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DESCRIPTION

BACKGROUND

[0001] Protein splicing is a post-translational process catalyzed by a family of proteins known as inteins.(1) During this process, an intein domain catalyzes its own excision from a larger precursor protein and simultaneously ligates the two flanking polypeptide sequences (exteins) together. While most inteins catalyze splicing in cis, a small subset of these proteins exist as naturally fragmented domains that are separately expressed but rapidly associate and catalyze splicing in trans. Given their capacity to make and break polypeptide bonds (inteins can be considered protein ligases), both cis and trans-splicing inteins have found widespread use as chemical biological tools.(2)

[0002] Despite the growing use of inteins in chemical biology, their practical utility has been constrained by two common characteristics of the family, namely (i) slow kinetics and (ii) context dependent efficiency with respect to the immediate flanking extein sequences.(3,4) Recently, a split intein from the cyanobacterium *Nostoc punctiforme* (Npu) was shown to catalyze protein trans-splicing on the order of a minute, rather than hours like most cis- or trans-splicing inteins.(5) Furthermore, this intein was slightly more tolerant of sequence variation at the critical +2 C-extein residue than other inteins.(6)

[0003] In addition to this finding, the following documents disclose facts regarding inteins and their uses. Neel H. Shah et al., (Journal of the American Chemical Society, 2012, vol. 134 no. 28, pages 11338-11341) discloses a kinetic analysis of the split DnaE inteins family and demonstrates that some of these inteins can catalyze protein trans-splicing in tens of seconds. The patent document WO 2009/132455 A1 reveals methods for producing fusion proteins that comprise a split intein N-fragment and a polypeptide. Yang J et al. (PNAS, 2002, vol. 100, no. 6, pages 3513-3518) refers to fusion proteins between a betaglucuronidase and N-fragments and/or C fragments of a DnaE intein of *Synechocystis* sp. strain PCC6B03. Neel H. Shah et al. (Angewandte Chemie International Edition, 2011 vol. 50, no. 29, pages 6511-6515) discloses the use of Npu_{wt} and a Npumut inteins for the generation of the full-length, active mammalian protein PARP1 through a one-pot three-piece ligation and demonstrates that electrostatic interactions can engender kinetic control in a complex enzymatic system. Finally, patent documents WO2011057163 and CN101333555 disclose fusion proteins between a polypeptide and a split intein N-fragment and methods of using split inteins in polypeptide modifications and patent documents WO2013045632A1 and CN101281201A disclose intein C-fragments and methods of using them.

[0004] However, a need still exists for more robust and more efficient split inteins for use in a variety of protein purification and protein modification applications.

SUMMARY

[0005] Provided herein is a method comprising

1. (a) contacting (1) a fusion protein comprising a polypeptide and a split intein N-fragment comprising a sequence selected from the group consisting of SEQ ID NO: 1-19, or a variant thereof, wherein the variant consists of a sequence selected from the group consisting of SEQ ID NO: 21-38 and 761 and (2) a split intein C-fragment comprising a sequence selected from the group consisting of SEQ ID NO: 57-74 and 708 or a variant thereof, wherein the variant consists of a sequence selected from the group consisting of SEQ ID NO: 75-128, 707 and 709-711, wherein contacting is performed under conditions that permit binding of the split intein N-fragment to the split intein C-fragment to form an intein intermediate; and
2. (b) contacting the intein intermediate with a nucleophile to form a conjugate of the protein and the nucleophile.

[0006] Provided herein is a complex comprising (i) a fusion protein comprising a split intein N-fragment and a polypeptide, wherein the split intein N-fragment comprises a sequence selected from the group consisting of SEQ ID NOs: 6, 1-5, 7-38 and 761, and (ii) a split intein C-fragment comprising a sequence selected from the group consisting of SEQ ID NOs: 57-128, 417-704, 707-711 or 745-759.

BRIEF DESCRIPTIONS OF THE DRAWINGS

[0007]

Figure 1 shows *trans*-splicing of split DnaE inteins. (a) Scheme depicting protein *trans*-splicing of the KanR protein with a variable local C-extein sequence. (b) *In vivo* relative *trans*-splicing efficiencies at 30°C with the endogenous "CFN" C-extein sequence and exogenous "CGN", "CEN", and "CRN" sequences. IC₅₀ values ($\pm$ SE, n = 3-4) are normalized relative to that of intact KanR proteins with the appropriate C-extein tri-peptide.

Figure 2 shows *in vitro* half-lives of *trans*-splicing reactions. Indicated split intein pairs fused to model exteins Ub or SUMO (Ub-Int^N and Int^C-SUMO) were mixed at either 30°C or 37°C, and the formation of products was monitored over time by gel electrophoresis. (a) Half-lives were extracted from the reaction progress curves fit to a standard first-order rate equation ($\pm$ SE, n = 3). Representative coomassie-stained SDS-PAGE gels showing (b) fast Ava splicing at 37°C and (c) inefficient Ssp splicing at 37°C.

Figure 3 shows sequence-activity relationships in split DnaE inteins. (a) Inteins in order of *in vivo* splicing activity with selected slices from the corresponding multiple sequence alignment. (b) Rendering of the Npu structure highlighting the proximity of position 120 to the terminal

catalytic residues C1 and N137. (c) *In vivo* analysis of the C120G mutation in the Aha intein ($\pm$ SD, $n = 3$). (d) Rendering of the Npu structure highlighting key catalytic residues (sticks) and important non-catalytic positions (spheres) that modulate Ssp activity. (e) *In vivo* analysis of Ssp-to-Npu point mutations that improve Ssp activity ($\pm$ SD, $n = 4$). Note that all residue numberings correspond to the relevant positions on Npu as defined by the NMR structure (PDB: 2KEQ).(21)

Figure 4 shows engineered versions of ultrafast DnaE inteins support efficient expressed protein ligation. (a) Scheme depicting the formation of the linear thioester intermediate and its use to generate a protein α -thioester for EPL. (b) Coomassie-stained SDS-PAGE gel depicting efficient MESNa thiolysis of ubiquitin from a fused AvaDnaE intein to yield the Ub-MES thioester, 4. (c) Fluorescent SDS-PAGE gels showing the formation of the Ub-CGK(Fluorescein) ligated product (6) from one-pot thiolysis and native chemical ligation reactions using the inteins indicated. (d) Reverse phase HPLC chromatographs showing pH dependence of the relative populations of precursor amide (1) and linear thioester (2).

Figure 5 shows sequence alignments of split DnaE inteins. Numbering follows that of Npu as assigned for the NMR structure (PDB 2KEQ). Critical catalytic residues are marked with an asterisk.

Figure 6 shows sequence logos for high- and low-activity inteins. Inteins are ranked based on *in vivo* activity with a "CFN" C-extein sequence. The high and low activity inteins are distinguished based on a cut-off IC_{50} value of 350 μ g/mL of kanamycin, and the Aha intein is included in the high-activity set, given that the C¹²⁰G mutation dramatically restores high activity.

Figure 7 shows purification of C-terminal α -thioesters using split-inteins. A) Scheme of the split-intein based purification of protein C-terminal α -thioesters. B) Sequence of WT Npu^C and its mutant Npu^C-AA having a linker to immobilize it onto a solid support (underlined). For the thiolysis experiments in solution the C-terminal Cys residue was previously alkylated with iodoacetamide.

Figure 8 shows Purification of soluble protein α -thioesters using the Npu^C-AA affinity column. A) Scheme of the purification strategy using split Npu DnaE intein. B) Purification of Ub-thioester (Ub-COSR) from cell lysates. C) Purification of MBP-thioester (MBP-COSR) from cell lysates. Both purifications were monitored by SDS-PAGE analysis stained with Coomassie (top) or Western Blot using an α -His antibody.

Figure 9 shows RP-HPLC and MS analysis of Ub and MBP α -thioesters. A) RP-HPLC (top) and MS (bottom) analysis of Ub-COSR eluted from the Npu^C-AA column. B) RP-HPLC (top) and MS (bottom) analysis of MBP-COSR eluted from the Npu^C-AA column.

Figure 10 shows the effect of the -1 residue on the efficiency of the on-resin thiolysis. 20 different Ub-Npu^N proteins were expressed containing each of the 20 proteinogenic amino

acids at the C-terminus of Ub (-1 residue) and purified over Npu^C-AA columns. Cleavage yields from the Npu^C-AA column were estimated by gel electrophoresis and amounts of thioester versus side reactions (mainly hydrolysis) were determined by RP-HPLC and MS analysis.

Figure 11 shows purification of H2B(1-116)- α -thioester under denaturing conditions. A) SDS-PAGE analysis of the purification of H2B(1-116) α -thioester over the Npu^C-AA column in the presence of 3 M urea. RP-HPLC (B) and MS (C) analysis of E1 from panel A confirmed the presence of the desired H2B thioester.

Figure 12 shows purification of α DEC thioesters expressed in 293T cells using the split-intein column. A) Expression levels of α DEC fused to different inteins in 293T cells. B) Purification of α DEC α -thioester through the Npu^C-AA affinity column. C) Expressed Protein Ligation (EPL) of α DEC-thioester with an N-terminal Cys containing fluorescent peptide.

Figure 13 shows EPL directly using Int^C-column eluted thioesters. RP-HPLC (30-73%B gradient, 214 nm and 440 nm detection) and MS analysis of the reactions between the H-CGK(F1)-NH₂ peptide and MBP (A) and PHPT1 (B) MES thioesters, purified from *E. coli* using the Int^C-column.

Figure 14 shows a one-pot purification/ligation experiment of ubiquitin to the H-CGK(Fluorescein)-NH₂ peptide (CGK(FI)). Ub-Npu^N from *E. coli* cell lysates was bound to the Int^C-column, and after removal of contaminants through extensive washes, intein cleavage and ligation were triggered by addition of 200 mM MES and 1 mM CGK(FI) peptide. Coomassie stained SDS-PAGE analysis and in gel fluorescence of the purification/ligation (left). RP-HPLC (detection at 214 and 440 nm) and ESI-TOF MS (right) of the eluted fractions confirms the desired ligated protein was obtained in one step directly from cell lysates with a ligation yield close to 95% (quantified by RP-HPLC).

Figure 15 shows the semi-synthesis of H2B-K120Ac under denaturing conditions. A) Coomassie stained SDS-PAGE analysis of H2B(1-116) α -thioester generation in the presence of 2 M urea (sup: cell lysate supernatant, trit: 1% triton wash of the inclusion bodies, inp: solubilized inclusion bodies used as input for the Int^C-column). E1-E6 were pooled, concentrated to 150 μ M and ligated to the peptide H-CVTK(Ac)YTSK-OH at 1 mM for 3 h at r.t. B) RP-HPLC (left) of the ligation reaction mixture and MS (right) of the ligated H2B-K120Ac product.

Figure 16 shows the characterization of α DEC205 ligated to the H-CGK(Fluorescein)-NH₂ peptide (CGK(F1)). Elution fractions from the Npu^C-column containing α DEC205-MES thioester were concentrated to 20 μ M and ligated to the CGK(F1) fluorescent peptide at 1 mM for 48 h at r.t. A) ESI-TOF MS analysis of deglycosylated and fully reduced HC after ligation, showing 75% of the HC are labeled. Expected mass for ligation product = 50221.2 Da. Free HC = 49575.0 Da. B) SEC-MALS analysis of the ligated antibody showing that it retains its tetrameric structure after thiolysis and ligation (MW = 151 kDa, MW calc = 148 kDa). C) Binding of

α DEC205-CGK(F1) to the DEC205 receptor. Dose dependent binding of α DEC205-CGK(F1) (left) or a control α -DEC205 antibody (right) to CHO cells expressing the mouse DEC205 receptor monitored by flow cytometry using a PE labeled α -mouse IgG. Binding to control CHO/NEO cells, which don't express the receptor is shown in gray.

