattcagat gcctgcaacg cttgcattcg attatcctat ggtagaccgt 4800

ttggctaagt ttatactgac tcaaatatgt ataaattctg agccagatac ctcagcagtt 4860

ctcacaccag atggaaatgg ggaggaaaaa gacagtaata aggacagaag taccagcact 4920

tccgttgact caaatattac ttccatggca gaagatttat tcgcactcga atccttacta 4980

aataaaataa aaagagatca ataa 5004

<210> 104
<211> 1667
<212> PRT
<213> Cylindrospermopsis raciborskii AWT205

<400> 104

Met Ser Gln Pro Asn Tyr Gly Ile Leu Met Lys Asn Ala Leu Asn Glu
1 5 10 15

Ile Asn Ser Leu Arg Ser Gln Leu Ala Ala Val Glu Ala Gln Lys Asn
20 25 30

Glu Ser Ile Ala Ile Val Gly Met Ser Cys Arg Phe Pro Gly Gly Ala
35 40 45

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

Ile Thr Glu Ile Pro Ala Asp Arg Trp Asp Val Asp Lys Tyr Tyr Asp
65 70 75 80

Ala Asp Pro Thr Ser Ser Gly Lys Met His Thr Arg Tyr Gly Gly Phe
85 90 95

Leu Asn Glu Val Asp Thr Phe Glu Pro Ser Phe Phe Asn Ile Ala Ala
100 105 110

Arg Glu Ala Val Ser Met Asp Pro Gln Gln Arg Leu Leu Leu Glu Val
115 120 125

Ser Trp Glu Ala Leu Glu Ser Gly Asn Ile Val Pro Ala Thr Leu Phe
130 135 140

Asp Ser Ser Thr Gly Val Phe Ile Gly Ile Gly Gly Ser Asn Tyr Lys
145 150 155 160

Ser Leu Met Ile Glu Asn Arg Ser Arg Ile Gly Lys Thr Asp Leu Tyr
165 170 175

Glu Leu Ser Gly Thr Asp Val Ser Val Ala Ala Gly Arg Ile Ser Tyr
180 185 190

Val Leu Gly Leu Met Gly Pro Ser Phe Val Ile Asp Thr Ala Cys Ser
195 200 205

Ser Ser Leu Val Ser Val His Gln Ala Cys Gln Ser Leu Arg Gln Arg
210 215 220

Glu Cys Asp Leu Ala Leu Ala Gly Gly Val Gly Leu Leu Ile Asp Pro
225 230 235 240

Asp Glu Met Ile Gly Leu Ser Gln Gly Gly Met Leu Ala Pro Asp Gly
245 250 255

Ser Cys Lys Thr Phe Asp Ala Asn Ala Asn Gly Tyr Val Arg Gly Glu
260 265 270

Gly Cys Gly Met Ile Val Leu Lys Arg Leu Ser Asp Ala Thr Ala Asp
275 280 285

Gly Asp Asn Ile Leu Ala Ile Ile Arg Gly Ser Met Val Asn His Asp
290 295 300

Gly His Ser Ser Gly Leu Thr Ala Pro Arg Gly Pro Ala Gln Val Ser
305 310 315 320

Val Ile Lys Gln Ala Leu Asp Arg Ala Gly Ile Ala Pro Asp Ala Val
325 330 335

Ser Tyr Leu Glu Ala His Gly Thr Gly Thr Pro Leu Gly Asp Pro Ile
340 345 350

Glu Met Asp Ser Leu Asn Glu Val Phe Gly Arg Arg Thr Glu Pro Leu
355 360 365

Trp Val Gly Ser Val Lys Thr Asn Ile Gly His Leu Glu Ala Ala Ser
370 375 380

Gly Ile Ala Gly Leu Ile Lys Val Val Leu Met Leu Lys Asn Lys Gln
385 390 395 400

Ile Pro Pro His Leu His Phe Lys Thr Pro Asn Pro Tyr Ile Asp Trp
405 410 415

Lys Asn Leu Pro Val Glu Ile Pro Thr Thr Leu His Ala Trp Asp Asp
420 425 430

Lys Thr Leu Lys Asp Arg Lys Arg Ile Ala Gly Val Ser Ser Phe Ser
435 440 445

Phe Ser Gly Thr Asn Ala His Ile Val Leu Ser Glu Ala Pro Ser Ser
450 455 460

Glu Leu Ile Ser Asn His Ala Ala Val Glu Arg Pro Trp His Leu Leu
