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Description

Technical Field

[0001] 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

[0002] 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.

[0003] 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.

[0004] *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.

[0005] 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, Aphanizomerzon 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.

[0006] 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.

Summary

[0007] In a first aspect, there is provided an isolated polynucleotide comprising a sequence according to SEQ ID NO: 1 or a variant sharing at least 80% identity with SEQ ID NO: 1 or fragment thereof wherein, 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.

[0008] 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.

[0009] In a third aspect, there is provided an isolated saxitoxin biosynthetic pathway polypeptide encoded by the fragment of the first aspect and comprising an amino acid sequence sharing at least 80%

identity 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: 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: 69.

[0010] 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.

[0011] It is described 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.

[0012] It is described a host cell comprising the vector.

[0013] In another embodiment, there is provided an isolated antibody capable of binding specifically to a polypeptide according to the third aspect.

[0014] In a fourth aspect, there is provided a method for detecting a cyanotoxic organism comprising the steps of obtaining a sample for use in the method and analyzing the sample for the presence of an *SXT*cluster gene present only in saxitoxin-producing organisms, wherein said analysing comprises detecting:

(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, and SEQ ID NO: 36;

(ii) a variant polynucleotide having at least 80% sequence identity with a polynucleotide of (i);

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

(iv) 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, and SEQ ID NO: 37; or,

(v) a variant polypeptide having at least 80% sequence identity with a polypeptide of (iv),

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

[0015] In one embodiment of the fourth aspect, the cyanotoxic organism is a cyanobacteria or a dinoflagellate.

[0016] In one embodiment of the fourth aspect, 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: 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 having at least 80% sequence identity with anyone of the said polynucleotide sequences.

[0017] In another embodiment of the fourth aspect, 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 having at least 80% sequence identity with anyone of the said polynucleotide sequences ,

(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 having at least 80% sequence identity with anyone of the said polypeptide sequences.

[0018] 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: 111, SEQ ID NO: 112, or variants having at least 80% sequence identity with anyone of the said polynucleotide sequences.

[0019] It is described 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.

[0020] Analysing the sample may comprise amplification of DNA from the sample by polymerase chain reaction and detecting the amplified sequences.

[0021] In one embodiment of the fourth aspect, 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.

[0022] In a fifth aspect, there is provided a kit for the detection of cyanotoxic organisms, the kit comprising at least one agent for detecting the presence of an *SXT* cluster gene present only in saxitoxin-producing organisms, wherein either:

(i) said agent can detect 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 having at least 80% sequence identity with any one of said polynucleotide sequences and said agent is a primer or a probe;

(ii) said agent can detect a ribonucleic acid or complementary DNA encoded by a sequence according to (i) and said agent is a primer or a probe; or

(iii) said agent can detect 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 having at least 80% sequence identity with any one of said polypeptide sequences, and said agent is an antibody capable of specifically binding to the polypeptide.

[0023] 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: 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: 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 having at least 80% sequence identity with any one of said polypeptide sequences.

[0024] In another embodiment of the fifth aspect, the kit further comprises 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 having at least 80% sequence identity with any one of said polynucleotide sequences,

(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 having at least 80% sequence identity with any one of said polypeptide sequences.

[0025] 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 having at least 80% sequence identity with any one of said polypeptide sequences.

[0026] It is described 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.

[0027] It is further described 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.

[0028] Modulating the expression or activity of one or more polypeptides may comprise inhibiting the expression or activity of said polypeptide.

[0029] Modulating the expression or activity of one or more polypeptides may comprise enhancing the expression or activity of said polypeptide.

Definitions

[0030] 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.

[0031] 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.

[0032] 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.

[0033] As used herein, the terms "polypeptide" and "protein" are used interchangeably and are taken to have the same meaning.

[0034] As used herein, the terms "nucleotide sequence" and "polynucleotide sequence" are used interchangeably and are taken to have the same meaning.

[0035] 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.

[0036] 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.

Brief Description of the Drawings

[0037] 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

[0038] 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.

[0039] 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.

[0040] 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

[0041] The inventors have determined the full polynucleotide sequence of the saxitoxin (*SXT*) gene cluster and the cylindrospermopsin (*CYR*) gene cluster.

[0042] 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.

[0043] The *SXT* gene cluster comprises 31 genes and 30 intergenic regions.

[0044] 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.

[0045] 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.

[0046] 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.

[0047] 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.

[0048] 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.

[0049] 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.

[0050] 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.

[0051] 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.

[0052] 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.

[0053] 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.

[0054] 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.

[0055] 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.

[0056] 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.

[0057] 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.

[0058] 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.

[0059] 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.

[0060] 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.

[0061] 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.

[0062] 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.

[0063] 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.

[0064] 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.

[0065] 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.

[0066] 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.

[0067] 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.

[0068] 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.

[0069] 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.

[0070] 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.

[0071] 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.

[0072] 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.

[0073] 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.

[0074] 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.

[0075] 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.

[0076] 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.

[0077] 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.

[0078] 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.

[0079] The *CYR* gene cluster comprises 15 genes and 14 intergenic regions.

[0080] 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.

[0081] 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.

[0082] 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.

[0083] 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.

[0084] 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.

[0085] 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.

[0086] 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.

[0087] 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.

[0088] 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.

[0089] 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.

[0090] 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.

[0091] 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.

[0092] 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.

[0093] 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.

[0094] 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.

[0095] In general, the nucleic acids and polypeptides of the invention are of an isolated or purified form.

[0096] *SXT* and *CYR* polynucleotides disclosed herein may be deoxyribonucleic acids (DNA), ribonucleic acids (RNA) or complementary deoxyribonucleic acids (cDNA).

[0097] 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 doublestranded 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.

[0098] 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.

[0099] 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.

[0100] 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.

[0101] 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.

[0102] 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.

[0103] 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.

[0104] 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.

[0105] 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).

[0106] 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.

[0107] 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.

[0108] 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.

[0109] 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 (seeHenikoff 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.

[0110] 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.

[0111] 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.

[0112] 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.

[0113] 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.

[0114] 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.

[0115] 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

[0116] 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.

[0117] 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.

[0118] 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.

[0119] Methods for the design and/or production of nucleotide probes and/or primers are generally known in the art, and are described inSambrook 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.

[0120] 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.

[0121] 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.

[0122] 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.

[0123] 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.

[0124] 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.

[0125] 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.

[0126] 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.

[0127] 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.

[0128] 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.

[0129] 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.

[0130] 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.

[0131] 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.

[0132] 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).

[0133] 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".

[0134] 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.

[0135] 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.

[0136] 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.

[0137] 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

[0138] 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.

[0139] 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.

[0140] 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.

[0141] Alternatively, the *SXT* polynucleotide may be an RNA or cDNA encoded by a sequence selected from the group consisting of SEQ 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.

[0142] 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: 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: 69, and variants and fragments thereof.

[0143] 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.

[0144] 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.

[0145] 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.

[0146] 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.

[0147] 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.

[0148] 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.

[0149] 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.

[0150] 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.

[0151] 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 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.

[0152] 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.

[0153] 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.

[0154] 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.

[0155] 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.

[0156] 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.

[0157] 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: 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: 69, and variants and fragments thereof.

[0158] 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.

[0159] 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.

[0160] 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.

[0161] 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: 41, SEQ ID NO: 43, SEQ 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: 69, and variants and fragments thereof.

[0162] 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.

[0163] 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.

[0164] 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.

[0165] 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. 7348147and PCT publication No. WO/2007/056723.

[0166] 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.

[0167] 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.

[0168] 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; andNeilan 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.

[0169] 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.

[0170] 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.

[0171] 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.

[0172] 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.

[0173] 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.

[0174] 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.

[0175] 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.

[0176] 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.

[0177] 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.

[0178] 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.

[0179] 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.

[0180] 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.

[0181] 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.

[0182] 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.

[0183] 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.

[0184] Methods for the design and/or production of nucleotide probes are generally known in the art, and are described, for example, inRobinson 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.

[0185] 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.

[0186] 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.

[0187] 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.

[0188] 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.

[0189] 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.

[0190] 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 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.

[0191] 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: 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: 69, and variants and fragments thereof.

[0192] 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.

[0193] 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.

[0194] 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.

[0195] 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.

[0196] 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.

[0197] 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.

[0198] 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.

[0199] 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 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.

[0200] 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.

[0201] 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.

[0202] 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.

[0203] The *CYR* polynucleotide may comprise a sequence selected from the group consisting of SEQ ID NO: 81, SEQ ID NO: 83, SEQ 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.

[0204] 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.

[0205] 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.

[0206] 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.

[0207] 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.

[0208] 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 m NO: 66, SEQ ID NO: 68, and variants and fragments thereof and/or polypeptides as disclosed herein, or a variant or fragment thereof.

[0209] 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.