Figure 17 shows purification of α DEC thioesters expressed in CHO cells using a split-intein column. Top) Coomassie stained SDS-PAGE gel of the purification of α DEC-MES thioester from CHO cells using an Npu^C-column. Bottom) Western blot analysis of the same purification.

Figure 18 shows purification of α DEC thioesters using an Ava^C split-intein column and Western blot analysis of the purification of α DEC thioesters from mammalian cell supernatants using an Ava^C-column.

Figure 19 shows expression tests of α DEC205 antibody fused to Ava^N split intein through the C-terminus of the antibody light chain and western blot analysis of CHO cell supernatants expressing the α DEC205-AvaN fusion at different timepoints.

DETAILED DESCRIPTION

[0008] Of the roughly 600 inteins currently catalogued, (7) less than 5% are split inteins, mostly from a family known as the cyanobacterial split DnaE inteins (8). Surprisingly, only six of these, including Npu, have been experimentally analyzed to any extent, (6,9,10) and only Npu and its widely-studied, low-efficiency ortholog from *Synechocystis* species PCC6803 (Ssp) have been rigorously characterized *in vitro*.(5,11)

[0009] A rapid survey of 18 split DnaE inteins was performed using an *in vivo* screening method to accurately compare the efficiencies of split inteins(12,13) In this assay, the two fragments of a split intein are co-expressed in *E. coli* as fusions to a fragmented aminoglycoside phosphotransferase (KanR) enzyme. Upon trans-splicing, the active enzyme is assembled, and the bacteria become resistant to the antibiotic kanamycin (Figure 1a). More active inteins confer greater kanamycin resistance and thus have a higher IC₅₀ value for bacterial growth as a function of kanamycin concentration. This assay can be carried out in the background of varying local C-extein sequences without significantly perturbing the dynamic range. Since all DnaE inteins splice the same local extein sequences in their endogenous context, this screen was originally carried out in a wild-type C-extein background (CFN) within the KanR enzyme. As expected, bacteria expressing the Npu intein had a high relative IC₅₀, whereas clones expressing Ssp showed poor resistance to kanamycin. Remarkably, more than half of the DnaE inteins showed splicing efficiency comparable to Npu *in vivo* at 30°C (Figure 1b).

[0010] To confirm that the high IC₅₀ values observed *in vivo* reflected rapid trans-splicing, a

series of kinetic studies were performed under standardized conditions *in vitro*. For this, individually expressed and purified split DnaE intein fragments fused to model N- and C-extein domains, ubiquitin and SUMO were made. The endogenous local extein residues were preserved as linkers between the extein domains and intein fragments to recapitulate a wild-type-like splicing context. Cognate intein fragments were mixed at 1 μ M, and the formation of the Ub-SUMO spliced product at 30°C and 37°C was monitored by gel electrophoresis. These assays validated that the new inteins with high-activity *in vivo* could catalyze trans-splicing *in vitro* in tens of seconds, substantially faster than Ssp (Figure 2a). Interestingly, all of the inteins analyzed except Ssp showed increased splicing rates at 37°C. Furthermore, all of the fast-splicing inteins showed low-to-undetectable levels of side reactions (Figure 2b), again in contrast to Ssp (Figure 2c).

[0011] The tolerance of the split inteins to C-extein sequence variation was investigated. Previously, the sensitivity of DnaE inteins was noted to changes at the +2 position in the C-extein.(6,12) Thus, all the split DnaE inteins were analyzed in the presence of a +2 glycine (CGN), glutamic acid (CEN), or arginine (CRN) in the *in vivo* screening assay (Figure 1b). Like Npu and Ssp, most of the inteins showed a dramatic decrease in activity in the presence of all three +2 mutations. Of the tested amino acids, glutamic acid was tolerated best for every intein, suggesting a conserved mechanism for accommodating a negative charge at this position. To more accurately assess the magnitude of the effect of C-extein mutations on trans-splicing, the Npu, Cra(CS505), and Cwa inteins were analyzed *in vitro* in the presence of a +2 glycine. All three of these reactions were characterized by rapid accumulation of thioester intermediates, which slowly resolved over tens of minutes into the spliced product and the N-extein cleavage product. Consistent with previously reported observations, these data indicate that split DnaE inteins require steric bulk at the +2 position for branched intermediate resolution and efficient splicing.(12) It is noteworthy that the Cra(CS505) and Cwa inteins showed greater C-extein promiscuity *in vivo*, while Ssp(PCC7002) did not tolerate any of the mutations tested. This demonstrates that subtle sequence variation between split inteins can afford differential promiscuity. Thus, this property may be further optimized through directed evolution(12) or rational design.

[0012] These data indicate that the split DnaE inteins are highly divergent in activity, despite all having evolved to catalyze trans-splicing on virtually identical substrates. Interestingly, the key catalytic residues involved in splicing are conserved across the entire family (Figure 5). Thus, residues that affect splicing activity are non-catalytic and perhaps only moderately conserved. The measurements of relative activity can facilitate the discovery of specific sequence features that differentiate high-activity inteins from inefficient ones. Indeed, sequence homology analysis indicates that inteins with high activity are more homologous to one another than they are to the low-activity inteins. One significant outlier to this observation is the intein from *Aphanothece halophytica* (Aha), which despite having greater than 65% sequence identity to the high-activity inteins, was inactive with the wild-type "CFN" C-extein motif *in vivo*. Closer inspection of a multiple sequence alignment indicated that this intein has a non-catalytic cysteine (position 120) in place of an otherwise absolutely conserved glycine (Figure 3a). Furthermore, this position is close to the intein active site, where an extra nucleophile may

facilitate undesirable side reactions (Figure 3b). Gratifyingly, mutating this cysteine to glycine reinstated high activity in the Aha intein whilst the reverse mutation destroyed the splicing activity of Npu (Figure 3c), validating the predictive capacity of these data.

[0013] Further analysis of the split intein sequence alignment indicated that several positions have strong amino acid conservation amongst the high-activity inteins but diverge for the low-activity inteins (Figures 3a, 6). These may be sites where the fast inteins have retained beneficial interactions that have been lost in slow ones. To test this idea, several positions were chosen where this sequence-activity correlation was apparent and replaced the residue in Ssp with the corresponding amino acid found in the fast inteins. Consistent with this hypothesis, several point mutations increased the activity of Ssp *in vivo* (Figures 3e). While the specific roles of these residues are not explicitly clear, especially given that they lie outside of the active site (Figure 3d), their locations on the intein fold (14) may provide some insights into their function. For example, at position 56, an aromatic residue is preferred in the high-activity inteins. This position is adjacent to the conserved catalytic TXXH motif (positions 69-72), and an aromatic residue may facilitate packing interactions to stabilize those residues. Similarly, a glutamate is preferred at position 122, proximal to catalytic histidine 125. The glutamate at position 89 is involved in an intimate ion cluster that was previously shown to be important for stabilizing the split intein complex.(13) Interestingly, E23 is distant from the catalytic site and has no obvious structural role. This position is conceivably important for fold stability or dynamics as has previously been observed for activating point mutations in other inteins. (15,16)

[0014] The discovery of new, fast trans-splicing inteins has broad implications for protein chemistry. Indeed, the discovery of Npu fueled a resurgence in the use of split intein-based technologies.(13,17,18) While no single intein may be ideal for every protein chemistry endeavor, the availability of several new fast-splicing split inteins can provide options to enhance the efficiency of most trans-splicing applications. For example, one common problem in working with split inteins is low expression yield or poor solubility of an intein fragment fusion to a protein of interest. Indeed, the over-expression and purification efforts here show that the Ub-IntN and IntC-SUMO fusions have markedly different yields of soluble expression, depending on the intein. Thus, a short-list of highly active split inteins with varying behavior will serve as starting point for empirical optimization of a given trans-splicing application.

[0015] Furthermore, the fragments of the different fast-splicing split inteins can be mixed as non-cognate pairs and still retain highly efficient splicing activity, further expanding the options available for any trans-splicing application. For example, the N-fragment split intein of Npu or variant thereof can bind to the C-fragment of Npu or variant thereof or any of the other split intein C-fragments or variants discussed below. Similarly, the N-fragment of Ssp or variant thereof can bind to the C-fragment of Ssp or variant thereof or any of the other split intein C-fragments or variants thereof discussed below; the N-fragment of Aha or variant thereof can bind to the C-fragment of Aha or variant thereof or any of the other split intein C-fragments or variants thereof discussed below; the N-fragment of Aov or variant thereof can bind to the C-fragment of Aov or variant thereof or any of the other split intein C-fragments or variants

thereof discussed below; the N-fragment of Asp or variant thereof can bind to the C-fragment of Asp or variant thereof or any of the other split intein C-fragments or variants thereof discussed below; the N-fragment of Ava or variant thereof can bind to the C-fragment of Ava or variant thereof or any of the other split intein C-fragments or variants thereof discussed below; the N-fragment of Cra(CS5505) or variant thereof can bind to the C-fragment of Cra(CS5505) or variant thereof or any of the other split intein C-fragments or variants thereof discussed below; the N-fragment of Csp(CCY0110) or variant thereof can bind to the C-fragment of Csp(CCY0110) or variant thereof or any of the other split intein C-fragments or variants thereof discussed below; the N-fragment of Csp(PCC8801) or variant thereof can bind to the C-fragment of Csp(PCC8801) or variant thereof or any of the other split intein C-fragments or variants thereof discussed below; the N-fragment of Cwa or variant thereof can bind to the C-fragment of Cwa or variant thereof or any of the other split intein C-fragments or variants thereof discussed below; the N-fragment of Maer(NIES843) or variant thereof can bind to the C-fragment of Maer(NIES843) or variant thereof or any of the other split intein C-fragments or variants thereof discussed below; the N-fragment of Mcht(PCC7420) or variant thereof can bind to the C-fragment of Mcht(PCC7420) or variant thereof or any of the other split intein C-fragments or variants thereof discussed below; the N-fragment of Oli or variant thereof can bind to the C-fragment of Oli or variant thereof or any of the other split intein C-fragments or variants thereof discussed below; the N-fragment of Sel(PC7942) or variant thereof can bind to the C-fragment of Sel(PC7942) or variant thereof or any of the other split intein C-fragments or variants thereof discussed below; the N-fragment of Ssp(PCC7002) or variant thereof can bind to the C-fragment of Ssp(PCC7002) or variant thereof or any of the other split intein C-fragments or variants thereof discussed below; the N-fragment of Tel or variant thereof can bind to the C-fragment of Tel or variant thereof or any of the other split intein C-fragments or variants thereof discussed below; the N-fragment of Ter or variant thereof can bind to the C-fragment of Ter or variant thereof or any of the other split intein C-fragments or variants thereof discussed below; and the N-fragment of Tvu or variant thereof can bind to the C-fragment of Tvu or variant thereof or any of the other split intein C-fragments or variants thereof discussed below.