465 470 475 480

Thr Leu Ser Ala Lys Asn Glu Glu Ala Leu Ala Asn Leu Val Gly Leu
485 490 495

Tyr Gln Ser Phe Ile Ser Thr Thr Asp Ala Ser Leu Ala Asp Ile Cys
500 505 510

Tyr Thr Ala Asn Thr Ala Arg Thr His Phe Ser His Arg Leu Ala Leu
515 520 525

Ser Ala Thr Ser His Ile Gln Ile Glu Ala Leu Leu Ala Ala Tyr Lys
530 535 540

Glu Gly Ser Val Ser Leu Ser Ile Asn Gln Gly Cys Val Leu Ser Asn
545 550 555 560

Ser Arg Ala Pro Lys Val Ala Phe Leu Phe Thr Gly Gln Gly Ser Gln
565 570 575

Tyr Val Gln Met Ala Gly Glu Leu Tyr Glu Thr Gln Pro Thr Phe Arg
580 585 590

Asn Cys Leu Asp Arg Cys Ala Glu Ile Leu Gln Ser Ile Phe Ser Ser
595 600 605

Arg Asn Ser Pro Trp Gly Asn Pro Leu Leu Ser Val Leu Tyr Pro Asn
610 615 620

His Glu Ser Lys Glu Ile Asp Gln Thr Ala Tyr Thr Gln Pro Ala Leu
625 630 635 640

Phe Ala Val Glu Tyr Ala Leu Ala Gln Met Trp Arg Ser Trp Gly Ile
645 650 655

Glu Pro Asp Ile Val Met Gly His Ser Ile Gly Glu Tyr Val Ala Ala
660 665 670

Cys Val Ala Gly Ile Phe Ser Leu Glu Asp Gly Leu Lys Leu Ala Ala
675 680 685

Glu Arg Gly Arg Leu Met Gln Ala Leu Pro Gln Asn Gly Glu Met Val
690 695 700

Ala Ile Ser Ala Ser Leu Glu Glu Val Lys Pro Ala Ile Gln Ser Asp
705 710 715 720

Gln Arg Val Val Ile Ala Ala Val Asn Gly Pro Arg Ser Val Val Ile
725 730 735

Ser Gly Asp Arg Gln Ala Val Gln Val Phe Thr Asn Thr Leu Glu Asp
740 745 750

Gln Gly Ile Arg Cys Lys Arg Leu Ser Val Ser His Ala Phe His Ser
755 760 765

Pro Leu Met Lys Pro Met Glu Gln Glu Phe Ala Gln Val Ala Arg Glu
770 775 780

Ile Asn Tyr Ser Pro Pro Lys Ile Ala Leu Val Ser Asn Leu Thr Gly
785 790 795 800

Asp Leu Ile Ser Pro Glu Ser Ser Leu Glu Glu Gly Val Ile Ala Ser
805 810 815

Pro Gly Tyr Trp Val Asn His Leu Cys Asn Pro Val Leu Phe Ala Asp
820 825 830

Gly Ile Ala Thr Met Gln Ala Gln Asp Val Gln Val Phe Leu Glu Val
835 840 845

Gly Pro Lys Pro Thr Leu Ser Gly Leu Val Gln Gln Tyr Phe Asp Glu
850 855 860

Val Ala His Ser Asp Arg Pro Val Thr Ile Pro Thr Leu Arg Pro Lys
865 870 875 880

Gln Pro Asn Trp Gln Thr Leu Leu Glu Ser Leu Gly Gln Leu Tyr Ala
885 890 895

Leu Gly Val Gln Val Asn Trp Ala Gly Phe Asp Arg Asp Tyr Thr Arg
900 905 910

Arg Lys Val Ser Leu Pro Thr Tyr Ala Trp Lys Arg Gln Arg Tyr Trp
915 920 925

Leu Glu Lys Gln Ser Ala Pro Arg Leu Glu Thr Thr Gln Val Arg Pro
930 935 940

Ala Thr Ala Ile Val Glu His Leu Glu Gln Gly Asn Val Pro Lys Ile
945 950 955 960

Val Asp Leu Leu Ala Ala Thr Asp Val Leu Ser Gly Glu Ala Arg Lys
965 970 975

Leu Leu Pro Ser Ile Ile Glu Leu Leu Val Ala Lys His Arg Glu Glu
980 985 990

Ala Thr Gln Lys Pro Ile Cys Asp Trp Leu Tyr Glu Val Val Trp Gln
995 1000 1005

Pro Gln Leu Leu Thr Leu Ser Thr Leu Pro Ala Val Glu Thr Glu