[0210] 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.

[0211] 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.

[0212] 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.

[0213] 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: 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: 69, and variants and fragments thereof.

[0214] 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

[0215] 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.

[0216] 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.

[0217] 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.

[0218] 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))

[0219] 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.

[0220] 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.

[0221] 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.

[0222] 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.

[0223] 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.

[0224] 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.

[0225] 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.

[0226] 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.

[0227] 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.

[0228] 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).

[0229] 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).

[0230] 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.

[0231] 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.

[0232] 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.

[0233] 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.

[0234] 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 $10^8 M^{-1}$.

[0235] 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.

[0236] 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.

[0237] 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).

[0238] 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. Doublestranded 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.

[0239] 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.

[0240] 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

[0241] 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.

[0242] 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).

[0243] 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.

[0244] 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

[0245] 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

[0246] 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.

[0247] 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.

[0248] *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.

[0249] 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).

[0250] 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.

[0251] *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'.

[0252] 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'.

[0253] 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.

[0254] 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.*

[0255] 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 SXTtailoring genes

[0256] 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.

[0257] *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.*

[0258] *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.

[0259] 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

[0260] *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

[0261] 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

[0262] 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.

[0263] 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.

[0264] 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).

[0265] 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

[0266] 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.

[0267] 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.

[0268] 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.

[0269] 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

[0270] 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).

[0271] 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.

[0272] 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.

[0273] 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.

[0274] 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.

[0275] 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.

[0276] 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.

[0277] 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

[0278] 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

[0279] 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

[0280] 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.

[0281] 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.

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<211> 1320

<212> DNA

<213> Cylindrospermopsis raciborskii T3

<400> 2

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<210> 3

<211> 439

<212> PRT

<213> Cylindrospermopsis raciborskii T3

<400> 3

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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
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    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
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Ser Ser Gly Ser Ile Thr Lys Leu Arg Gln Arg Gly Met Gly Thr Glu
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Phe Ala Glu Leu Arg Asn Tyr Cys Met Gly Asp Asp Leu Arg Leu Ile
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Asp Trp Lys Ala Thr Ala Arg Arg Ala Tyr Gly Asn Leu Ser Pro Leu
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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
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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
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<210> 4

<211> 759

<212> DNA

<213> Cylindrospermopsis raciborskii T3

<400> 4

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<210> 5

<211> 252

<212> PRT

<213> Cylindrospermopsis raciborskii T3

<400> 5

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            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
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        115                 120                 125
Trp Trp Leu Ser Gly Asn Lys Asp Ser Phe Thr Gly Gly Leu Leu Tyr
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145                 150                 155                 160
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                165                 170                 175
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            180                 185                 190
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        195                 200                 205
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    210                 215                 220
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<210> 6

<211> 396

<212> DNA

<213> Cylindrospermopsis raciborskii T3

<400> 6

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<210> 7

<211> 131

<212> PRT

<213> Cylindrospermopsis raciborskii T3

<400> 7

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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

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ttatctacaa ctgtccagac ccatatcttg ttttttttta ccaataaatg tttccaactc     60
atccagttga caaacttcag gtgtttggga attattatta ctatctgata actgacgacc    120
tagcttttg acccaacgaa tgactgtatt gtgatttact ttagtcattc tttcaattgc     180
cctaaatcca ttcccattta catacatggt taaacatgct tcctttactt cttgggaata    240
acctctagga gaataagatt caataaattg acgaccacaa ttcttgcatt gataattttg    300
ttttcccctt ctctggccat ttttttctaat attattggaa tcacagtttg aacagttcat   360
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<210> 9

<211> 119

<212> PRT

<213> Cylindrospermopsis raciborskii T3

<400> 9

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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

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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 atttttcaa 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

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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

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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

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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

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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
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<210> 15

<211> 1245

<212> PRT

<213> Cylindrospermopsis raciborskii T3

<400> 15

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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 Se
        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
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<210> 16

<211> 387

<212> DNA

<213> Cylindrospermopsis raciborskii T3

<400> 16

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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
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<210> 17

<211> 128

<212> PRT

<213> Cylindrospermopsis raciborskii T3

<400> 17

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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

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atggaaacaa cctcaaaaaa atttaagtca gatctgatat tagaagcacg agcaagccta     60
aagttgggaa tcccccttagt 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 gaatacegcc    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 acccctttggg 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
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<210> 19

<211> 471

<212> PRT

<213> Cylindrospermopsis raciborskii T3

<400> 19

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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

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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
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<210> 21

<211> 377

<212> PRT

<213> Cylindrospermopsis raciborskii T3

<400> 21

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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

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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

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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

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atgcagatct taggaatttc agcttactac cacgatagtg ctgccgcgat ggttatcgat     60
```

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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
ttttttccca 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

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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

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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

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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

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atgctaaaag acacttggga ttttattaaa gacattgccg gatttattaa agaacaaaaa     60
aactatttgt tgattcccct aattatcacc ctggtatcct tgggggcgct gattgtcttt    120
gctcaatctt ctgcgatcgc acctttcatt tacactcttt tttaa                    165
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<210> 29

<211> 54

<212> PRT

<213> Cylindrospermopsis raciborskii T3

<400> 29

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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 tcccttcaa     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
aagccttttct 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 agaaaaacctt 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 tcgttttttg 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 ggatatttcc    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 ttacctttte 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
gggggggatag 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

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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 ctttcagcg 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 atccgccccc 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

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atgagttggt ccacaatgaa ggacgtcttg attttaatag tcaaatccct ccaaatccat     60
tataatccca tgaatgctct ttcaattcct acctggatta tccatatttc tagtgtcatt    120
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<213> Cylindrospermopsis raciborskii AWT205

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<213> Cylindrospermopsis raciborskii AWT205

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Thr Leu  Val Lys Ala Ile Gly  Phe Val Leu Arg Glu  Ala Ser Pro
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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
```

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    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
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<210> 83

<211> 4074

<212> DNA

<213> Cylindrospermopsis raciborskii AWT205

<400> 83

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cacaatgggg ttgatgctat ccaagagatt ccaaaaagcc gttgggatat tgacgactat    240
tatgatccca caccagcaac acccggcaaa atgtatacac gttttggtgg ttttctcgac    300
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gaccctcaac agagattgct tctggaagtg agttgggaag ccttagaacg ggctgggctg    420
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cttgataccg cctgttcgtc ctctttggtt tgtgtggcat tggctgtcaa gagcctacgt    660
caacaggagt gtgatttggc attggcgggt ggtgtacaga tacaagtgat accagatggc    720
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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
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ggctttagtg gcacaaactc tcatatcgta ctagaggcag ccccaaacat agagcaacct   1380
actgatgata ttaatcaaac gccgcatatt ttgaccttag ctgcaaaaac acccgcagcc   1440
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gcggacattt gtttcacagc acacataggg cgtaaacatt ttaaacatag gtttgcggta   1560
gtcacggaat ctaaagagca actgcgtttg caattggatg catttgcaca atcaggggat   1620
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gcccattgtg atgacatctt gcgtgctggt gcatatttcg accgatcact actttcgatt   1800
ctctacccag agggaaaatc agaagccatt caccaaaccg cttatactca gcccgcgctt   1860
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gaggatgggc tgaaactaat tgctactcgt ggtcgtctga tgcaatccct acctcaagac   2040
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gatcgcatca atttactcaa cagtggtgat atgccttggt tctgggtaat ggagcgatca   3540
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aatgtgtata ttgtcgcggg tgggtctagc aacctcccca cggtagccag ccacctcatg   3720
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tggcctgtta ccccatcgtt tcgtgttctg cgagacggtt atccacctga tcgagattct   3960
ggtggtcacg cagttagtac ggttttccag ctcaatgatt tcgatggagc gatcgaagaa   4020
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<210> 84

<211> 1357

<212> PRT

<213> Cylindrospermopsis raciborskii AWT205

<400> 84

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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
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<210> 85

<211> 1437

<212> DNA

<213> cylindrospermopsis raciborskii awt205

<400> 85

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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
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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
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caagcctgtg gcaacaactg ttgtaacatc ttcaatgaaa tgaagctgac cgccttattc   1020
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accatcgaag gagcgcaggc gattggttta gatcacaaga ttggctctct tcaagtgggc   1140
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tccgctattc tcgctgaagc gcaagtacaa gctcaacaac tctgccaacg tgtgaccgct   1380
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<210> 86

<211> 478

<212> PRT

<213> Cylindrospermopsis raciborskii AWT205

<400> 86

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            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

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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

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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

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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 ccatttttct cccgtcccag aaaccagcca agcaggacaa agttgagcaa   960
aatggcaggc gctccccaac tctgggtgtt aaaatacgct tgagctgaag acttcacctc  1020
tgggccgaca tctagtatag aaaaccccaa caccctaac gggtactgta acagtatgat  1080
cgccaccccc 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