[0016] The most widely used intein-based technology, expressed protein ligation, exploits *cis*-acting inteins to generate recombinant protein α -thioester derivatives.(2) In principle, any split intein can be artificially fused and then utilized as a *cis*-splicing intein in this application (1 in Figure 4a). Ultrafast split inteins are especially attractive in this regard due to their speed and efficiency. To test this notion, artificially fused variants of Npu, Ava, and Mcht with an N-terminal ubiquitin domain were generated. To prevent splicing, premature C-terminal cleavage or undesired high levels of competing hydrolysis residues Asn137 and Cys+1 were mutated to Ala. Upon reaction with the exogenous thiol sodium 2-mercaptoethanesulfonate (MESNa), the fused DnaE inteins were rapidly cleaved to generate the ubiquitin α -thioester, 4, in a few hours (Figures 4b). By contrast, MESNa thiolysis of the commonly used MxeGyrA intein was not complete even after one day under identical conditions. The fused DnaE inteins were sufficiently fast to allow for a one-pot thiolysis and native chemical ligation reaction with an N-terminal cysteine-containing fluorescent peptide, 5, to give semisynthetic protein 6 (Figure 4c). Furthermore, these inteins could be used to efficiently generate α -thioesters of four other

structurally unique proteins domains with different C-terminal amino acid residues. These results demonstrate that fused versions of split DnaE inteins will be of general utility for protein semisynthesis.

[0017] The rapid rate of thiolysis observed for the fused DnaE inteins has mechanistic implications as well as practical ones. Without wishing to be bound by theory, one possible explanation for their enhanced reactivity over the MxeGyrA intein is that these inteins drive the N-to-S acyl shift reaction more efficiently, generating a larger population of the reactive linear thioester species 2 (Figure 4a). This thioester intermediate is generally thought to be transiently populated in protein splicing, and to our knowledge, it has never been directly observed.⁽¹⁾ Surprisingly, when analyzing the ubiquitin-DnaE intein fusions by reverse phase HPLC, two major peaks and a third minor peak were often observed, all bearing the same mass. The relative abundance of these species could be modulated by unfolding the proteins or by changes in pH, and the two major species were almost equally populated from pH 4-6 (Figure 4d). The major peaks most likely correspond to the precursor amide, 1, and the linear thioester, 2, and the minor peak as the tetrahedral oxythiazolidine intermediate. Importantly, only a single HPLC peak was seen for the ubiquitin-MxeGyrA fusion under identical conditions. These observations, along with the enhanced thiolysis rates, strongly support the notion that these DnaE inteins have a hyper-activated N-terminal splice junction.

[0018] Splicing activities in an entire family of split inteins has been characterized. Ultrafast protein trans-splicing may be the norm, rather than the exception, in this family. Furthermore, different split inteins have varying degrees of tolerance for C-extein mutations, suggesting that traceless protein splicing may be attainable by modestly engineering any highly active intein. A thorough comparison of the activities of a small family of homologous proteins can be used to identify important non-catalytic positions that modulate activity. Finally, by artificially fusing split DnaE intein fragments, new constructs have been provided for the efficient synthesis of protein α -thioesters used in expressed protein ligation. These results will guide the development of improved protein chemistry technologies and should lay the groundwork towards a more fundamental understanding of efficient protein splicing.

Fusion Proteins of Split Intein N-Fragment (not covered by the claimed invention)

[0019] Disclosed herein are fusion proteins of a polypeptide and a split intein N-fragment. As used herein, the term "polypeptide" refers to any amino acid based polymer, interchangeable referred to as a "protein" throughout, and can include glycoproteins and lipoproteins. In some cases, the polypeptide is a polypeptide excreted from a cell (e.g., a mammalian cell). In various cases, the polypeptide is an antibody or a fragment thereof. The polypeptide can be any naturally occurring or synthetic polypeptide of interest, including polypeptides having one or more amino acid residues other than the 20 naturally occurring amino acids.

[0020] In some cases, the polypeptide has a molecular weight of 45 kDa or greater, 50 kDa or greater, 60 kDa or greater, 75 kDa or greater, 100 kDa or greater, 120 kDa or greater, or 150

kDa or greater. The polypeptide can be, e.g., an antibody or a fragment thereof. In cases of antibodies, the split intein N-fragment can be fused to one or both of the heavy chains, and/or to one or both of the light chains. In some cases, the polypeptide is a protein secreted from a cell, e.g., a mammalian cell.

[0021] The split intein N-fragment comprises a sequence as shown in Figure 5, e.g., Npu (SEQ ID NO: 1), Ssp (SEQ ID NO: 2), Aha (SEQ ID NO: 3), Aov (SEQ ID NO: 4), Asp (SEQ ID NO: 5), Ava (SEQ ID NO: 6), Cra(CS505) (SEQ ID NO: 7), Csp(CCY0110) (SEQ ID NO: 8), Csp(PCC8801) (SEQ ID NO: 9), Cwa (SEQ ID NO: 10), Maer(NIES843) (SEQ ID NO: 11), Mcht(PCC7420) (SEQ ID NO: 12), Oli (SEQ ID NO: 13), Sel(PC7942) (SEQ ID NO: 14), Ssp(PCC7002) (SEQ ID NO: 15), Tel (SEQ ID NO: 16), Ter (SEQ ID NO: 17), Tvu (SEQ ID NO: 18), or a variant thereof. In some cases, the split intein N-fragment sequence comprises a sequence other than Npu (SEQ ID NO: 1) or Ssp (SEQ ID NO: 2), and in other cases, comprises a sequence other than Npu (SEQ ID NO: 1), Ssp (SEQ ID NO: 2), or Aha (SEQ ID NO: 3). In some specific cases, the split intein N-fragment sequence comprises a sequence of Ava (SEQ ID NO: 6), Cra (SEQ ID NO: 7), Csp(PCC8801) (SEQ ID NO: 9), Cwa (SEQ ID NO: 10), Mcht(PCC7420) (SEQ ID NO: 12), Oli (SEQ ID NO: 13), Ter (SEQ ID NO: 17) and Tvu (SEQ ID NO: 18). In some cases, the split intein N-fragment has a sequence comprising a consensus sequence of SEQ ID NO: 19:

(CLSYDTEILTVEYGAVPIGKIVEENIECTVYSVDENGFVYTQPIAQWHDRGEQEVFE
YCLEDGSTIRATKDHKFMTEDEMLPIDEIFEQGLDLKQVKGLPD).

[0022] As used herein, a variant of a split intein N-fragment is a mutated split intein N-fragment as disclosed herein that maintains the activity of the split intein N-fragment (e.g., its ability to bind to a split intein C-fragment and/or catalyze nucleophilic attack of the polypeptide fused to it). Contemplated variants of a split intein N-fragments disclosed herein include mutation of one or more C residues, except for Cys1, to an aliphatic residue, such as an A, I, L, or F, or to a S residue. One such variant contemplated is a mutant Npu with Cys28 and Cys59 mutated to Ser, SEQ ID NO: 20

(CLSYETEILTVEYGLLPKIVEKRIESTVYSVDNNGNIYTQPVAQWHDRGEQEVFEY
SLEDGSLIRATKDHKFMTEVDGQMLPIDEIFERELDLMRVDNLPN).

Mutated Split Intein C-Fragments and Binding to a Support (not covered by the claimed invention)

[0023] The split intein C-fragments disclosed herein are mutated from the naturally occurring sequences to mutate the N137 and C+1 residues to a residue other than Asn or Gln for N137 and a residue other than Cys for C+1 (SEQ ID NOs: 129-146). In some cases, the mutations at these two positions are to a hydrophobic residue, e.g., not containing a free SH thiol (Cys), a carboxylic acid (Asp, Glu), or a base (Arg, His, Lys) or other undesired group (e.g., Asn, Gln)

on the side chain. In various cases, the two mutated aliphatic residues can be the same or different and can be A, V, I, S, M, H, L, F, Y, G, or W or can be an unnatural (e.g., not encoded by genetic code) aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, norvaline, 2-aminopentanoic acid, or 2-aminohexanoic acid (SEQ ID NOs: 219-236). Specifically contemplated are mutations where both residues are selected from A, I, V, L, Y, G and F (SEQ ID NOs: 309-326). In various cases, at least one of the two mutated residues is A.

[0024] Thus, provided herein is a mutated split intein C-fragment comprising a mutation at N137 and Cys+1 of Npu (SEQ ID NOs: 129, 147, 165, 183, 201, 219, 237, 255, 273, 291, 309, 327, 345, 363, 381 and 399), Ssp (SEQ ID NOs: 130, 148, 166, 184, 202, 220, 238, 256, 274, 292, 310, 328, 346, 364, 382 and 400), Aha (SEQ ID NOs: 131, 149, 167, 185, 203, 221, 239, 257, 275, 293, 311, 329, 347, 365, 383 and 401), Aov (SEQ ID NOs: 132, 150, 168, 186, 204, 222, 240, 258, 276, 294, 312, 330, 348, 366, 384 and 402), Asp (SEQ ID NOs: 133, 151, 169, 187, 205, 223, 241, 259, 277, 295, 313, 331, 349, 367, 385 and 403), Ava (SEQ ID NOs: 134, 152, 170, 188, 206, 224, 242, 260, 278, 296, 314, 332, 350, 368, 386 and 404), Cra(CS505) (SEQ ID NOs: 135, 153, 171, 189, 207, 225, 243, 261, 279, 297, 315, 333, 351, 369, 387 and 405), Csp (CCY0110) (SEQ ID NOs: 136, 154, 172, 190, 208, 226, 244, 262, 280, 298, 316, 334, 352, 370, 388 and 406), Csp(PCC8801) (SEQ ID NOs: 137, 155, 173, 191, 209, 227, 245, 263, 281, 299, 317, 335, 353, 371, 389 and 407), Cwa (SEQ ID NOs: 138, 156, 174, 192, 210, 228, 246, 264, 282, 300, 318, 336, 354, 372, 390 and 408), Maer(NIES843) (SEQ ID NOs: 139, 157, 175, 193, 211, 229, 247, 265, 283, 301, 319, 337, 355, 373, 391 and 409), Mcht(PCC7420) (SEQ ID NOs: 140, 158, 176, 194, 212, 230, 248, 266, 284, 302, 320, 338, 356, 374, 392 and 410), Oli (SEQ ID NOs: 141, 159, 177, 195, 213, 231, 249, 267, 285, 303, 321, 339, 357, 375, 393 and 411), Sel(PC7942) (SEQ ID NOs: 142, 160, 178, 196, 214, 232, 250, 268, 286, 304, 322, 340, 358, 376, 394 and 412), Ssp(PCC7002) (SEQ ID NOs: 143, 161, 179, 197, 215, 233, 251, 269, 287, 305, 323, 341, 359, 377, 395 and 413), Tel (SEQ ID NOs: 144, 162, 180, 198, 216, 234, 252, 270, 288, 306, 324, 342, 360, 378, 396 and 414), Ter (SEQ ID NOs: 145, 163, 181, 199, 217, 235, 253, 271, 289, 307, 325, 343, 361, 379, 397 and 415), or Tvu (SEQ ID NOs: 146, 164, 182, 200, 218, 236, 254, 272, 290, 308, 326, 344, 362, 380, 398 and 416), where the mutation at N137 and Cys+1 is a naturally occurring or unnatural hydrophobic residue. In some specific cases, at least one of the mutations is A (SEQ ID NOs: 183-200, 255-272, 327-344, and 345-416) and in more specific cases, both mutations are A (SEQ ID NOs: 399-416).