1010 1015 1020

Gly Arg Gln Trp Leu Ile Phe Ala Asp Ala Ser Gly His Gly Glu
1025 1030 1035

Ala Leu Ala Ala Gln Leu Arg Gln Gln Gly Asp Ile Ile Thr Leu
1040 1045 1050

Val Tyr Ala Gly Leu Lys Tyr His Ser Ala Asn Asn Lys Gln Asn
1055 1060 1065

Thr Gly Gly Asp Ile Pro Tyr Phe Gln Ile Asp Pro Ile Gln Arg
1070 1075 1080

Glu Asp Tyr Glu Arg Leu Phe Ala Ala Leu Pro Pro Leu Tyr Gly
1085 1090 1095

Ile Val His Leu Trp Ser Leu Asp Ile Leu Ser Leu Asp Lys Val
1100 1105 1110

Ser Asn Leu Ile Glu Asn Val Gln Leu Gly Ser Gly Thr Leu Leu
1115 1120 1125

Asn Leu Ile Gln Thr Val Leu Gln Leu Glu Thr Pro Thr Pro Ser
1130 1135 1140

Leu Trp Leu Val Thr Lys Asn Ala Gln Ala Val Arg Lys Asn Asp
1145 1150 1155

Ser Leu Val Gly Val Leu Gln Ser Pro Leu Trp Gly Met Gly Lys
1160 1165 1170

Val Ile Ala Leu Glu His Pro Glu Leu Asn Cys Val Ser Ile Asp
1175 1180 1185

Leu Asp Gly Glu Gly Leu Pro Asp Glu Gln Ala Lys Phe Leu Ala
1190 1195 1200

Ala Glu Leu Arg Ala Ala Ser Glu Phe Arg His Thr Thr Ile Pro
1205 1210 1215

His Glu Ser Gln Val Ala Trp Arg Asn Arg Thr Arg Tyr Val Ser
1220 1225 1230

Arg Phe Lys Gly Tyr Gln Lys His Pro Ala Thr Ser Ser Lys Met
1235 1240 1245

Pro Ile Arg Pro Asp Ala Thr Tyr Leu Ile Thr Gly Gly Phe Gly
1250 1255 1260

Gly Leu Gly Leu Leu Val Ala Arg Trp Met Val Glu Gln Gly Ala
1265 1270 1275

Thr His Leu Phe Leu Met Gly Arg Ser Gln Pro Lys Pro Ala Ala
1280 1285 1290

Gln Lys Gln Leu Gln Glu Ile Ala Ala Leu Gly Ala Thr Val Thr
1295 1300 1305

Val Val Gln Ala Asp Val Gly Ile Arg Ser Gln Val Ala Asn Val
1310 1315 1320

Leu Ala Gln Ile Asp Lys Ala Tyr Pro Leu Ala Gly Ile Ile His
1325 1330 1335

Thr Ala Gly Val Leu Asp Asp Gly Ile Leu Leu Gln Gln Asn Trp
1340 1345 1350

Ala Arg Phe Ser Lys Val Phe Ala Pro Lys Leu Glu Gly Ala Trp
1355 1360 1365

His Leu His Thr Leu Thr Glu Glu Met Pro Leu Asp Phe Phe Ile
1370 1375 1380

Cys Phe Ser Ser Thr Ala Gly Leu Leu Gly Ser Gly Gly Gln Ala
1385 1390 1395

Asn Tyr Ala Ala Ala Asn Ala Phe Leu Asp Ala Phe Ala His His
1400 1405 1410

Arg Arg Ile Gln Gly Leu Pro Ala Leu Ser Ile Asn Trp Asp Ala
1415 1420 1425

Trp Ser Gln Val Gly Met Thr Val Arg Leu Gln Gln Ala Ser Ser
1430 1435 1440

Gln Ser Thr Thr Val Gly Gln Asp Ile Ser Thr Leu Glu Ile Ser
1445 1450 1455

Pro Glu Gln Gly Leu Gln Ile Phe Ala Tyr Leu Leu Gln Gln Pro
1460 1465 1470

Ser Ala Gln Ile Ala Ala Ile Ser Thr Asp Gly Leu Arg Lys Met
1475 1480 1485

Tyr Asp Thr Ser Ser Ala Phe Phe Ala Leu Leu Asp Leu Asp Arg
1490 1495 1500

Ser Ser Ser Thr Thr Gln Glu Gln Ser Thr Leu Ser His Glu Val
1505 1510 1515

Gly Leu Thr Leu Leu Glu Gln Leu Gln Gln Ala Arg Pro Lys Glu
1520 1525 1530