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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

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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

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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

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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

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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

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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
tggccccca tggaggtcga gttgaacgaa aaactagccc cttggtacag caccgtagca    660
agttctacgc attttcactc gtatcagaat aaaaatgagt cgttgccgct atatcttgtc    720
gatatttgta aacgctgcga tgaaatatat caggaattat atcaatttcg actttattag    780
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<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

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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
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<212> PRT

<213> Cylindrospermopsis raciborskii AWT205

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Lys Arg His Leu Glu Pro Arg Arg Phe Arg Val His Asp Ile His Phe
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Ser Leu His Cys Ala Thr Trp Asp Ile His Arg Thr Gly Thr Cys Glu
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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
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Asp Val Ala Lys Lys Leu Ala Leu Thr Ile Pro Ala Leu Gln Glu Cys
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Gln Thr Val Tyr Leu Asp Gln Glu Ile Phe Glu Tyr Asp Phe His Phe
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Leu Ala Ile Ala Lys Leu Leu His Asn Gln Tyr Leu Arg Leu Leu His
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Ile Ser Gln Gln Lys Ile Glu Lys Leu Phe Leu Pro Val Ile Ala Leu
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Leu Phe Asn Asn Pro Ala Tyr Val Lys Ala Gly Ala Val Leu Glu Gly
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Ala Phe Glu Arg Ala Gly Tyr Asn Pro Glu Thr Tyr Pro Glu Pro Val
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Gln Thr Ala Cys Ser Thr Ser Leu Val Ala Val His Met Ala Cys Gln
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Val Val Val Pro Gln Lys Gly Gly Tyr Leu Tyr Glu Glu Gly Met Val
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Val Asp Gly Gln Ala Asp Val Ile Ser Glu Ala Ile Ala Ile Ala Asp
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Gln Leu Gly Asp Pro Ile Glu Val  Ala Gly Leu Ala Arg  Ala Phe Gln
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Ser Val  Lys Thr Asn Ile Gly  His Leu Asp Glu Ala  Ala Gly Ile
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Pro Ile  Ile Arg Gln Arg Gln  Ser Val Leu Gln Ala  Thr Asn Thr
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Thr Lys  Leu Thr Arg Asn Ala  Ser Val Ala Gln His  Pro Leu Leu
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Gly Gln  Arg Leu His Leu Ser  Arg Thr Gln Glu Ile  Tyr Phe Gln
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<210> 102

<211> 1888

<212> PRT

<213> Cylindrospermopsis raciborskii AWT205

<400> 102

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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
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    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
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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
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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
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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
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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
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Glu Glu  Leu Gln Ala Gly Cys  Pro Gln Glu Ile Asp  Leu Asn Leu
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Phe Tyr  Gln Thr Phe Thr Asp  Lys Gly Phe Val Phe  Gly Ser Arg
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Phe Arg  Trp Leu Glu Gln Ile  Trp Val Gly Asp Gly  Glu Ala Leu
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Ala Arg  Leu Arg Gln Pro Glu  Ser Ile Glu Ser Phe  Lys Gly Tyr
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Val Ile  His Pro Gly Leu Leu  Asp Ala Cys Thr Gln  Val Pro Phe
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Ala Ile  Ser Ser Asp Asp Glu  Asn Arg Gln Ser Glu  Thr Thr Met
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Pro Phe  Ala Leu Asn Glu Leu  Arg Cys Tyr Gln Pro  Ala Asn Gly
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Gln Met  Trp Trp Val His Ala  Thr Glu Lys Asp Arg  Tyr Thr Trp
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Asp Val  Ser Leu Phe Asp Glu  Ser Gly Gln Val Ile  Ala Glu Phe
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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
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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
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Ile Asn  Pro Ala Ser Pro His  Asp Tyr Lys Tyr Phe  Leu Glu Thr
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Leu Thr  Asp Ile Arg Leu Pro  Cys Glu His Ile Leu  Tyr Leu Trp
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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
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Arg Ala  Glu His Pro Glu Phe  Asp Cys Arg Cys Leu  Asp Phe Asp
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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
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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
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Met Tyr  Tyr Arg His Ile Lys  Gly Ser Asn Ser Leu  Ser Ile Asn
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Glu Gln  Arg Gly Ile Ala Ala  Ile Ser Pro Lys Gln  Gly Arg His
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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
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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
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Leu Ala  Gln Ala Leu Asn Ile  Ala Phe Glu
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<210> 103

<211> 5004

<212> DNA

<213> Cylindrospermopsis raciborskii AWT205

<400> 103

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<210> 104

<211> 1667

<212> PRT .

<213> Cylindrospermopsis raciborskii AWT205

<400> 104

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            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
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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