[0025] A variety of supports can be used. Generally, the solid support is a polymer or substance that allows for linkage of the split intein C-fragment, optionally via a linker. The linker can be further amino acid residues engineered to the C-terminus of the split intein C-fragment or can be other known linkers for attachment of a peptide to a support. One contemplated linker is a small peptide -SGGC (SEQ ID NO: 705), where the thiol of the C-terminal Cys can be used to attach the split intein C-fragment to the support. Thus, specifically contemplated are mutated split intein C-fragments of the Npu, Ssp, etc. sequences noted above having a -SGGC peptide linker (SEQ ID NO: 705) (e.g., specifying the residues starting at the N137 position: AAFN-SGGC) (SEQ ID NO: 706). The length of a peptide linker can be modified to provide varying lengths and flexibility in any individual situation (e.g., more than 2 Gly residues). It will

also be apparent that the C-terminus residue of a peptide linker can be modified to introduce an appropriately reactive functional group to attach the split intein C-fragment to a surface of choice (e.g., Lys to react via an amine, Cys to react via a thiol, or Asp or Glu to react via a carboxylic acid). Other, unnatural amino acid residues are also contemplated for use in a peptide linker to provide other functional group moieties to allow for different attachment chemistry of the C-fragment to a support of interest (e.g., azide, alkynes, carbonyls, amino-oxy, cyano-benzothiazoles, tetrazoles, alkenes, alkylhalides). The linker can alternatively be a polymeric linker.

[0026] Based upon an analysis of the sequences of the highly active split intein C-fragments investigated, a consensus sequence for the split intein C-fragment is derived: SEQ ID NO: 707 (VKIISRQSLGKQNVYDIGVEKDHNFLLANGLIASN), as well as a mutated version where the N137 is mutated to other than Asn or Gln (SEQ ID NO:708), or more specifically, N137 is mutant to a naturally occurring or unnaturally occurring hydrophobic residue, such as A, V, I, M, H, L, F, Y, G, S, H, or W or can be a unnatural (e.g., not encoded by genetic code) aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentanoic acid, or 2-aminohexanoic acid (SEQ ID NO: 709). Specifically contemplated mutations at N137 for the consensus sequences include A, I, V, L, Y, G, and F (SEQ ID NO: 710). Also contemplated is where N137 is mutated to A (SEQ ID NO: 711).

[0027] Further contemplated are variants of the consensus sequence having a residue at the +1 position other than Cys (SEQ ID NOs: 712, 716, 720, and 724). More specifically the +1 position can be a naturally occurring or unnaturally occurring hydrophobic residue such as A, V, I, M, H, L, F, Y, G, S, H, or W or can be a unnatural (e.g., not encoded by genetic code) aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentanoic acid, or 2-aminohexanoic acid (SEQ ID NOs: 713, 717, 721, and 725). Specifically contemplated are mutation at +1 position is selected from A, I, V, L, Y, G, and F (SEQ ID NOs: 714, 718, 722, and 726). In various cases, at least one of the mutated residues of the consensus sequence is A (SEQ ID NOs: 715, 719, and 723). In some cases, the consensus C-fragment sequence has both mutations as Ala (SEQ ID NO:727). Further contemplated is a consensus sequence comprising FN at the +2 and +3 positions (SEQ ID NO:728-743). Also contemplated is a consensus sequence comprising a peptide linker for attachment to a solid support, and one example is -SGGC at positions +4-+7 (SEQ ID NO: 744-759).

[0028] The split intein C-fragment or variant thereof as disclosed herein can be attached to a solid support via a linker. In various cases, the linker is a polymer, including but not limited to a water-soluble polymer, a nucleic acid, a polypeptide, an oligosaccharide, a carbohydrate, a lipid, or combinations thereof. It is not critical what the linker's chemical structure is, since it serves primarily as a linker. The linker should be chosen so as not to interfere with the activity of the C-fragment. The linker can be made up of amino acids linked together by peptide bonds. Thus, in some aspects, the linker comprises Y_n , wherein Y is a naturally occurring amino acid or a stereoisomer thereof and "n" is any one of 1 through 20. The linker is therefore can be made up of from 1 to 20 amino acids linked by peptide bonds, wherein the amino acids are

selected from the 20 naturally-occurring amino acids. In some cases, the 1 to 20 amino acids are selected from Gly, Ala, Ser, Cys. In some cases, the linker is made up of a majority of amino acids that are sterically un-hindered, such as Gly.

[0029] Non-peptide linkers are also possible. For example, alkyl linkers such as $--HN-(CH_2)_s--CO--$, wherein $s=2-20$ can be used. These alkyl linkers may further be substituted by any non-sterically hindering group such as lower alkyl (e.g., C_1-C_6), halogen (e.g., Cl, Br), CN, NH_2 , phenyl, etc.

[0030] Another type of non-peptide linker is a polyethylene glycol group, such as: $--HN-(CH_2)_2-(O-CH_2-CH_2)_n-O-CH_2-CO-$, wherein n is such that the overall molecular weight of the linker ranges from approximately 101 to 5000, preferably 101 to 500.

[0031] In some cases, the linker has a length of about 0-14 sub-units (e.g., amino acids).

[0032] In instances wherein the linker is a polynucleotide, the length of the linker in various aspects is at least about 10 nucleotides, 10-30 nucleotides, or even greater than 30 nucleotides. In various aspects, the bases of the polynucleotide linker are all adenines, all thymines, all cytidines, all guanines, all uracils, or all some other modified base.

[0033] In another aspect, a non-nucleotide linker comprises a basic nucleotide, polyether, polyamine, polyamide, peptide, carbohydrate, lipid, polyhydrocarbon, or other polymeric compounds. Specific examples include those described by Seela and Kaiser, *Nucleic Acids Res.* 1990, 18:6353 and *Nucleic Acids Res.* 1987, 15:3113; Cload and Schepartz, *J. Am. Chem. Soc.* 1991, 113:6324; Richardson and Schepartz, *J. Am. Chem. Soc.* 1991, 113:5109; Ma et al., *Nucleic Acids Res.* 1993, 21:2585 and *Biochemistry* 1993, 32:1751; Durand et al., *Nucleic Acids Res.* 1990, 18:6353; McCurdy et al., *Nucleosides & Nucleotides* 1991, 10:287; Jsche et al., *Tetrahedron Lett.* 1993, 34:301; Ono et al., *Biochemistry* 1991, 30:9914; Arnold et al., International Publication No. WO 89/02439; Usman et al., International Publication No. WO 95/06731; Dudycz et al., International Publication No. WO 95/11910 and Ferentz and Verdine, *J. Am. Chem. Soc.* 1991, 113:4000. A "non-nucleotide" further means any group or compound that can be incorporated into a nucleic acid chain in the place of one or more nucleotide units, including either sugar and/or phosphate substitutions, and allows the remaining bases to exhibit their enzymatic activity. The group or compound can be abasic in that it does not contain a commonly recognized nucleotide base, such as adenosine, guanine, cytosine, uracil or thymine, for example at the C1 position of the sugar.

[0034] In various aspects, linkers contemplated include linear polymers (e.g., polyethylene glycol, polylysine, dextran, etc.), branched chain polymers (see, for example, U.S. Patent 4,289,872 to Denkenwalter et al., issued September 15, 1981; 5,229,490 to Tam, issued July 20, 1993; WO 93/21259 by Frechet et al., published 28 October 1993); lipids; cholesterol groups (such as a steroid); or carbohydrates or oligosaccharides. Other linkers include one or more water soluble polymer attachments such as polyoxyethylene glycol, or polypropylene

glycol as described U.S. Patent Nos: 4,640,835, 4,496,689, 4,301,144, 4,670,417, 4,791,192 and 4,179,337. Other useful polymers as linkers known in the art include monomethoxy-polyethylene glycol, dextran, cellulose, or other carbohydrate based polymers, poly-(N-vinyl pyrrolidone) polyethylene glycol, propylene glycol homopolymers, a polypropylene oxide/ethylene oxide co-polymer, polyoxyethylated polyols (e.g., glycerol) and polyvinyl alcohol, as well as mixtures of these polymers.

[0035] In still other aspects, oligonucleotide such as poly-A or hydrophilic or amphiphilic polymers are contemplated as linkers, including, for example, amphiphiles (including oligonucleotides).

[0036] Contemplated solid supports include resins, particles, and beads. More specific solid supports include polyhydroxy polymers, e.g. based on polysaccharides, such as agarose, dextran, cellulose, starch, pullulan, or the like, and synthetic polymers, such as polyacrylic amide, polymethacrylic amide, poly(hydroxyalkylvinyl ethers), poly(hydroxyalkylacrylates) and polymethacrylates (e.g. polyglycidymethacrylate), polyvinyl alcohols and polymers based on styrenes and divinylbenzenes, and copolymers in which two or more of the monomers corresponding to the above-mentioned polymers are included. Specific solid supports contemplated include agarose, sepharose, cellulose, polystyrene, polyethylene glycol, derivatized agarose, acrylamide, sephadex, sepharose, polyethyleneglycol (PEG)-acrylamide, and polystyrene-PEG based supports. In some cases, the solid support can be a resin such as p-methylbenzhydrylamine (pMBHA) resin (Peptides International, Louisville, Ky.), polystyrenes (e.g., PAM-resin obtained from Bachem Inc., Peninsula Laboratories, etc.), including chloromethylpolystyrene, hydroxymethylpolystyrene and aminomethylpolystyrene, poly (dimethylacrylamide)-grafted styrene co-divinyl-benzene (e.g., POLYHIPE resin, obtained from Aminotech, Canada), polyamide resin (obtained from Peninsula Laboratories), polystyrene resin grafted with polyethylene glycol (e.g., TENTAGEL or ARGOGEL, Bayer, Tübingen, Germany) polydimethylacrylamide resin (obtained from Milligen/Bioscience, California), or Sepharose (Pharmacia, Sweden). In various aspects, the solid support can be a magnetic bead, a glass slide, a glass bead, or a metal or inorganic particle (e.g., gold, silica, iron, or mixture thereof).

Methods of Purifying and Modifying Polypeptides

[0037] Site-specific modification of proteins is an invaluable tool to study the molecular details of protein function (19). Moreover, its potential for the discovery and development of protein therapeutics has also been recently acknowledged (20). Several methods have been developed over the years to generate site-specifically modified proteins; one of the most widely used is Expressed Protein Ligation (EPL), which has been applied to many different proteins in a variety of studies to address fundamental questions of protein function. EPL was first described in 1998 (21), as an expansion to recombinant proteins of Native Chemical Ligation (NCL) (19,22), and it consists on the reaction between a C-terminal recombinant protein α -thioester with a synthetic peptide containing a Cys at its N-terminus through the formation of a

new native peptide bond between the two fragments. The synthetic nature of the Cys containing peptide allows for the incorporation of almost any chemical modification into the protein of interest.

[0038] In order to apply EPL to any given protein the generation of protein C-terminal thioesters in good yields and high purity is an absolute requirement. A family of single turnover enzymes, named inteins, has been used since the dawn of EPL for the generation of such thioesters. Inteins are able to catalyze protein splicing, a naturally occurring post-translational modification by which they excise themselves from the polypeptide in which they are embedded, concomitantly forming a new peptide bond between their flanking protein regions (23). Importantly, this reaction occurs via several protein α -thioesters, which can be trapped through a trans-thioesterification reaction with an exogenous thiol.