Arg Glu Lys Met Leu Leu Arg His Leu Gln Thr Gln Val Ala Ala
1535 1540 1545

Val Leu Arg Ser Pro Glu Leu Pro Ala Val His Gln Pro Phe Thr
1550 1555 1560

Asp Leu Gly Met Asp Ser Leu Met Ser Leu Glu Leu Met Arg Arg
1565 1570 1575

Leu Glu Glu Ser Leu Gly Ile Gln Met Pro Ala Thr Leu Ala Phe
1580 1585 1590

Asp Tyr Pro Met Val Asp Arg Leu Ala Lys Phe Ile Leu Thr Gln
1595 1600 1605

Ile Cys Ile Asn Ser Glu Pro Asp Thr Ser Ala Val Leu Thr Pro
1610 1615 1620

Asp Gly Asn Gly Glu Glu Lys Asp Ser Asn Lys Asp Arg Ser Thr
1625 1630 1635

Ser Thr Ser Val Asp Ser Asn Ile Thr Ser Met Ala Glu Asp Leu
1640 1645 1650

Phe Ala Leu Glu Ser Leu Leu Asn Lys Ile Lys Arg Asp Gln
1655 1660 1665

<210> 105
<211> 318
<212> DNA
<213> Cylindrospermopsis raciborskii AWT205

<400> 105
ttatgctgca tctaaataga agttccatag ccctgcactg accaacatca attgatcatc 60

aaaatcggtc acacgattcc tatatgtggg ataaaatttg cagtacagca ggatataaaa 120

tagtttttcc tctatacttc tgagtgtagg cttgcgtccg cccccgggcg cacgtttgcg 180

gtttgctaag gagttgaaca cggtgcgttc ataggtatca gcaaactgag ataacagctc 240

gttgaatgct tggcggttaa gtccagtcat tgctcgtagc agtcgctctt gattcaggat 300

gcggtctaag ttcaacat 318

<210> 106
<211> 105
<212> PRT
<213> Cylindrospermopsis raciborskii AWT205

<400> 106

Met Leu Asn Leu Asp Arg Ile Leu Asn Gln Glu Arg Leu Leu Arg Ala
1 5 10 15

Met Thr Gly Leu Asn Arg Gln Ala Phe Asn Glu Leu Leu Ser Gln Phe
20 25 30

Ala Asp Thr Tyr Glu Arg Thr Val Phe Asn Ser Leu Ala Asn Arg Lys
35 40 45

Arg Ala Pro Gly Gly Gly Arg Lys Pro Thr Leu Arg Ser Ile Glu Glu
50 55 60

Lys Leu Phe Tyr Ile Leu Leu Tyr Cys Lys Phe Tyr Pro Thr Tyr Arg
65 70 75 80

Asn Arg Val Thr Asp Phe Asp Asp Gln Leu Met Leu Val Ser Ala Gly
85 90 95

Leu Trp Asn Phe Tyr Leu Asp Ala Ala
100 105

<210> 107
<211> 600
<212> DNA
<213> Cylindrospermopsis raciborskii AWT205

<400> 107
ctactgagtg aaagtgaact tctttcccac gtattcgagt agctgttgta agctggcctc 60

gatggaaagt tccgaagttt ccaccagtaa atctggtgtt ctcggtggtt cgtagggagc 120

gctaattccc gtaaaagact caatttctcc acggcgtgct tttgcataga gacccttggg 180

gtcacgttgt tcacaaattt ccatcggagt tgcaatatat acttcatgaa acagatctcc 240

ggacagaata cggatttgct cccggtcttt cctgtaaggt gaaatgaaag cagtaatcac 300

taaacaaccc gaatccgcaa aaagtttggc cacctcgcca atacgacgaa tattttccgc 360

acgatcagca gcagaaaatc ccaagtcagc acataatcca tgacggatat tgtcaccatc 420

aaggacaaaa gtataccaac ctttctggaa caaaatccgc tctaattcta gagccaatgt 480

tgttttacct gatcctgata atccagtgaa ccatagaatt ccatttcggt gaccattctt 540

taaacaacga tcaaatgggg acacaagatg ttttgtatgt tgaatattgc ttgatttcat 600

<210> 108
<211> 199
<212> PRT
<213> Cylindrospermopsis raciborskii AWT205

<400> 108

Met Lys Ser Ser Asn Ile Gln His Thr Lys His Leu Val Ser Pro Phe