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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
```

<210> 109

<211> 1548

<212> DNA

<213> Cylindrospermopsis raciborskii AWT205

<400> 109

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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
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<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
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<210> 181

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<210> 182

<211> 19

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<400> 183

aatctatagc caaaacccct aa 22

<210> 184

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<400> 184
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gcaacaagac tacatttagt agatttaga 29
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gctttttcaa ttacacgttc aatccaa 27

Patentkrav

1. Fremgangsmåde til detektering af en cyanotoksisk organisme omfattende trinnene med opnåelse af en prøve til anvendelse i fremgangsmåde og analyse af prøven for tilstedeværelse af et *SXT*-clustergen, der kun er til stede i saxitoxin-producerende organismer, hvor analysen omfatter detektering af:

(i) et polynukleotid omfattende en sekvens, der er udvalgt fra gruppen bestående af: SEQ ID NO: 14, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24 og SEQ ID NO: 36;

(ii) en polynukleotidvariant med mindst har 80 % sekvensidentitet med et polynukleotid af (i);

(iii) en ribonukleinsyre eller komplementært dna kodet for af en sekvens ifølge (i);

(iv) et polypeptid omfattende en sekvens, der er udvalgt fra gruppen bestående af: SEQ ID NO: 15, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, og SEQ ID NO: 37; eller

(v) en polypeptidvariant med mindst 80 % sekvensidentitet med et polypeptid af (iv),

og hvor tilstedeværelsen er en indikation for cyanotoksiske organismer i prøven.

2. Fremgangsmåde ifølge krav 1, hvor den cyanotoksiske organisme er en cyanobakterie eller en dinoflagellat.

3. Fremgangsmåde ifølge krav 1, hvor analysen omfatter amplifikation af DNA fra prøven ved polymerasekædereaktion ved anvendelse af én eller flere primere omfattende en sekvens, der er udvalgt fra gruppen bestående af 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 og varianter, der mindst har 80 % sekvensidentitet med en hvilken som helst af primersekvenserne.

4. Fremgangsmåde ifølge et hvilket som helst af kravene 1 til 3, hvilken fremgangsmåde endvidere omfatter analyse af prøven for forekomst af én eller flere af:

(i) et polynukleotid omfattende en sekvens, der er udvalgt fra gruppen bestående af: 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 og varianter, der mindst har 80 % sekvensidentitet med en hvilken som helst af polynukleotidsekvenserne,

(ii) en ribonukleinsyre eller komplementært dna kodet for af en sekvens ifølge (i),

(iii) et polypeptid omfattende en sekvens, der er udvalgt fra gruppen bestående af: 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 og SEQ ID NO: 110 samt varianter, der mindst har 80 % sekvensidentitet med en hvilken som helst af polypeptidsekvenserne.

5. Fremgangsmåde ifølge krav 4, hvor analysen omfatter amplifikation af dna fra prøven ved polymerasekædereaktion ved anvendelse af én eller flere primere omfattende en sekvens, der er udvalgt fra gruppen bestående af SEQ ID NO: 111, SEQ ID NO: 112 og varianter, der mindst har 80 % sekvensidentitet med en hvilken som helst af sekvenserne.

6. Kit til detektering af cyanotoksiske organismer, hvilket kit omfatter mindst ét stof til detektering af tilstedeværelsen af et *SXT*-clustergen, der kun er til stede i saxitoxin-producerende organismer, hvor enten:

(i) stoffet kan detektere et polynukleotid omfattende en sekvens, der er udvalgt fra gruppen bestående af: SEQ ID NO: 14, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 36, og varianter, der mindst har 80 % sekvensidentitet med en hvilken som helst af polynukleotidsekvenserne, og stoffet er en primer eller en sonde;

(ii) stoffet kan detektere en ribonukleinsyre eller komplementært dna kodet for af en sekvens ifølge (i) og stoffet er en primer eller en sonde; eller

(iii) stoffet kan detektere et polypeptid omfattende en sekvens, der er udvalgt fra gruppen bestående af: SEQ ID NO: 15, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 37 og varianter, der mindst har 80 % sekvensidentitet med en hvilken som helst af polypeptidsekvenserne, og stoffet er et antistof, der specifikt kan bindes til polypeptidet.

7. Kit ifølge krav 6, hvor det mindst ene stof er en primer eller sonde, der omfatter en nukleotidsekvens udvalgt fra gruppen bestående af 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 og varianter, der mindst har 80 % sekvensidentitet med en hvilken som helst af nukleotidsekvenserne.

8. Kit ifølge krav 6 eller krav 7, hvilket kit endvidere omfatter mindst ét supplerende stof til detektering af tilstedeværelsen af én eller flere af:

(i) et polynukleotid omfattende en sekvens, der er udvalgt fra gruppen bestående af: 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 og varianter, der mindst har 80 % sekvensidentitet med en hvilken som helst af polynukleotidsekvenserne,

(ii) en ribonukleinsyre eller komplementært dna kodet for af en sekvens ifølge (i) eller

(iii) et polypeptid omfattende en sekvens, der er udvalgt fra gruppen bestående af: 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 og SEQ ID NO: 110 samt varianter, der mindst har 80 % sekvensidentitet med en hvilken som helst af polypeptidsekvenserne.

9. Kit ifølge krav 8, hvor det mindst ene supplerende stof er et antistof, en primer eller sonde, hvor primeren eller sonden omfatter en sekvens, der er udvalgt fra gruppen bestående af SEQ ID NO: 111, SEQ ID NO: 112 og varianter, der mindst har 80 % sekvensidentitet med en hvilken som helst af sekvenserne.

10. Isoleret polynukleotid omfattende en nukleotidsekvens, der deler mindst 80 % sekvensidentitet med SEQ ID NO: 1 eller en nukleotidsekvens, der deler mindst 80 % sekvensidentitet med en sekvens, der er udvalgt fra gruppen bestående af 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 og SEQ ID NO: 68.

11. Isoleret ribonukleinsyre eller isoleret komplementært dna kodet for af en sekvens ifølge krav 10.

12. Isoleret polypeptid fra saxitoxins biosyntesevej, hvilket polypeptid er kodet for af et fragment ifølge krav 10 og som omfatter en aminosyresekvens, der deler mindst 80 % sekvensidentitet med en sekvens, der er udvalgt fra gruppen bestående af 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: 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 NO: 59, SEQ ID NO: 61, SEQ ID NO: 63 og SEQ ID NO: 69.

13. Sonde eller primer, der specifikt hybridiseres med én eller flere af:

(i) et polynukleotid ifølge krav 10 eller

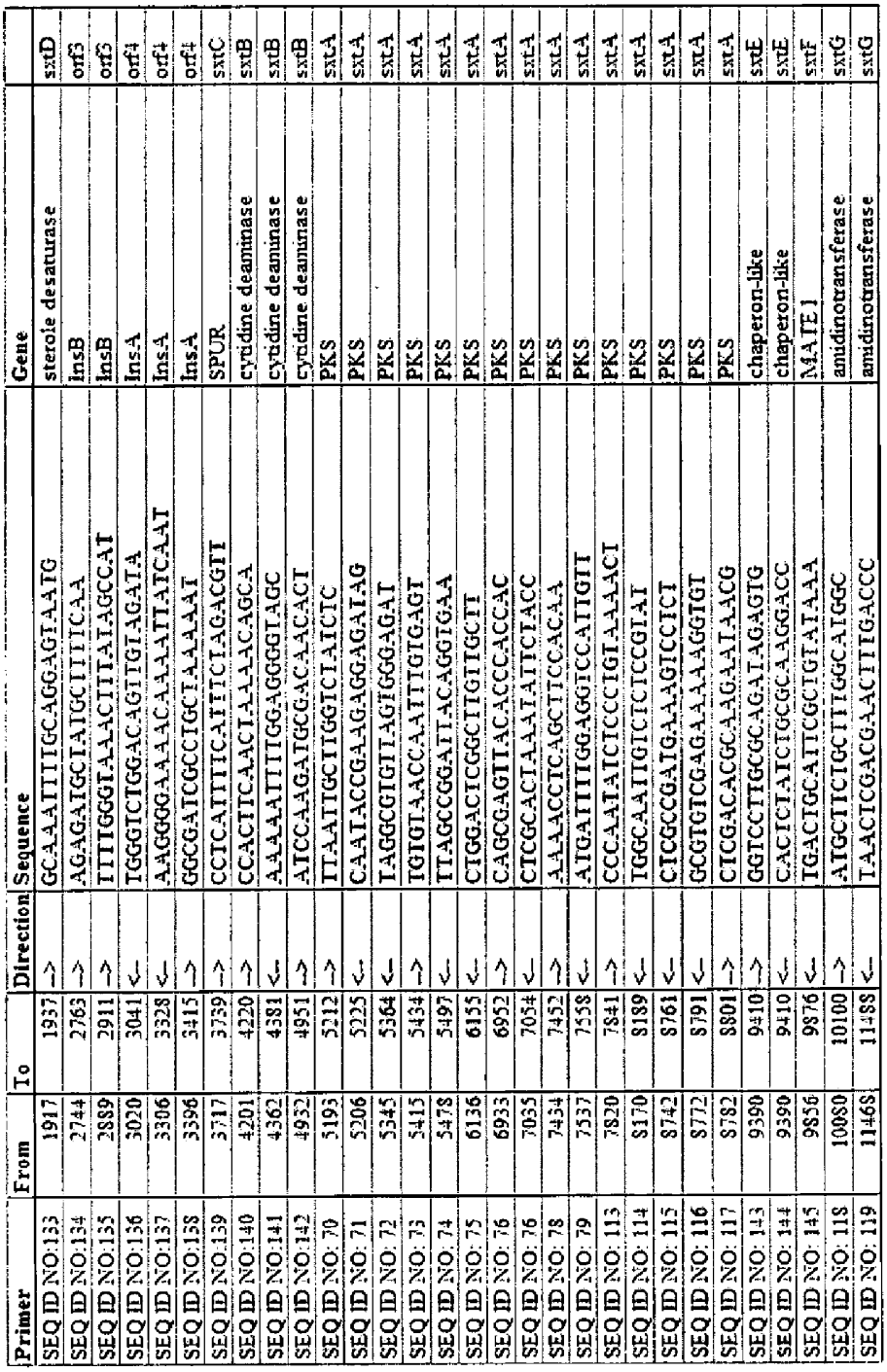
(ii) en ribonukleinsyre eller komplementært dna ifølge krav 11,

hvor primeren eller sonden omfatter en sekvens, der er udvalgt fra gruppen bestående af 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: 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: 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, og varianter, der mindst har 80 % sekvensidentitet med en hvilken som helst af polynukleotidsekvenserne.

14. Isoleret antistof, der specifikt kan bindes til et polypeptid ifølge krav 12.

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	-->	TTTTGGGTAAACTTTATAGCCAT	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	<--	AAAAATTTTTGGAGGGGTAGC	cytidine deaminase	sxtB