[0039] Inteins, such as GyrA or VMA, have been successfully harnessed to prepare a wide variety of protein thioesters. In order to isolate the desired protein thioesters inteins are usually fused to affinity tags such as the chitin binding domain or the hexa-His tag. However, despite the notable success of this strategy, the reaction conditions required for efficient thiolysis (reducing agents, large concentration of thiols and long incubation times) affect the performance of such tags and subsequent additional purification steps are often required to obtain the desired pure product for ligation (24-26). Moreover, depending on the identity of the C-terminal residue of the protein of interest, significant levels of *in vivo* premature cleavage can occur, significantly reducing the final product yield.

[0040] An ideal system should combine the thioester formation capabilities of inteins with a built-in affinity purification strategy (fully compatible with the thiolysis reaction conditions) and reduced risk of premature cleavage. Naturally split-inteins were investigated, which can perform a reaction analogous to protein splicing but in which the intein itself is split into two different polypeptides. Each of the two intein fragments are completely inactive by themselves but have a strong affinity for each other and, upon binding, they adopt their splicing competent active conformation and are able to carry out protein trans-splicing. Recently, an artificially split version of the DnaB intein has been reported for the purification of unmodified proteins (27). Thus, a purification strategy is provided using naturally split-inteins instead and to harness them for the one pot purification and generation of recombinant protein α -thioesters (Figure 7) directly from cell lysates.

[0041] Due to the extremely fast reaction kinetics of naturally split inteins, several mutations were introduced to allow efficient thioester formation and minimize *in vivo* and *in vitro* undesired cleavage reactions. Specifically, both the C-intein C-terminal catalytic Asn137 and the Cys+1 residues had to be mutated to Ala to prevent premature C- and N-terminal cleavage, respectively. Mutation to two sequential aliphatic residues, natural or unnatural, is also expected to yield comparable results as the AA mutation. Other mutated split intein C-fragments as described above can be used in the described purification and /or modification methods, and are specifically contemplated.

[0042] To develop a split-intein based purification and thioester formation strategy the Npu split-intein was chosen, which is one of the fastest DnaE split-inteins previously known [10]. Initially the ability of split Npu to generate protein thioesters in solution was tested by mixing the model protein ubiquitin fused to NpuN with a mutant NpuC (Asn¹³⁷ and Cys⁺¹ to Ala) in the presence (and absence) of the thiol MESNa. SDS-PAGE, HPLC and MS analysis of the reactions showed the formation of the desired ubiquitin C-terminal α -thioester in a few hours. Encouraged by these results an affinity purification strategy was designed based on the covalent immobilization of the NpuC intein mutant onto a solid support. The immobilized mutated NpuC could then be used to purify NpuN tagged proteins from complex mixtures and addition of an exogenous thiol would cleave off the desired protein α -thioester, which would elute from the column in a highly purified form. Other split intein N-fragments as described above can be used in the methods disclosed herein, and are specifically contemplated.

[0043] An NpuC mutant (Asn¹³⁷ and Cys⁺¹ mutated to Ala, NpuC-AA (SEQ. ID NO: 777) was prepared with a Cys residue at the C-terminus of its C-extein, which was used to immobilize the peptide onto a iodoacetyl resin. With the NpuC-AA affinity resin in hand, it was shown that several protein C-terminal α -thioesters (Ubiquitin, MBP, PHPT1) could be easily produced and purified out of cell lysates (Figure 8). HPLC and MS analysis confirmed the formation of the desired protein thioesters with very low levels of undesired hydrolysis (Figure 9). Recovery yields varied between 75 and 95% and the NpuC-AA resin had a consistent loading capacity of 3-6 mg of protein per mL. The utility of the α -thioester derivatives of Ub, MBP, and PHPT1 obtained from the column was demonstrated by ligating each of them to an N-terminal Cys-containing fluorescent peptide (CGK(FI)) to give the corresponding semisynthetic products in excellent yield (Figure 13). Importantly, one-pot thiolysis/ligation reactions can be carried out, which provides a site-specifically modified protein directly from cell lysates without isolating the intermediate thioester (Figure 14).

[0044] A concern when working with split-inteins (and also inteins) is the effect of the flanking amino acid sequences on splicing and/or thiolysis activity. Although the N-terminal junction is regarded as more tolerant towards deviations from the native N-extein residues it was important to evaluate the effect that the C-terminal amino acid of the protein of interest (-1 residue according to intein numbering conventions) would have on the yields of thioester formation. A complete library of Ub-X-NpuN fusion proteins was constructed where the C-terminal Ub residue (X) was varied from its native Gly to all other 19 proteinogenic amino acids. Proteins were expressed in *E. coli* and cell lysates, applied to the NpuC-AA affinity resin and purified. Protein yields were estimated from the SDS-PAGE analysis for each purification and hydrolysis levels from RP-HPLC and MS analysis of the elution fractions (Figure 10). Results show similar trends to those known for non-split inteins, such as GyrA (29), and most amino acids display high yields of cleavage after overnight incubation with MESNa, the exceptions being Pro and Glu, for which recovery were 49 and 50%, respectively. As expected, the Asn α -thioester could not be isolated due to the well-known reaction of its side-chain with the adjacent α -thioester to form a succinimide.

[0045] This purification strategy was very successful for the purification of several soluble

proteins under native conditions. However, protein fragments required for EPL sometimes suffer from poor solubility and high toxicity and tend to accumulate in cellular inclusion bodies during expression. The Npu split-intein has been shown to retain a significant level of activity in the presence of denaturants (28), which suggested that this strategy would be compatible under such conditions. Using the model Ub-NpuN protein fusion it was confirmed that both, binding to the NpuC-AA-resin and thioester formation, worked well in the presence of 2 and 4 M urea. Similar levels of both, binding and thiolysis, were obtained than in the absence of denaturant and same reaction conditions.

[0046] The system was next tested for the purification from inclusion bodies of a fragment of the histone H2B. Preparation of site-specifically modified histones using EPL is a topic of major interest due to their crucial role in the understanding of epigenetic regulation. However, histone fragments are remarkably poorly behaved and the preparation of their recombinant C-terminal α -thioesters particularly challenging. A H2B(1-116) fragment fused to NpuN was expressed in *E. coli* and the inclusion bodies extracted with 6 M urea. The H2B-NpuN fusion was subsequently diluted into a 3 M urea buffer and the corresponding C-terminal α -thioester generated concomitant with purification over the NpuC-AA affinity resin (Figure 11). Due to its tendency of aggregation, very dilute protein solutions bound more efficiently to the resin, and also longer reaction times were required for efficient thioester generation, obviously, these are parameters that would need to be optimized on a protein to protein basis. Using these conditions, H2B(1-116) C-terminal thioester was obtained in excellent purity (> 90 % by RP-HPLC) and isolated yield (~20 mg per L of culture). This represents a significant improvement over previous protocols which afford less protein (4 mg per L of culture) and require the use of multiple chromatographic purification steps including RP-HPLC. Importantly, the H2B(1-116)-MES thioester obtained from the IntC-column can be directly used in EPL reactions without further purification. Accordingly, the protein was successfully ligated to a synthetic H2B(117-125) peptide containing an acetylated Lys at position 120 to yield semi-synthetic H2B-K120Ac (Figure 15).

[0047] The potential of this thioester formation purification strategy was demonstrated by applying it to the site-specific modification of a monoclonal antibody. Thus, specifically contemplated is a method of purifying an antibody by using a fusion protein of an antibody and a split intein N-fragment as disclosed herein and a mutated split intein C-fragment as disclosed herein.

[0048] The modification of antibodies is a field of intense research, specially focused on the development of therapeutic antibody-drug-conjugates (30). The identity of the N-intein could have a significant effect on the expression levels of its fusion to a given protein of interest. The N-fragment of several of the fastest split DnaE inteins cross-reacted with NpuC, allowing one to use any of them with the same NpuC based affinity column. Accordingly, the expression levels of a model antibody (α DEC, antibody against the DEC205 receptor) were tested and found the highest levels of expression were obtained when α DEC was fused to the AvaN intein (Figure 12A). α DEC-AvaN fusions were transfected into 293T cells and after 4 days of culture the supernatants were collected and purified over the NpuC-AA-column. The presence of a C-

terminal thioester in the purified α DEC was confirmed by reacting it with a short fluorescent peptide with an N-terminal Cys residue (Figure 12B and C). MS of the deglycosylated and reduced α DEC-fluorophore conjugate was used to confirm its identity and SEC-MALS demonstrate the product was monodisperse and of the expected size for an IgG antibody.

[0049] Split-inteins can be engineered for the preparation of protein α -thioesters and that the strong affinity between the two split-intein fragments provides a powerful handle for their purification. The generality of the approach is demonstrated by using it to generate highly pure thioesters of both soluble (ubiquitin, MBP, PHPT) and insoluble proteins (H2B fragment) as well as monoclonal antibodies (α DEC). Moreover, several N-inteins can be tested for optimal expression levels of the protein of interest and used with one single NpuCcolumn.

[0050] Thus, the split inteins disclosed herein can be used to purify and modify a polypeptide of interest. A polypeptide of interest is provided in a fusion protein with a split intein N-fragment, e.g., via well-known recombinant protein methods. The fusion protein is then contacted with a corresponding split intein C-fragment under conditions that allow binding of the N-fragment and C-fragment to form an intein intermediate. The split intein C-fragment can be bound to a support (e.g., a solid support such as a resin) or can subsequently (e.g., after binding to the split intein N-fragment to form the intein intermediate) be bound to a support. This allows for the removal via washing of components that were in the mixture due to the recombinant protein synthesis, allowing the fusion protein to be isolated from the other components. Washes can include detergents, denaturing agents and salt solutions (e.g., NaCl).

[0051] Then, the intein intermediate can be reacted with a nucleophile to release the polypeptide of interest from the bound N- and C-fragment inteins wherein the C-terminus of the polypeptide is modified by the nucleophile added. The nucleophile can be a thiol to directed yield the polypeptide as an α -thioester, which in turn can be further modified, e.g., with a different nucleophile (e.g., a drug, a polymer, another polypeptide, a oligonucleotide), or any other moiety using the well-known α -thioester chemistry for protein modification at the C-terminus. One advantage of this chemistry is that only the C-terminus is modified with a thioester for further modification, thus allowing for selective modification only at the C-terminus and not at any other acidic residue in the polypeptide.

[0052] The nucleophile that is used in the methods disclosed herein either with the intein intermediate or as a subsequent nucleophile reacting with, e.g., a α -thioester, can be any compound or material having a suitable nucleophilic moiety. For example, to form a α -thioester, a thiol moiety is contemplated as the nucleophile. In some cases, the thiol is a 1,2-aminothiol, or a 1,2-aminoselenol. An α -selenothioester can be formed by using a selenothiol (R-SeH). Alternative nucleophiles contemplated include amines (i.e. aminolysis to give amides directly), hydrazines (to give hydrazides), amino-oxy groups (to give hydroxamic acids). Additionally, the nucleophile can be a functional group within a compound of interest for conjugation to the polypeptide of interest (e.g., a drug to form a protein-drug conjugate) or could alternatively bear an additional functional group for subsequent known bioorthogonal reactions

such as an azide or an alkyne (for a click chemistry reaction between the two function groups to form a triazole), a tetrazole, an α -ketoacid, an aldehyde or ketone, or a cyanobenzothiazole.