1 5 10 15

Asp Arg Cys Leu Lys Asn Gly His Arg Asn Gly Ile Leu Trp Phe Thr
20 25 30

Gly Leu Ser Gly Ser Gly Lys Thr Thr Leu Ala Leu Glu Leu Glu Arg
35 40 45

Ile Leu Phe Gln Lys Gly Trp Tyr Thr Phe Val Leu Asp Gly Asp Asn
50 55 60

Ile Arg His Gly Leu Cys Ala Asp Leu Gly Phe Ser Ala Ala Asp Arg
65 70 75 80

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

Ser Gly Cys Leu Val Ile Thr Ala Phe Ile Ser Pro Tyr Arg Lys Asp
100 105 110

Arg Glu Gln Ile Arg Ile Leu Ser Gly Asp Leu Phe His Glu Val Tyr
115 120 125

Ile Ala Thr Pro Met Glu Ile Cys Glu Gln Arg Asp Pro Lys Gly Leu
130 135 140

Tyr Ala Lys Ala Arg Arg Gly Glu Ile Glu Ser Phe Thr Gly Ile Ser
145 150 155 160

Ala Pro Tyr Glu Pro Pro Arg Thr Pro Asp Leu Leu Val Glu Thr Ser
165 170 175

Glu Leu Ser Ile Glu Ala Ser Leu Gln Gln Leu Leu Glu Tyr Val Gly
180 185 190

Lys Lys Phe Thr Phe Thr Gln
195

<210> 109
<211> 1548
<212> DNA
<213> Cylindrospermopsis raciborskii AWT205

<400> 109
atgcctaaat actttaatac tgctggaccc tgtaaatccg aaatccacta tatgctctct 60

cccacagctc gactaccgga tttgaaagca ctaattgacg gagaaaacta ctttataatt 120

cacgcgccgc gacaagtcgg caaaactaca gctatgatag ccttagcacg agaattgact 180

gatagtggaa aatataccgc agttattctt tccgttgaag tgggatcagt attctcccat 240

aatccccagc aagcggagca ggttatttta gaagaatgga aacaggcaat caaattttat 300

ttacccaaag aactacaacc atcctattgg ccagagcgtg aaacagactc aggaataggc 360

aaaactttaa gtgagtggtc cgcacaatct ccaagacctc ttgtaatctt tttacatgaa 420

atcgattccc taacagatga agctttaatc ctaattttaa gacaattacg ctcaggtttt 480

ccccgtcgtc ctcggggatt tccccattcg gtggggttaa ttggtatgcg ggatgtgcgg 540

gactataagg ttaaatctgg tggaagtgaa cgactgaata cgtcaagtcc tttcaatatc 600

aaagcggaat ccttgacttt aagtaatttc actctgtcag aggtggaaga actttactta 660

caacatacgc aagctacagg acaaattttt accccggaag caattaaaca agcattttat 720

ttaaccgatg ggcaaccatg gttagtaaac gccctagctc gtcaagccac tcaggtgtta 780

gtgaaagata ttactcaacc cattaccgct gaagtaatta accaagccaa agaagttctg 840

attcagcgcc aggataccca tttggatagt ttggcagagc gcttacggga agatcgggtc 900

aaagccatta ttcaacctat gttagctgga tcggacttac cagatacccc agaggatgat 960

cgccgtttct tgctagattt aggcttggta aagcgcagtc ccttgggagg actaaccatt 1020

gccaatccca tttaccagga ggtgattcct cgtgttttgt cccagggtag tcaggatagt 1080

ctaccccaga ttcaacctac ttggttaaat actgataata ctttaaatcc tgacaaactc 1140

ttaaatgctt tcctagagtt ttggcgacaa catggggaac cattactcaa aagtgcgcct 1200

tatcatgaaa ttgctcccca tttagttttg atggcgtttt tacatcgggt agtgaatggt 1260

ggtggcactt tagaacggga atatgccgtt ggttctggaa gaatggatat ttgtttacgc 1320

tatggcaagg tagtgatggg catagagtta aaggtttggg ggggaaaatc ggatccgtta 1380

acgaagggtt tgacccaatt ggataaatat ctgggtgggt taggattaga tagaggttgg 1440