SEQ ID NO:142	4932	4951	-->	ATCCAAGATGCGACAACACT	cytidine deaminase	sxtB
SEQ ID NO: 70	5193	5212	-->	TTAATTGCTTGGTCTAATCTC	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	<--	CTCGCACTAAATATTCTACC	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	<--	CTCGCCGATGAAGTCCTCT	PKS	sxtA
SEQ ID NO: 116	8772	8791	<--	GCGTGTCGAGAAAAAGGTGT	PKS	sxtA
SEQ ID NO: 117	8782	8801	-->	CTCGACACGCAAGAATAACG	PKS	sxtA
SEQ ID NO: 143	9390	9410	-->	GGTCCTTGCGCAGATAGAGTG	chaperon-like	sxtE
SEQ ID NO: 144	9390	9410	<--	CACTCTATCTGCGCAAGGACC	chaperon-like	sxtE
SEQ ID NO: 145	9856	9876	<--	TGACTGCATTCGCTGTATAAA	MATE1	sxtF
SEQ ID NO: 118	10080	10100	-->	ATGCTTCTGCTTTGGCATGGC	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	-->	GCCGCCAATCCTCCGCGATG	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	<--	ctcgagTTAAAAAAAGAGTGTAAATGAAAGG	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	-->	TCTGCCATATCCCCCAACCTA	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
nxtD	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
nxtC	unknown protein	354	no similarity found		regulatory
nxtB	cytidine deaminase	957	EAS64681.1 *Vibrio anguillarum*	62	cyclisation
nxtA	methyltransferase	1506	ABF89568.1 *Myxococcus xanthus*	64	methylation
	GNAT	633	AAT78096.1 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
nxtE	unknown protein	387	ABE53436.1 *Shewanella denitrificans*	52	unknown
nxtF	MATE	1416	NcaM ABC44739.1 *Salinibacter ruber*	52	export of PSTs
nxtG	amidinotransferase	1134	ABA05575.1 *Nitrobacter winogradskyi*	71	amidinotransfer
nxtH	phenylpropionate dioxygenase	1005	ZP_00243439.1 *Rubrivivax gelatinosus*	50	C-12 hydroxylation
nxtI	carbamoyltransferase	1839	ABG50968.1 *Trichodesmium erythraeum*	82	carbamoylation

FIGURE 2

sxtJ	unknown protein	444	EAM51043.1 *Cyanothece watsonii*	72	regulatory
sxtK	unknown protein	165	ABG50954.1 *Trichodesmium erythraeum*	81	regulatory
sxtL	GDSL-lipase	1299	ABG50952.1 *Trichodesmium erythraeum*	60	cyclisation
sxtM	MATE	1449	NorM ABC44739.1 *Salinibacter ruber*	53	export of PSTs
sxtN	sulfotransferase	831	ABG53102.1 *Trichodesmium erythraeum*	57	sulfotransfer
sxtX	cephalosporin hydroxylase	774	ABG50679.1 *Trichodesmium erythraeum*	77	N-1 hydroxylation
sxtW	ferredoxin	327	ZP_00106179.2 *Nostoc punctiforme*	99	electron carrier
sxtV	succinate dehydrogenase	1653	ABA24604.1 *Anabaena variabilis*	92	dioxygenase reductase
sxtU	alcohol dehydrogenase	750	ZP_00111652.1 *Nostoc punctiforme*	83	reduction of C-1
sxtT	phenylpropionate dioxygenase	1005	ZP_00243439.1 *Rubrivivax gelatinosus*	48	C-12 hydroxylation