[0053] Additional aspects and details of the invention will be apparent from the following examples, which are intended to be illustrative rather than limiting.

EXAMPLES

Materials

[0054] All buffering salts, isopropyl- β -D-thiogalactopyranoside (IPTG), and N,N-diisopropylethylamine (DIPEA) were purchased from Fisher Scientific (Pittsburgh, PA). Kanamycin sulfate (Kan), β -Mercaptoethanol (BME), DL-dithiothreitol (DTT), sodium 2-mercaptoethanesulfonate (MESNa), ethanedithiol (EDT), Coomassie brilliant blue, N,N-dimethylformamide (DMF), Tetrakis(triphenylphosphine)palladium(0) ($\text{Pd}(\text{PPh}_3)_4$), phenylsilane, triisopropylsilane (TIS), sodium diethyldithiocarbamate trihydrate, and 5(6)-carboxyfluorescein were purchased from Sigma-Aldrich (St. Louis, MO). Tris(2-carboxyethyl)phosphine hydrochloride (TCEP) was purchased from Thermo Scientific (Rockford, IL). Fmoc-Gly-OH, Fmoc-Lys(Alloc)-OH, and Boc-Cys(Trt)-OH were purchased from Novabiochem (Läufelfingen, Switzerland). Piperidine was purchased from Alfa Aesar (Ward Hill, MA). Dichloromethane (DCM) and rink amide resin were purchased from EMD Chemicals (Billerica, MA). 1-Hydroxybenzotriazole hydrate (HOBt) was purchased from AnaSpec (Fremont, Ca). Trifluoroacetic acid (TFA) was purchased from Halocarbon (North Augusta, SC). Complete protease inhibitor tablets were purchased from Roche Diagnostics (Mannheim, Germany). Nickel-nitrilotriacetic acid (Ni-NTA) resin was from Novagen (Gibbstown, NJ). The QuikChange XL II site directed mutagenesis kit was from Agilent (La Jolla, CA). DpnI and the Phusion High-Fidelity PCR kit were from New England Biolabs (Ipswich, MA). DNA purification kits (QIAprep spin minikit, QIAquick gel extraction kit, QIAquick PCR purification kit) were from Qiagen (Valencia, CA). Sub-cloning efficiency DH5 $\square$ competent cells and One Shot BL21(DE3) chemically competent E. coli were purchased from Invitrogen (Carlsbad, CA) and used to generate "in-house" high-competency cell lines. Oligonucleotides were purchased from Integrated DNA Technologies (Coralville, IA). The new intein genes were generated synthetically and purchased from GENEWIZ (South Plainfield, NJ). All plasmids used in this study were sequenced by GENEWIZ.

[0055] Criterion XT Bis-Tris gels (12%), Immun-blot PVDF membrane (0.2 μm), and Bradford reagent dye concentrate were purchased from Bio-Rad (Hercules, CA). 20x MES-SDS running buffer was purchased from Boston Bioproducts (Ashland, MA). Mouse antimyc monoclonal antibody (a-myc) was purchased from Invitrogen (Carlsbad, CA). Anti-His Tag, clone HIS.H8 mouse monoclonal antibody (α -His6) was purchased from Millipore (Billerica, MA). Mouse HA. 11 monoclonal antibody (a-HA) was purchased from Covance (Princeton, NJ). IRDye 800CW

goat anti-Mouse IgG secondary antibody (Licor mouse 800) and Licor Blocking Buffer were purchased from LI-COR Biotechnology (Lincoln, NE).

Equipment

[0056] Size-exclusion chromatography was carried out on an ÄKTA FPLC system from GE Healthcare. Both preparative and analytical FPLC were carried out on a Superdex 75 10/300 or S200 10/300 column. For all runs, proteins were eluted over 1.35 column volumes of buffer (flow rate: 0.5 mL/min). Analytical RP-HPLC was performed on Hewlett-Packard 1100 and 1200 series instruments equipped with a C18 Vydac column (5 μ m, 4.6 $\times$ 150 mm) at a flow rate of 1 mL/min. Preparative RP-HPLC was performed on a Waters prep LC system comprised of a Waters 2545 Binary Gradient Module and a Waters 2489 UV detector. Purifications were carried out on a C18 Vydac 218TP1022 column (10 μ M; 22 $\times$ 250 mm). All runs used 0.1 % TFA (trifluoroacetic acid) in water (solvent A) and 90 % acetonitrile in water with 0.1% TFA (solvent B). For all runs, a two minute isocratic period in initial conditions was followed by a 30 minute linear gradient with increasing buffer B concentration. Electrospray ionization mass spectrometric analysis (ESI-MS) was performed on a Bruker Daltonics MicroTOF-Q II mass spectrometer. In vivo intein activity assays were carried out on a VersaMax tunable microplate reader from Molecular Devices. Cells were lysed using an S-450D Branson Digital Sonifier. Western blots and coomassie-stained in vitro splicing assay gels were imaged on a LI-COR Odyssey Infrared Imager. Fluorescent fluorescein-containing gels were imaged using the GE ImageQuant LAS 4000 imager.

Compilation of the DnaE sequence library and sequence analysis

[0057] Protein sequences of the split DnaE inteins were obtained from the NEB InBase1. This list consisted of 23 entries as of May 2011. Of these entries, two were discarded from the study as they did not have a C-intein sequence: Csp(PCC7822) and Nosp(CCY9414). Two pairs of inteins had identical sequences: Nsp(PCC7120) with Asp (these are most likely the same organism with two different names) and Sel(PCC6301) with Sel(PC7942). Thus, Nsp(PCC7120) and Sel(PCC6301) were removed from the library. The Mcht(PCC7420) and Oli C-intein sequences were identical, but both inteins were kept in the library as their N-intein sequences were different. In the InBase, the Aov intein had an "X" at position 87 in place of an absolutely conserved isoleucine (I), so 187 was utilized at this position. The plasmid for the kanamycin resistance assays bearing the Csp(PCC7424) intein proved to be unstable and yielded highly variable results; thus this intein was excluded from the analyses. The final library contained 18 inteins, Table 1.

Table 1

DnaE Intein Name	Genus	Species	Strain
Npu	Nostoc	punctiforme	PCC73102
Ssp	Synechocystis	species	PCC6803

DnaE Intein Name	Genus	Species	Strain
Aha	Aphanothece	halophytica	
Aov	Aphanizomenon	ovalisporum	
Asp	Anabaena	species	PCC7120
Ava	Anabaena	variabilis	A TCC29413
Cra(CS505)	Cylindrospermopsis	raciborskii	CS-505
Csp(CCY0110)	Cyanothece	species	CCY0110
Csp(PCC8801)	Cyanothece	species	PCC8801
Cwa	Crocospaera	watsonii	WH 8501
Maer(NIES843)	Microcystis	aeruginosa	NIES-843
Mcht(PCC7420)-2	Microcoleus	chthonoplastes	PCC7420
Oli	Oscillatoria	limnetica	Solar Lake
Sel(PC7942)	Synechococcus	elongatus	PC7942
Ssp(PCC7002)	Synechococcus	species	PCC7002
Tel	Thermosynechococcus	elongatus	BP-1
Ter-3	Trichodesmium	erythraeum	IMS101
Tvu	Thermosynechococcus	vulcanus	

[0058] Given the high homology of DnaE intein sequences, the N- and C-inteins were manually aligned using the multiple alignment software Jalview2. All N-intein sequences were "left-justified" to align the first cysteine residue, and the variable N-intein tail region was not aligned. All C-intein sequences were "right-justified" to align the C-terminal asparagine. The residue numbering used in this study is based on the numbering for the NMR structure of a fused Npu intein (PDB code 2KEQ). Thus, the variable N-intein tail region after residue 102 (the last residue of NpuN) is excluded from the numbering, as is the N-terminal methionine of the C-intein. The C-intein numbering starts at 103, except for the Tel and Tvu inteins, which have a gap at this position and start at 104. For the sequence logos (Figure 6), the N- and C-intein alignments were each separated into two alignments based on high and low activity. The high activity sequence logos were comprised of Cwa, Cra(CS505), Csp(PCC8801), Ava, Npu, Csp(CCY0110), Mcht(PCC7420), Maer(NIES843), Asp, Oli, and Aha (which was included based on the high activity of the C120G mutant). The low activity sequence logos were comprised of Aov, Ter, Ssp(PCC7002), Tvu, Tel, Ssp, and Sel(PC7942). The sequence logos were generated using WebLogo. (4) Heat maps were generated using the statistical computing and graphics program "R".

Cloning of plasmids for in vivo screening

[0059] The aminoglycoside phosphotransferase (KanR) and Npu gene fragments were cloned into a pBluescript KS (+) vector between KpnI and SacI restriction sites as previously described (36,37). This construct contained the following architecture:

[KanR promoter]-[RBS]-[myc-KanRN]-[IntN]-[iRBS]-[IntC]-[CFN-KanRC] where the KanR promoter is the constitutive promoter found in most kanamycin-resistant plasmids, RBS is a common *E. coli* ribosomal binding site, iRBS is an intervening ribosomal binding site preceded by a linker, myc encodes for a c-myc epitope tag (EQKLISEEDL) (SEQ ID NO: 760), KanRN and KanRC are fragments of the KanR protein, and IntN and IntC are split intein fragments. An analogous Ssp plasmid was also constructed as previously described (36,37). These plasmids are referred to as myc-KanR-NpuDnaE-Split and myc-KanR-SspDnaE-Split. To generate the screening vectors for the remaining split inteins, synthetic genes were designed and purchased from GENEWIZ containing the following architecture:

[5' overhang]-[IntN]-[iRBS]-[IntC]-[3' overhang] where the 5' and 3' overhangs were the exact 39 bp found upstream of NpuN and 25 bp found downstream of NpuC, respectively, in the myc-KanR-NpuDnaE-Split plasmid. For all inteins, the purchased gene sequences were codon-optimized with the default *E. coli* codon usage table generated based on all *E. coli* coding sequences in GenBank8. The synthetic genes were received in pUC57 vectors.

[0060] To clone the screening plasmids, the entire synthetic gene was amplified with Phusion High-Fidelity Polymerase using primers annealing to the 5' and 3' overhangs. The resulting megaprimer was inserted into the myc-KanR plasmid in place of Npu by overlap-extension PCR with Phusion polymerase (39). This resulted in 18 homologous plasmids containing identical backbones, promoters, and KanR genes, but with different codon-optimized intein genes. The plasmids are named as: myc-KanR-XYZDnaE-Split (where XYZ indicates the intein name as given in Table 1). Specific point mutations were made to various inteins using a QuikChange Site-Directed Mutagenesis kit with the standard recommended protocol.