ttagtaattt ttgatcaccg tccgggatta ccacccatgg gtgagaggat tagtatggaa 1500

caggccatta gtccagaggg aagaaccatt acagtgattc gtagctag 1548

<210> 110
<211> 515
<212> PRT
<213> Cylindrospermopsis raciborskii AWT205

<400> 110

Met Pro Lys Tyr Phe Asn Thr Ala Gly Pro Cys Lys Ser Glu Ile His
1 5 10 15

Tyr Met Leu Ser Pro Thr Ala Arg Leu Pro Asp Leu Lys Ala Leu Ile
20 25 30

Asp Gly Glu Asn Tyr Phe Ile Ile His Ala Pro Arg Gln Val Gly Lys
35 40 45

Thr Thr Ala Met Ile Ala Leu Ala Arg Glu Leu Thr Asp Ser Gly Lys
50 55 60

Tyr Thr Ala Val Ile Leu Ser Val Glu Val Gly Ser Val Phe Ser His
65 70 75 80

Asn Pro Gln Gln Ala Glu Gln Val Ile Leu Glu Glu Trp Lys Gln Ala
85 90 95

Ile Lys Phe Tyr Leu Pro Lys Glu Leu Gln Pro Ser Tyr Trp Pro Glu
100 105 110

Arg Glu Thr Asp Ser Gly Ile Gly Lys Thr Leu Ser Glu Trp Ser Ala
115 120 125

Gln Ser Pro Arg Pro Leu Val Ile Phe Leu His Glu Ile Asp Ser Leu
130 135 140

Thr Asp Glu Ala Leu Ile Leu Ile Leu Arg Gln Leu Arg Ser Gly Phe
145 150 155 160

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

Arg Asp Val Arg Asp Tyr Lys Val Lys Ser Gly Gly Ser Glu Arg Leu
180 185 190

Asn Thr Ser Ser Pro Phe Asn Ile Lys Ala Glu Ser Leu Thr Leu Ser
195 200 205

Asn Phe Thr Leu Ser Glu Val Glu Glu Leu Tyr Leu Gln His Thr Gln
210 215 220

Ala Thr Gly Gln Ile Phe Thr Pro Glu Ala Ile Lys Gln Ala Phe Tyr
225 230 235 240

Leu Thr Asp Gly Gln Pro Trp Leu Val Asn Ala Leu Ala Arg Gln Ala
245 250 255

Thr Gln Val Leu Val Lys Asp Ile Thr Gln Pro Ile Thr Ala Glu Val
260 265 270

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

Asp Ser Leu Ala Glu Arg Leu Arg Glu Asp Arg Val Lys Ala Ile Ile
290 295 300

Gln Pro Met Leu Ala Gly Ser Asp Leu Pro Asp Thr Pro Glu Asp Asp
305 310 315 320

Arg Arg Phe Leu Leu Asp Leu Gly Leu Val Lys Arg Ser Pro Leu Gly
325 330 335

Gly Leu Thr Ile Ala Asn Pro Ile Tyr Gln Glu Val Ile Pro Arg Val
340 345 350

Leu Ser Gln Gly Ser Gln Asp Ser Leu Pro Gln Ile Gln Pro Thr Trp
355 360 365

Leu Asn Thr Asp Asn Thr Leu Asn Pro Asp Lys Leu Leu Asn Ala Phe
370 375 380

Leu Glu Phe Trp Arg Gln His Gly Glu Pro Leu Leu Lys Ser Ala Pro
385 390 395 400

Tyr His Glu Ile Ala Pro His Leu Val Leu Met Ala Phe Leu His Arg
405 410 415

Val Val Asn Gly Gly Gly Thr Leu Glu Arg Glu Tyr Ala Val Gly Ser
420 425 430

Gly Arg Met Asp Ile Cys Leu Arg Tyr Gly Lys Val Val Met Gly Ile
435 440 445

Glu Leu Lys Val Trp Gly Gly Lys Ser Asp Pro Leu Thr Lys Gly Leu
450 455 460

Thr Gln Leu Asp Lys Tyr Leu Gly Gly Leu Gly Leu Asp Arg Gly Trp
465 470 475 480

Leu Val Ile Phe Asp His Arg Pro Gly Leu Pro Pro Met Gly Glu Arg
485 490 495

Ile Ser Met Glu Gln Ala Ile Ser Pro Glu Gly Arg Thr Ile Thr Val