sxtS	phytanoyl-CoA dioxygenase	726	ABG30370.1 *Rasobacter denitrificans*	41	ring formation
orf24	unknown protein	576	no similarity found		unknown
sxtR	acyl transferase	777	AAU26161.1 *Legionella pneumophila*	54	unknown
sxtQ	unknown protein	777	EAR64935.1 *Bacillus* sp. NRRL B-14911	46	unknown
sxtP	RTX-toxin	1227	ABA20206.1 *Anabaena variabilis*	68	binding of PSTs
sxtO	adenylylsulfate kinase	603	ZP_00033494.2 *Magnetospirillum magneticum*	76	PAPS biosynthesis
orf29	transposase, IS4	1350	EAQ22567.1 *Synechococcus fluviatilis*	61	transposition
sxtY	PhoU	666	BAB76200.1 *Nostoc* PCC7120	87	signal transduction
sxtZ	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)

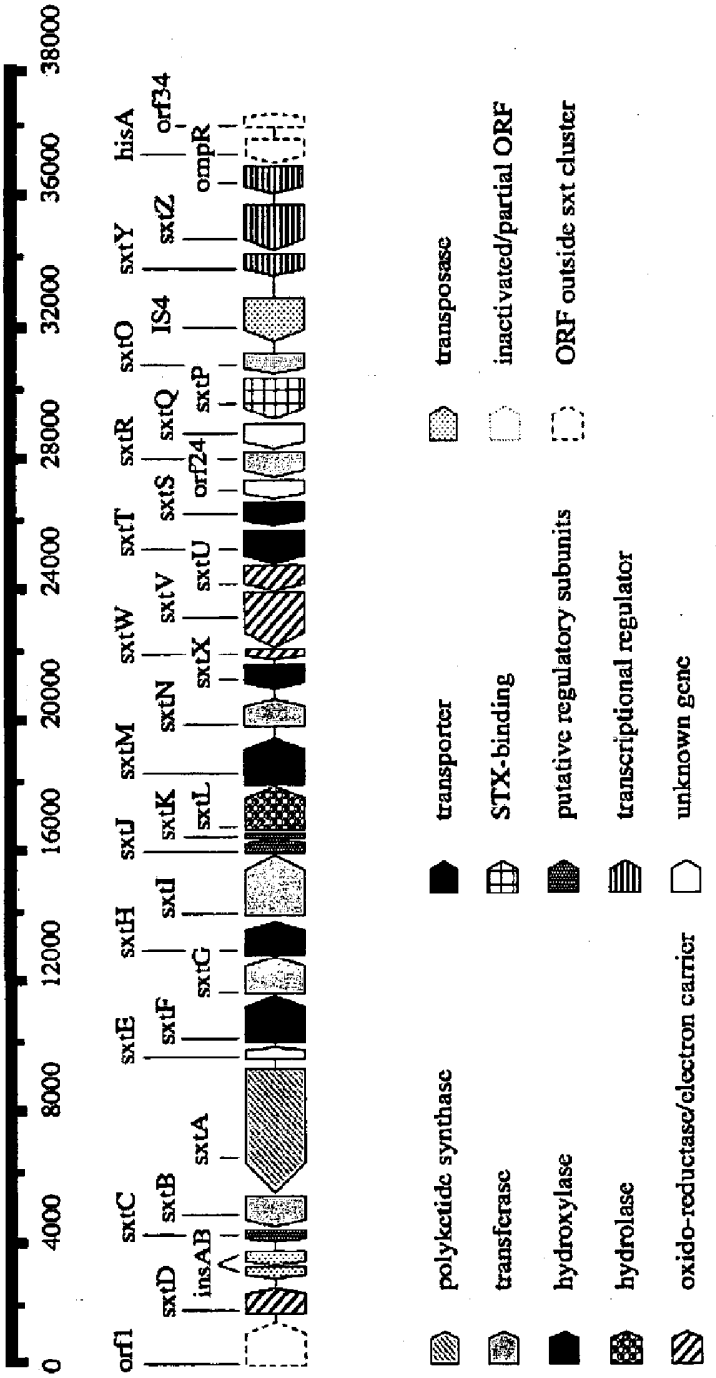

0
4000
8000
12000
16000
20000
24000
28000
32000
36000
38000
orf1
sxtD
insAB
sxtC
sxtB
sxtA
sxtE
sxtF
sxtG
sxtH
sxtI
sxtJ
sxtK
sxtL
sxtM
sxtN
sxtX
sxtW
sxtV
sxtU
sxtT
sxtS
orf24
sxtR
sxtQ
sxtP
sxtO
IS4
sxtY
sxtZ
ompR
hisA
orf34
polyketide synthase
transferase
hydroxylase
hydrolase
oxido-reductase/electron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

FIGURE 3

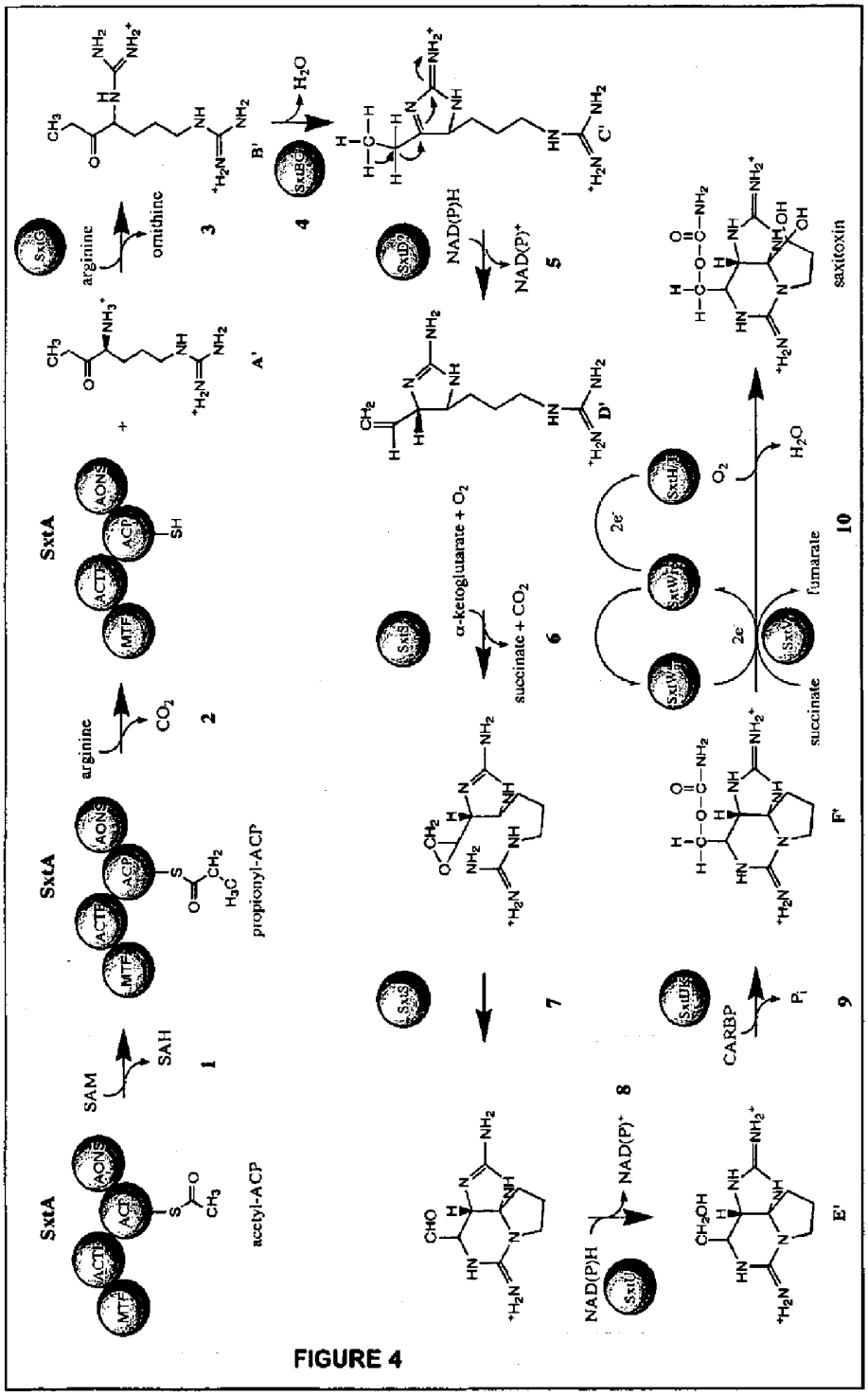

SxtA
SxtA
SxtA
acetyl-ACP
propionyl-ACP
SAM
SAH
arginine
CO2
ornithine
A'
B'
H2O
NAD(P)H
NAD(P)+
α-ketoglutarate + O2
succinate + CO2
CARBP
Pi
NAD(P)H
NAD(P)+
2e
2e
O2
H2O
fumarate
succinate
saxitoxin
1
2
3
4
5
6
7
8
9
10
C'
D'
E'
F'

FIGURE 4

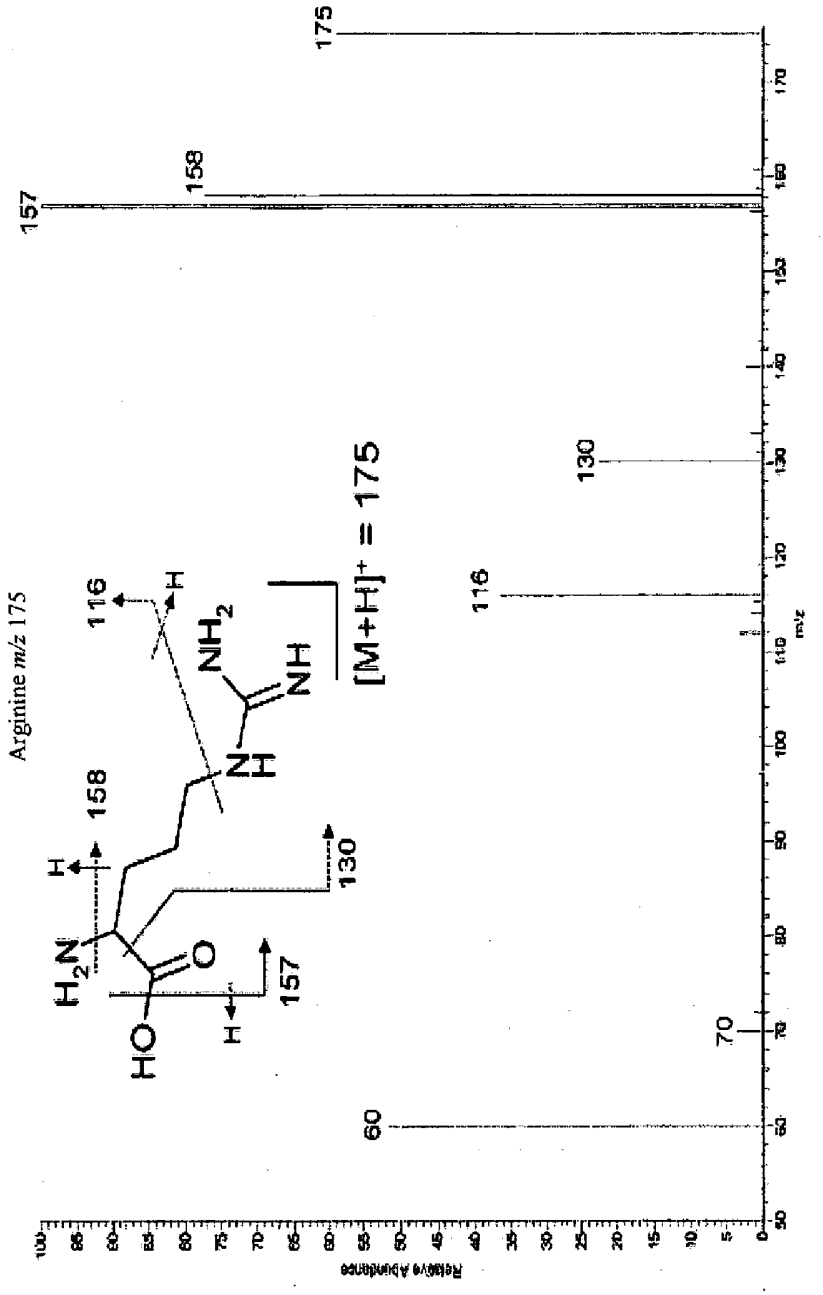

Arginine m/z 175
[M+H]+ = 175
175
158
157
130
116
70
60
m/z
Relative Abundance

FIGURE 5A

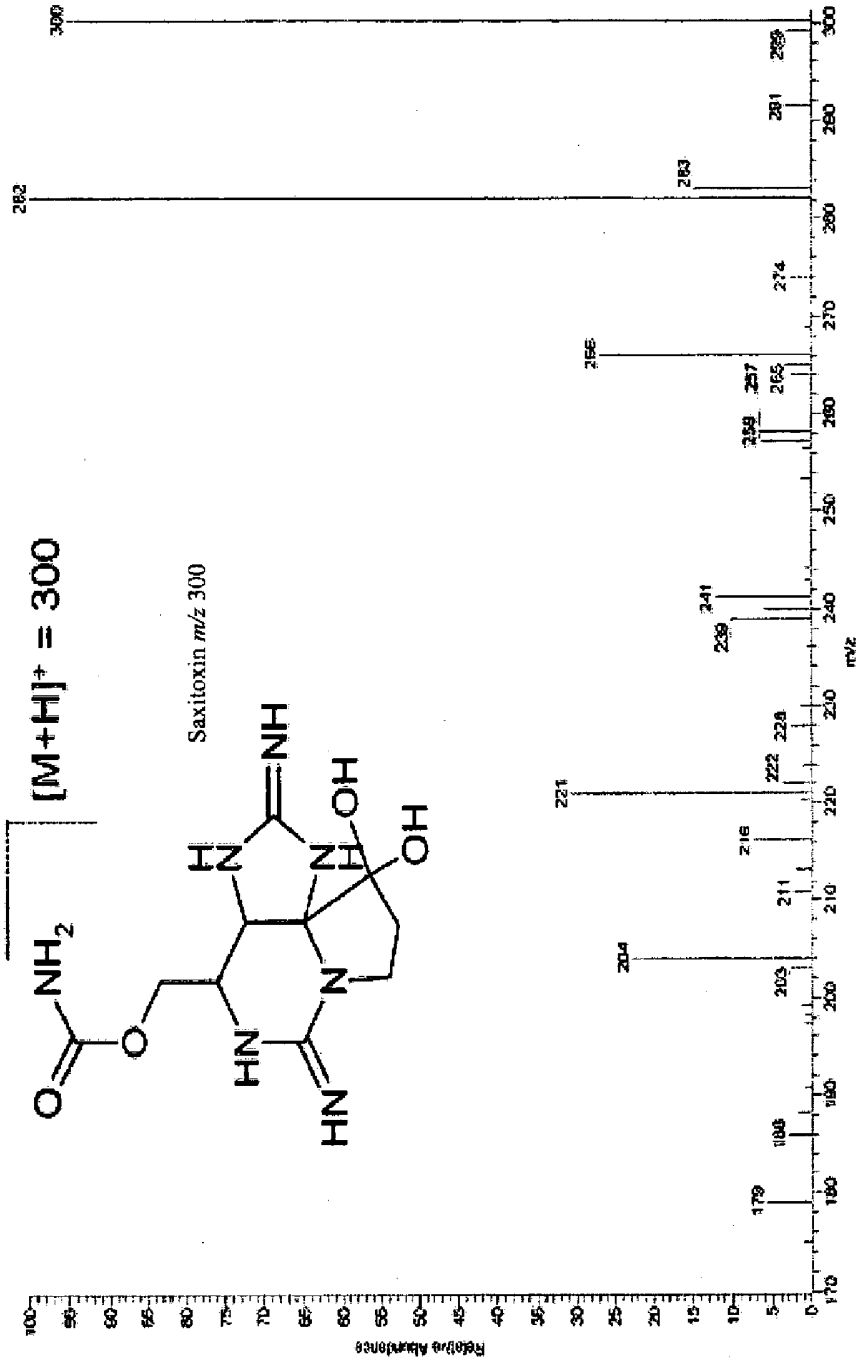

[M+H]+ = 300
Saxitoxin m/z 300
NH2
O
NH
HN
OH
OH
m/z
Relative Abundance

FIGURE 5B

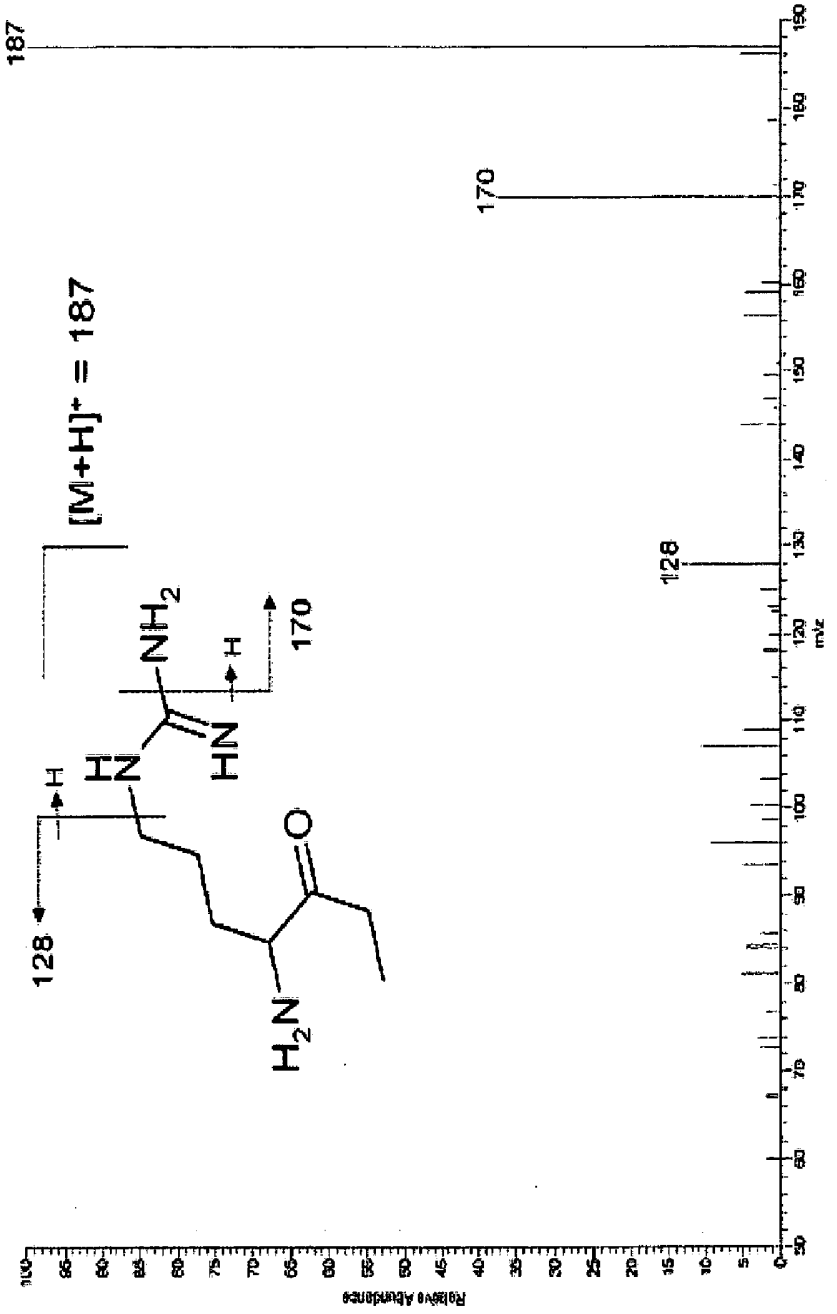

187
170
128
[M+H]+ = 187
NH2
H
170
HN
HN
H
128
O
H2N
m/z
Relative Abundance

FIGURE 5C

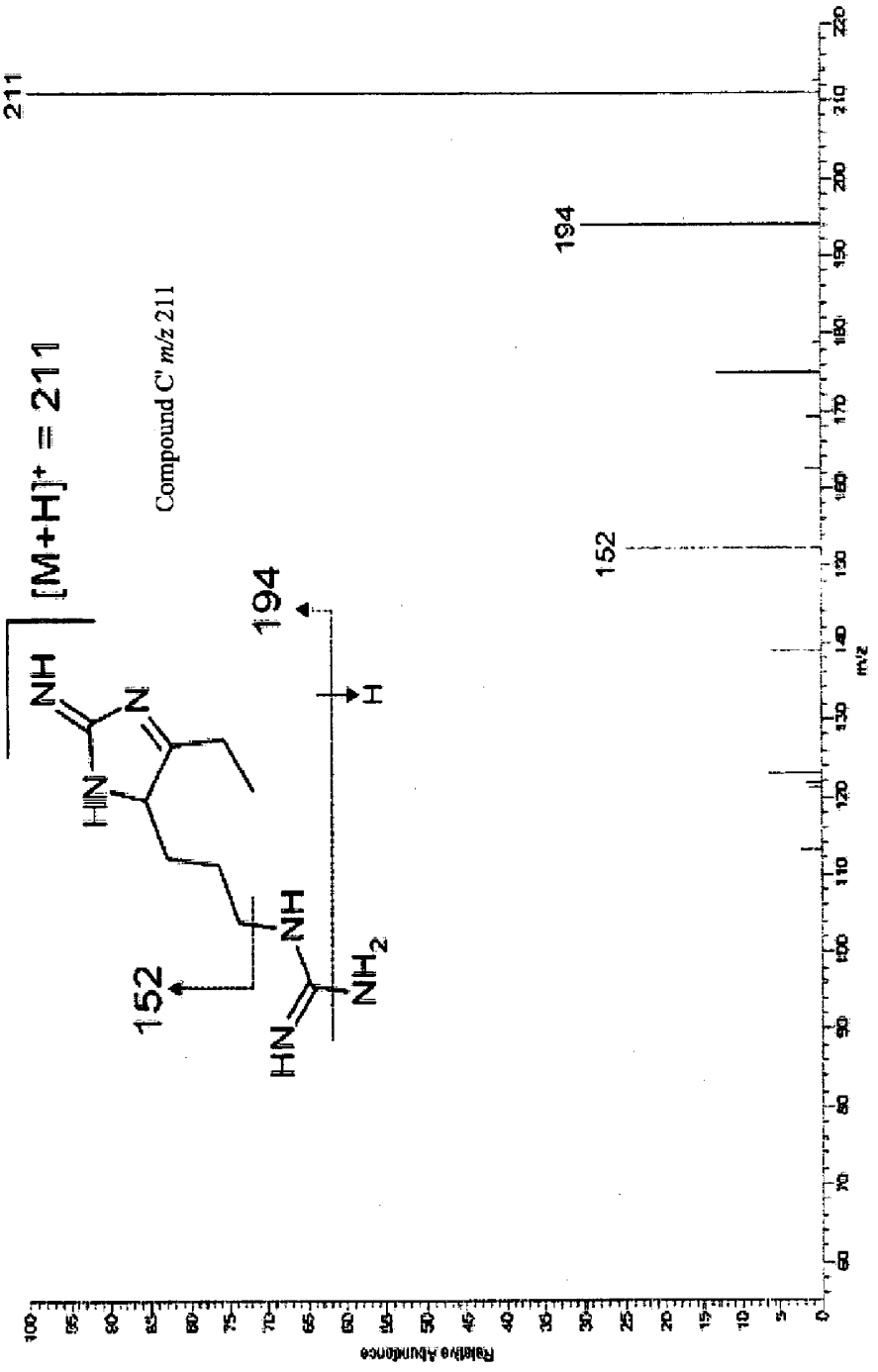

211
194
152
[M+H]+ = 211
Compound C' m/z 211
194
H
152
NH
N
HN
NH
NH2
HN
m/z
Relative Abundance

FIGURE 5D

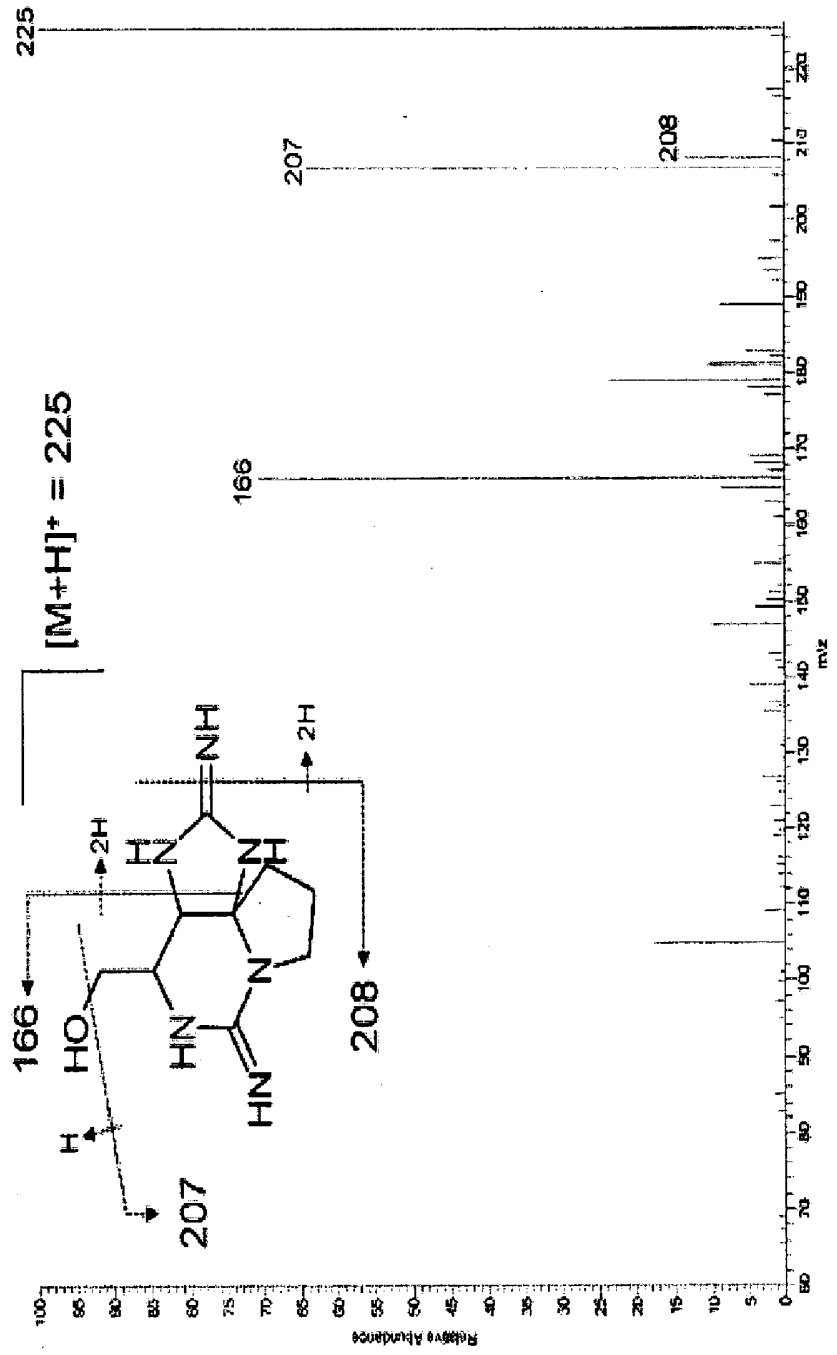

[M+H]+ = 225
225
207
208
166
m/z
Relative Abundance
166
208
207
2H
2H
HO
H
HN
NH
NH
HN
N

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

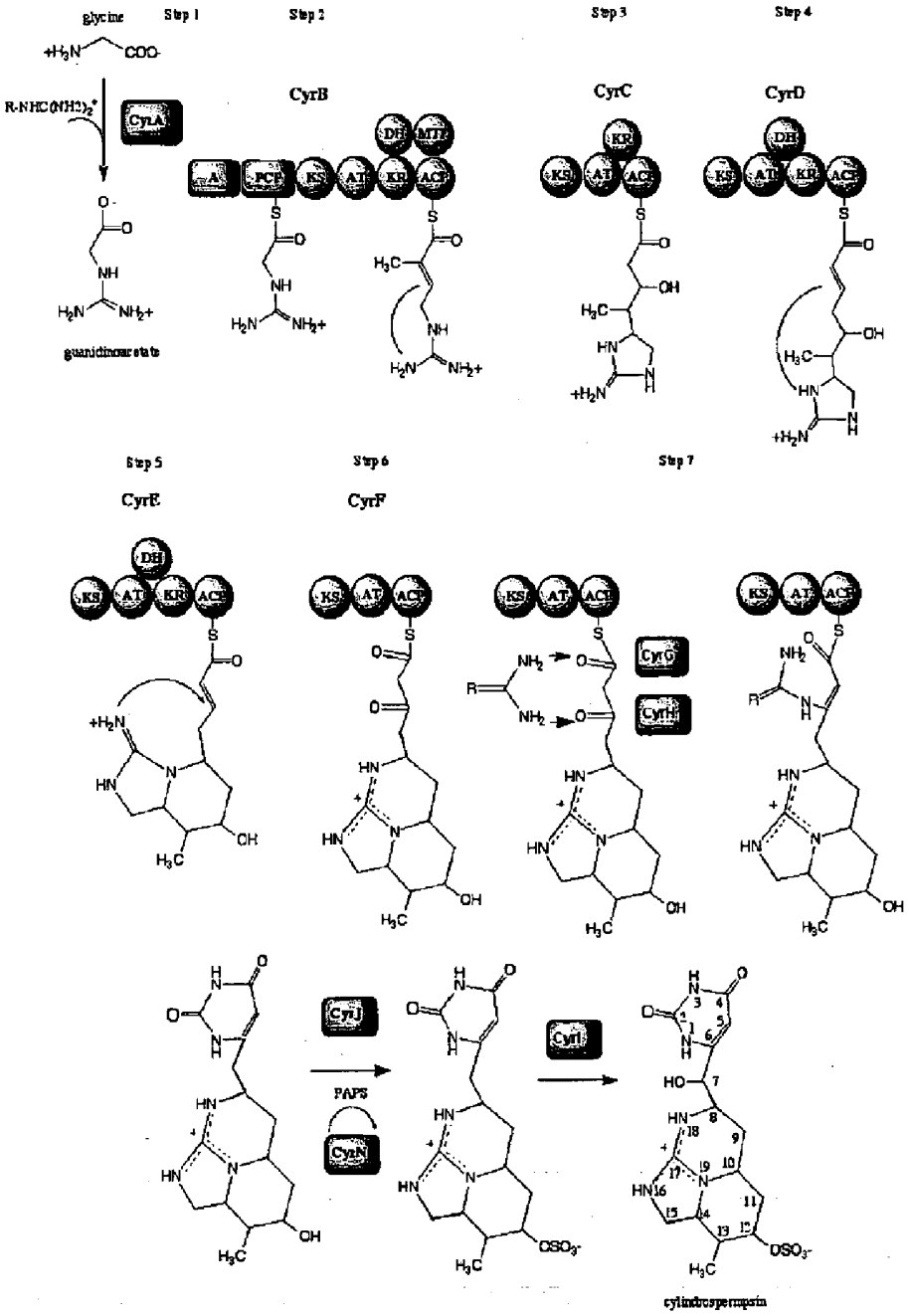

glycine
Step 1
Step 2
Step 3
Step 4
CyrA
CyrB
CyrC
CyrD
guanidinoacetate
Step 5
Step 6
Step 7
CyrE
CyrF
CyrG
CyrH
CyrJ
CyrI
CyrN
PAPS
cylindrospermopsin

FIGURE 8

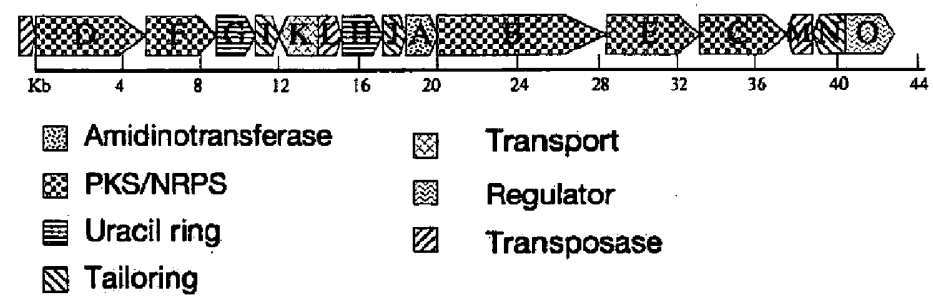

D
F
G
I
K
L
M
N
A
B
E
C
M
N
O
Kb
4
8
12
16
20
24
28
32
36
40
44
Amidinotransferase
PKS/NRPS
Uracil ring
Tailoring
Transport
Regulator
Transposase

FIGURE 9