In vivo screening of relative intein activities

[0061] 96-well plate assay: Intein activity-coupled kanamycin resistance (KanR) assays were conducted in 96-well plate format as previously described (36,37). Typically, plasmids were transformed into 15 µL of sub-cloning efficiency DH5α cells by heat shock, and the transformed cells were grown for 18 hours at 37°C in 3 mL of Luria-Bertani (LB) media with 100 µg/mL of ampicillin (LB/amp). The over-night cultures were diluted 250-fold into LB/amp solutions containing 8 different kanamycin concentrations (150 µL per culture). The cells were grown at 30°C on a 96-well plate, monitoring optical density (OD) at 650 nm every 5 minutes for 24 hours while shaking for one minute preceding each measurement. The endpoint of this growth curve (typically in the stationary phase) was plotted as a function of kanamycin concentration to visualize the dose-response relationship and fitted to a variable slope dose-response equation to determine IC₅₀ values.

$$OD_{Obs} = OD_{Min} + \frac{(OD_{Max} - OD_{Min})}{1 + 10^{[(\log IC_{50} - \log [Kan]) \cdot HillSlope]}}$$

In each regression analysis, typically three or four independent dose response curves were

collectively fit to the equation above using the GraphPad Prism software. In each fit, OD_{Min} was fixed to the background absorbance at 650 nm, and all other parameters were allowed to vary. The reported error bars for the IC_{50} bar graphs (Figure 1b) represent the standard error in the best-fit IC_{50} value from three or four collectively fit dose-response curves.

[0062] Western blot analysis of *in vivo* splicing: For the western blot analyses, DH5 α cells were transformed with the assay plasmids identically as for the 96-well plate setup and grown for 18 hours at 37°C while shaking. The overnight cultures were used to inoculate 3 mL of fresh LB/amp at a 1:300 dilution, and the cells were incubated at 30°C for 24 hours. The ODs of the 30°C cultures were measured at 650nm to assess relative bacterial levels, then 150 μ L of each culture was transferred to an Eppendorf tube and centrifuged at 17,000 rcf for 2 minutes. The supernatant was aspirated off, and the cell pellets were resuspended/lysed in ~200 μ L of 2 $\times$ SDS gel loading dye containing 4% BME (the resuspension volumes were varied slightly to normalize for differences in OD). The samples were boiled for 10 minutes, then centrifuged at 17,000 rcf for 1 minute. Each sample (5 μ L) was loaded onto a 12% Bis-Tris gel and run in MES-SDS running buffer. The proteins were transferred to PVDF membrane in Towbin transfer buffer (25 mM Tris, 192 mM glycine, 15% methanol) at 100V for 90 minutes. Membranes were blocked with 4% milk in TBST, then the primary antibody (α -myc, 1:5000) and secondary antibody (Licor mouse 800, 1:15,000) were sequentially applied in 4% milk in TBST. The blots were imaged using the Licor Odyssey scanner.

Cloning of plasmids for *in vitro* splicing assays

[0063] Ub-IntN plasmids: The N-intein expression plasmids were derived from a previously described NpuN plasmid, pMR-Ub-NpuN(WT) (36,37). This plasmid encoded for the following protein sequence:

MHHHHHHGGMQIFVKTLTGKTTITLEVESSDTIDNVKSKIQDKEGIPPDQQELIFAGKQLE
 DGRTLSYDNIQKESTLHLVLRRLRGGGGGGKFAEY**CLSYETEILTVEYGLLP**IGKIVEKRI
 ECTVYSVDNNGNIYTQPVAAQWHDGEQEVFEYCLEDGSLIRATKDHKFMTVDGQMLPIDE
IFERELDLMRVDNLPN (SEQ ID NO: 761)

where the NpuN sequence is given in bold, the immediate native local extein residues are underlined, and these residues are preceded by His₆-Ub with a Gly₄ linker. Significant *in vivo* proteolysis was previously observed during expression of this construct, so this plasmid was modified using QuikChange to remove the Gly₄ sequence. The resulting plasmid, pMR-Ub-NpuN- Δ Gly₄ was used as the template for all other Ub-IntN plasmids and encoded for the following protein sequence:

MHHHHHHGGMQIFVKTLTGKTTITLEVESSDTIDNVKSKIQDKEGIPPDQQELIFAGKQLE
 DGRTLSYDNIQKESTLHLVLRRLRGGGGGGKFAEY**CLSYETEILTVEYGLLP**IGKIVEKRIECTV
 YSVDNNGNIYTQPVAAQWHDGEQEVFEYCLEDGSLIRATKDHKFMTVDGQMLPIDE**IFERE**
ELDLMRVDNLPN (SEQ ID NO: 762)

[0064] All other IntN plasmids were cloned using overlap-extension PCR to generate Ub-IntN fusion genes in homologous plasmids in a traceless manner (39). Specifically, N-intein genes were amplified by Phusion polymerase from the synthetic gene plasmids using primers with overhangs that anneal to the plasmid sequences surrounding NpuN in pMR-Ub-NpuNΔGly₄. The resulting megaprimer was then used to insert the new N-intein gene in place of NpuN to generate a new plasmid called pMR-Ub-IntN that was identical to the NpuN plasmid except for the N-intein gene.

[0065] IntC-SUMO plasmids: The C-intein plasmids were all derived from a previously described NpuC plasmid, pET-NpuC(WT)-SUMO (37). This plasmid encoded for the following protein sequence:

MGSSHHHHHHGENLY FQ | **G****I****K****I****A****T****R****K****Y****L****G****K****Q****N****V****D****I****G****V****E****R****D****H****N****F****A****L****K****N****G****F****T****A****S****N****C****E****N****S****G****L****V**

PRGSASMSDSEVNQEAKPEVKPEVKPETHINLKVSDGSSEIFFKIKKTTPLRRLMEAFAK

RQ GKEMDSLRF~~LY~~DGIRIQADQTPEDLDMEDNDIIEAHREQIGGYPYDVPDYA (SEQ ID

NO: 763)

where the NpuC sequence is given in bold, and the immediate native local extein residues are underlined, followed by a linker sequence and SUMO-HA. This construct is preceded by a His₆-tag and a tobacco etch virus (TEV) protease recognition sequence. The TEV protease cleavage site is indicated by "|" and leaves behind a glycine residue in place of an N-terminal IntC methionine.

[0066] All other IntC plasmids were cloned using overlap-extension PCR to generate IntC-SUMO fusion genes in homologous plasmids in a traceless manner (39). Specifically, C-intein genes were amplified by Phusion polymerase from the synthetic gene plasmids using primers with overhangs that anneal to the plasmid sequences surrounding NpuC in pET-NpuC(WT)-SUMO. The resulting megaprimer was then used to insert the new C-intein gene in place of NpuC to generate a new plasmid called pET-IntC-SUMO that was identical to the NpuC plasmid except for the C-intein gene.

Purification of proteins for in vitro splicing assays

[0067] Over-expression and purification of Ub-IntN constructs (except Ub-CwaN): *E. coli* BL21(DE3) cells transformed with each N-intein plasmid were grown in 1 L of LB containing 100 µg/mL of ampicillin at 37°C until OD₆₀₀ = 0.6. The cells were then cooled down to 18 °C, and expression was induced by addition of 0.5 mM IPTG for 16 hours at 18 °C. After harvesting the cells by centrifugation (10,500 rcf, 30 min), the cell pellets were transferred to 50 mL conical tubes with 5 mL of lysis buffer (50 mM phosphate, 300 mM NaCl, 5 mM imidazole, 2 mM BME, pH 8.0) and stored at -80°C. The cell pellets were resuspended by adding an additional 15 mL of lysis buffer supplemented with Complete protease inhibitor cocktail. Cells were lysed by sonication (35% amplitude, 8x 20 second pulses separated by 30 seconds on ice). The soluble fraction was recovered by centrifugation (35,000 rcf, 30 min). The soluble fraction was mixed with 2 mL of Ni-NTA resin and incubated at 4°C for 30 minutes.

After incubation, the slurry was loaded onto a fritted column. After discarding the flow-through, the column was washed with 5 column volumes (CV) of lysis buffer, 5 CV of wash buffer 1 (lysis buffer with 20 mM imidazole), and 3 CV of wash buffer 2 (lysis buffer with 50 mM imidazole). The protein was eluted with elution buffer (lysis buffer with 250 mM imidazole) in four 1.5 CV elution fractions. The wash and elution fractions were analyzed by SDS-PAGE.

[0068] After enrichment over the Ni-NTA column, the proteins were purified by gel filtration. The wash and elution fractions were all treated with 50 mM DTT for 30 minutes on ice. For well-expressing proteins, the first elution fraction was then directly injected on an S75 10/300 gel filtration column (3x 1 mL injections) and eluted over 1.35 CV in freshly prepared, degassed splicing buffer (100 mM phosphates, 150 mM NaCl, 1 mM DTT, 1 mM EDTA, pH 7.2). For the more dilute, low-yielding proteins, typically the 50 mM imidazole wash fraction and the first two elution fractions were pooled and concentrated four-fold to 3 mL. Then, the concentrated protein was purified by gel filtration identically to the highyielding constructs. FPLC fractions were analyzed by SDS-PAGE, and the purest fractions were pooled and analyzed by analytical gel filtration, analytical RP-HPLC, and mass spectrometry. The concentration of pure proteins were determined by UV A280nm and by the Bradford assay.

[0069] Over-expression and purification of Ub-CwaN: The Ub-CwaN protein did not express well in the soluble fraction, and all of the enriched protein was aggregated, as observed by gel filtration analysis. Thus, after expression, cell lysis, and fractionation, as described above, the protein was extracted from the insoluble fraction of the lysate as follows. First, the lysate pellet was resuspended in 20 mL of Triton wash buffer (lysis buffer with 0.1% Triton X-100) and incubated at room temperature for 30 minutes. The Triton wash was centrifuged at 35,000 rcf for 30 minutes, and the supernatant was discarded. Next, the pellet was resuspended in 20 mL of lysis buffer containing 6 M urea, and the mixture was incubated overnight at 4°C. The mixture was centrifuged at 35,000 rcf for 30 minutes, and then the supernatant was mixed with 2 mL of NiNTA resin. The Ni column was run identically as for the native purifications described above, except that every buffer had a background of 6 M urea. Following enrichment over a Ni-NTA column, the 50 mM imidazole wash and the first two elution fractions were pooled and diluted to 0.2 mg/mL. The diluted protein was refolded into lysis buffer (without urea) by step-wise dialysis removal of the urea at 4°C. The protein was concentrated four-fold to 3 mL and immediately purified by gel filtration as indicated for the native purifications above. The pure protein was analyzed by analytical gel filtration, analytical RP-HPLC, and mass spectrometry. Note that this construct was highly susceptible to aggregation. When re-folded at 2 mg/mL rather than 0.2 mg/mL, less than 10% of the obtained protein was monomeric, whereas more dilute refolding yielded roughly 50% monomeric protein. The obtained protein was 80% monomeric, and the monomer to aggregate ratio did not change after 24 hours of storage at 4°C. The concentration of pure protein was determined by the Bradford assay.

[0070] Over-expression and purification of IntC-SUMO constructs: *E. coli* BL21(DE3) cells transformed with each C-intein plasmid were grown in 1 L of LB medium containing kanamycin (50 µg/mL) at 37 °C until OD₆₀₀ = 0.6. Then, expression was induced by addition of 0.5 mM IPTG for 3 hours at 37 °C. The cells were lysed, and the desired protein was enriched over Ni-

NTA resin identically as for the natively purified Ub-IntN proteins. The AvaC-SUMO and Csp(PCC8801)C-SUMO proteins did not express well at 37 °C, so the proteins were re-expressed by induction at 18 °C for 16 hours. For each protein, the 50 mM imidazole wash and the first two elution fractions were pooled and dialyzed into TEV cleavage buffer (50 mM phosphate, 300 mM NaCl, 5 mM imidazole, 0.5 mM EDTA, 0.5 mM DTT, pH 8.0) then treated with 40 µg of His-tagged TEV protease overnight at room temperature. The cleavage was confirmed by RP-HPLC/MS, after which the reaction solution was incubated with Ni-NTA resin at room temperature for 30 min. The flow-through and two 1.5 CV washes with wash buffer 1 were collected and pooled. The protein was then concentrated to 3-4 mL, injected onto the S75 10/300 gel filtration column (3x 1 mL injections), and eluted over 1.35 CV in freshly prepared, degassed splicing buffer (100 mM phosphates, 150 mM NaCl, 1 mM DTT, 1 mM EDTA, pH 7.2). FPLC fractions were analyzed by SDS-PAGE, and the purest fractions were pooled and analyzed by analytical gel filtration, analytical RP-HPLC, and mass spectrometry. The concentration of pure protein was determined by UV $A_{280\text{nm}}$ and by the Bradford assay.