500 505 510

Ile Arg Ser
515

<210> 111
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii AWT205 sequence

<400> 111
acttctctcc tttccctatc 20

<210> 112
<211> 22
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii AWT205 sequence

<400> 112
gagtgaaaat gcgtagaact tg 22

<210> 113
<211> 22
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 113
cccaatatct ccctgtaaaa ct 22

<210> 114
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 114
tggcaattgt ctctccgtat 20

<210> 115
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 115
ctcgccgatg aaagtcctct 20

<210> 116
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 116
gcgtgtcgag aaaaaggtgt 20

<210> 117
<211> 20

<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 117
ctcgacacgc aagaataacg 20

<210> 118
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 118
atgcttctgc tttggcatgg c 21

<210> 119
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 119
taactcgacg aactttgacc c 21

<210> 120
<211> 19
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3

<400> 120
gccgccaatc ctcgcgatg 19

<210> 121
<211> 22
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 121
gaacgtctaa tgttgcacag tg 22

<210> 122
<211> 23
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 122
ctggtacgta gtcgcaaagg tgg 23

<210> 123
<211> 26
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 123
ctgacggtac atgtatttcc tgtgac 26

<210> 124
<211> 30
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 124
cgtctcatat gcagatctta ggaatttcag 30

<210> 125
<211> 25
<212> DNA
<213> Artificial

<220>

<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 125
gcttactacc acgatagtgc tgccg 25

<210> 126
<211> 22
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 126
tctatgttta gcaggtggtg tc 22

<210> 127
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 127
ttctgcaaga cgagccataa 20

<210> 128
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 128
ggttcgccgc ggacattaaa 20

<210> 129
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 129
atgctaatgc ggtgggagta 20

<210> 130
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 130
aaagcagttc cgacgacatt 20

<210> 131
<211> 23
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 131
cctatttcga ttattgtttt cgg 23

<210> 132
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 132
gataccgatc ataaactacg 20

<210> 133
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 133
gcaaattttg caggagtaat g 21

<210> 134
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 134
gcaaattttg caggagtaat g 21

<210> 135
<211> 23
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 135
ttttgggtaa actttatagc cat 23

<210> 136
<211> 22
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 136
tgggtctgga cagttgtaga ta 22

<210> 137
<211> 23
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 137
aaggggaaaa caaaattatc aat 23

<210> 138
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 138
ggcgatcgcc tgctaaaaat 20

<210> 139
<211> 23
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 139
cctcattttc atttctagac gtt 23

<210> 140
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 140
ccacttcaac taaaacagca 20

<210> 141
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 141
aaaaattttg gaggggtagc 20

<210> 142
<211> 20

<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 142
atccaagatg cgacaacact 20

<210> 143
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 143
ggtccttgcg cagatagagt g 21

<210> 144
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 144
cactctatct gcgcaaggac c 21

<210> 145
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 145
tgactgcatt cgctgtataa a 21

<210> 146
<211> 22
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 146
ttcataagac ggctgttgaa tc 22

<210> 147
<211> 30
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 147
ctcgagttaa aaaagagtgt aaatgaaagg 30

<210> 148
<211> 23
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 148
ttctataact gctgccaaat ttt 23

<210> 149
<211> 23
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 149
aattttggag tgactggtta tgg 23

<210> 150
<211> 23
<212> DNA
<213> Artificial

<220>

<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 150
ccataaccag tcactccaaa att 23

<210> 151
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 151
ttttagttgt tacttttggc g 21

<210> 152
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 152
acagcagatg agagaaagta 20

<210> 153
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 153
gggttgtctt gctgattttc 20

<210> 154
<211> 22
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 154
cattaaaata agtccggaca gg 22

<210> 155
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 155
ttaaacagaa tgaggagcaa 20

<210> 156
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 156
aaacaacaca cccatctaag 20

<210> 157
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 157
ttaataaggc atccccaaga 20

<210> 158
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 158
gaaatggctg tgtaaaaact 20

<210> 159
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 159
tctgccatat ccccaaccta 20

<210> 160
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 160
gatcgcccga caggaagact 20

<210> 161
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 161
tccggcttga cctgctggac 20

<210> 162
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 162
tgcgatgatt ttgcctctgt 20

<210> 163
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 163
aaaatttgca cacccacacg 20

<210> 164
<211> 27
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 164
ttggattgaa cgtgtaattg aaaaagc 27

<210> 165
<211> 27
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 165
gctttttcaa ttacacgttc aatccaa 27

<210> 166
<211> 19
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 166
aaatggcgta tcgactaac 19

<210> 167
<211> 21

<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 167
atataggagc gcataaagtg c 21

<210> 168
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 168
cttggtataa gtcttgtgat 20

<210> 169
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 169
aacactcatt agattcatct 20

<210> 170
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 170
tccactaaat cctttgaatt g 21

<210> 171
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 171
tgtttgtctg gatgcgatcc t 21

<210> 172
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 172
gcagttcagg tccatgaaac 20

<210> 173
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 173
agcccagtca caaccttcgt 20

<210> 174
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 174
tctggaagta cttgcactgt c 21

<210> 175
<211> 22
<212> DNA
<213> Artificial

<220>

<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 175
tgtaactccg tcaggacata aa 22

<210> 176
<211> 23
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 176
tgcaaatttt agtagcaata acg 23

<210> 177
<211> 27
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 177
ctttactaat tatagcgggg atattat 27

<210> 178
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 178
cagtggggaa atagatggat 20

<210> 179
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 179
tggtcataaa agcgggattc 20

<210> 180
<211> 18
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 180
ggatcttggc gcaattta 18

<210> 181
<211> 23
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 181
gttagagact tggaacgtat tgg 23

<210> 182
<211> 19
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 182
ccaaacccag aagaaatcc 19

<210> 183
<211> 22
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 183
aatctatagc caaaacccct aa 22

<210> 184
<211> 19
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 184
actgtgtgaa caattcccc 19

<210> 185
<211> 29
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 185
gcaacaagac tacatttagt agatttaga 29

<210> 186
<211> 27
<212> DNA
<213> Artificial

<220>
<223> Based on Cylindrospermopsis raciborskii T3 sequence

<400> 186
gctttttcaa ttacacgttc aatccaa 27