[0071] Usage and storage of the Ub-IntN and IntC-SUMO constructs: All of the purified proteins were stored at 4°C and used within two days for splicing assays with their cognate IntC-SUMO. The remaining protein (2 vol. eq.) was mixed with splicing buffer containing 60% glycerol (1 vol. eq.) to yield a 20% glycerol stock that was aliquoted and flash frozen in liquid N₂. The protein aliquots were stored at -80°C. The proteins were fully functional after thawing on ice and could be flash-frozen and re-thawed at least once without detectable loss of function.

In vitro splicing assays

[0072] Kinetic assay procedure: For a typical assay, individual protein stock solutions of Ub-IntN and IntC-SUMO constructs were prepared in filtered splicing buffer (100 mM phosphate, 150 mM NaCl, 1 mM DTT, 1 mM EDTA, pH 7.2) at 2x the final concentration (e.g. 2.0 µM stock solution for a 1.0 µM reaction). 1 mM TCEP was added (from a pH-neutralized 100 mM stock solution) to each protein solution, and the proteins were incubated at 30 °C or 37 °C for 5 min depending on the reaction temperature. To initiate a reaction, the N- and C-intein were mixed at equal volumes (i.e. equimolar ratios). A typical reaction volume was 300 µL and was carried out in an Eppendorf tube on a heat block. During the reaction, 20 µL aliquots of the reaction solution were removed at the desired time points and quenched in 20 µL of 2× concentrated SDS gel loading dye on ice to afford a final quenched solution with 40 mM Tris (~pH 7.0), 10% (v/v) glycerol, 1% (w/v) SDS, 0.02% (w/v) bromophenol blue, and 2% (v/v) BME. For each reaction, an artificial zero time point was taken by mixing equivalent amounts of starting materials directly into the quencher solution. Samples were boiled for 10 minutes then centrifuged at 17,000 rcf for 1 minute. Aliquots of starting materials and time points (15 µL) were loaded onto Bis-Tris gels and run in MES-SDS running buffer. The gels were Coomassie-stained then imaged using the Licor Odyssey scanner.

[0073] Note that for the reactions with a CGN C-extein sequence, no BME was used in the quencher solution. Furthermore, before boiling the samples, each sample was treated with 1 μ L of 2 N HCl. After boiling and cooling the samples, they were treated with 1 μ L of 2 N NaOH. This procedure prevented undesired hydrolysis or thiolysis of the branched intermediate.

[0074] Determination of kinetic parameters: To determine reaction rates, each lane of a gel was analyzed using the Licor Odyssey quantification function or ImageJ. Given the close proximity of the starting material bands, these bands were typically integrated together. To normalize for loading error, the integrated intensity of each band in a lane was expressed as a fraction intensity of the total band intensity in that lane (which remained relatively constant between lanes). These normalized intensities were plotted as a function of time, and data from three independent reactions were collectively fit to first-order rate equations using the GraphPad Prism software:

For reactant depletion:

$$Y = S(e^{-k_{obs}t}) + Z$$

For product formation:

$$Y = Y_{max}(1 - e^{-k_{obs}t})$$

Y is the fractional intensity of a species, t is time in minutes, S is a scaling factor for reactant depletion (allowed to vary), Z indicates the fraction of reactant remaining at the reaction endpoint (allowed to vary), Y_{max} is a scaling factor for product formation, and k_{obs} is the observed first-order rate constant for the splicing reaction (allowed to vary). Half-lives were calculated from the best-fit value for the first-order rate constant:

$$t_{1/2} = \frac{\ln 2}{k_{obs}}$$

For reactions with no detectable side product formation, the rate of product (Ub-SUMO) and IntN formation were consistent with the rate of starting material depletion.

[0075] Western blot analysis of reactions: Western blots of the zero time point and reaction endpoint were carried out to confirm the identities of the observed bands. The quenched time points from the reactions described above were loaded onto 12% Bis-Tris gels (5 μ L per sample, two identical gels) and run in MES-SDS running buffer. The resolved proteins were transferred from the gel onto PVDF membrane in CAPS transfer buffer (10 mM *N*-cyclohexyl-3-aminopropanesulfonic acid, 10% (v/v) methanol, pH 10.5) at 100 V for 60 minutes. Membranes were blocked with Licor Blocking Buffer, then the primary antibody (α -His₆, 1:3000, or α -HA, 1:25,000) was applied in Licor Blocking Buffer. The secondary antibody (Licor mouse 800, 1:15,000) was applied in 4% milk in TBST. The blots were imaged using the Licor Odyssey scanner. Blots from the 30 °C and 37 °C reactions were virtually identical.

HPLC/MS analysis of Npu-CGN and Cra(CS505)-CGN reactions

[0076] For the HPLC/MS analysis of Npu-CGN and Cra(CS505)-CGN, individual protein stock

solutions of Ub-IntN and IntC-CGN-SUMO were prepared in filtered splicing buffer (100 mM phosphate, 150 mM NaCl, 1 mM DTT, 1 mM EDTA, pH 7.2) at 8.0 μ M. 1 mM TCEP was added (from a pH-neutralized 100 mM stock solution) to each protein solution, and the proteins were incubated at 30 °C for 5 min. To initiate a reaction, the N- and C-intein were mixed at equal volumes (i.e. equimolar ratios) and incubated at 30 °C. During the reaction, 90 μ L aliquots of the reaction solution were removed at the desired time points and quenched in 30 μ L of a quenching solution (6 M guanidine hydrochloride with 4 % trifluoroacetic acid). 100 μ L of each quenched time point were injected onto an analytical C18 RP-HPLC column and eluted over a 25-73% buffer B gradient in 30 minutes, preceded by a two minute isocratic phase in 25% buffer B (see Equipment section for column and running buffer specifications). At different time points, various HPLC peaks were collected and their identities were confirmed by mass spectrometry. The IntC-(Ub)SUMO species were identified by MS, verifying branched intermediate formation and depletion.

Kinetic Modeling

[0077] When comparing the Npu, Cra(CS505), and Cwa reactions in the presence of CGN, higher amounts of cleaved ubiquitin (i.e. N-extein cleavage) were obtained than splice product, despite the fact that the rate of the former was slower than the latter. This observation is inconsistent with N-extein cleavage and splice product formation only occurring from the branched intermediate, since in this scenario splicing and cleavage would be competing first-order reactions occurring from the same reactant (the branched intermediate), leading to more splice product than cleavage (the opposite of that observed). In an attempt to reconcile these observations, a series of kinetic modeling simulations were carried out. All modeling was carried out using the kinetic modeling applet from BPREid (40). The models have three basic assumptions about the splicing pathway:

1. 1. The forward and reverse reactions in the first equilibrium are fast. In addition, the position of this equilibrium lies slightly towards the amide.
2. 2. The second equilibrium is also fast and should have K_{eq} close to 1, since both intermediates are cysteinyl thioesters.
3. 3. For fast inteins, the rate of branched intermediate resolution (k_s) is on the same order of magnitude as the rates of the first two reversible steps, whereas the cleavage rates from L (k_6) and B (k_7) are relatively slow. For slow inteins, branched intermediate resolution (k_s) is also slow, on the same order of magnitude as the cleavage.

[0078] With these assumptions, six scenarios were devised that assess how the relative rates of cleavage and branched intermediate resolution and the equilibrium between the linear and branched intermediates could affect the rates and extents of formation of the cleavage and spliced products. For slow inteins, such as those bearing exogenous C-extein residues, the rate of branched intermediate resolution is similar to the rate of N-extein cleavage. Under

these circumstances, three factors are important:

1. 1. The relative rates of cleavage from L versus B (k_6 vs. k_7).
2. 2. The relative rates of branched intermediate resolution versus cleavage (k_s vs. $k_6 + k_7$).
3. 3. Most importantly, the rates of exchange between the linear and branched intermediates (k_3/k_4).

These analyses suggest not only that cleavage should be occurring both from the linear and branched intermediate, but also that cleavage at the linear intermediate may be favored.

Protein thiolysis and ligation from fused DnaE inteins and MxeGyrA

[0079] Solid-phase synthesis and purification of H-Cys-Gly-Lys(Fluorescein)-NH₂ (CGK-Fluorescein): Fmoc-based solid phase peptide synthesis (SPPS) was used to produce a peptide with the sequence H-Cys-Gly-Lys(Fluorescein)-NH₂. The peptide was synthesized on Rink amide resin at a 0.2 mmol scale as follows: 20% piperidine in DMF was used for Fmoc deprotection using a one minute equilibration of the resin followed by a 20 minute incubation. After Fmoc deprotection, amino acids were coupled using DIC/HOBt as activating agents. First, the amino acid (1.1 mmol) was dissolved in 50:50 DCM:DMF (2 mL) and was activated with DIC (1.0 mmol) and HOBt (1.2 mmol) at 0 °C for 15 minutes. The mixture was added to the N-terminally deprotected resin and coupled for 10 minutes at room temperature.

[0080] After the cysteine was coupled, the lysine side chain was deprotected by treatment with Pd(Ph₃)₄ (0.1 eq.) and phenylsilane (25 eq.) in dry DCM for 30 minutes. The peptidyl resin was washed with DCM (2 × 5 mL) and DMF (2 × 5 mL) followed by two washes with 0.5% DIPEA in DMF (v/v) and two washes with 0.5% sodium diethyldithiocarbamate trihydrate in DMF (w/v) to remove any remaining traces of the Pd catalyst. 5(6)-Carboxyfluorescein was then coupled to the lysine side chain using the DIC/HOBt activation method overnight at room temperature. Finally, the peptide was cleaved off the resin using 94% TFA, 1% TIS, 2.5% EDT, and 2.5% H₂O (6.5 mL) for one hour. After cleavage, roughly half of the TFA was evaporated under a stream of nitrogen. The crude peptide was precipitated with cold ether and washed with cold ether twice. Finally, the peptide was purified by RP-HPLC on C18 prep column over a 15-80% buffer B gradient in 40 minutes. The purified peptide was analyzed by analytical RP-HPLC and ESI-MS to confirm its identity. Note that no attempt was made to separately isolate the 5-carboxyfluorescein and 6-carboxyfluorescein conjugates, thus the peptide is a mixture of these two isomers.

[0081] Cloning of Ub-Intein fusions: All Ub-Intein fusions were cloned into a modified pTXB1 vector from NEB containing ubiquitin in which a His₆-tag and stop codon were inserted between the MxeGyrA intein and the chitin binding domain. This resulted in a plasmid, pTXB1-Ub-MxeGyrA-ATEA-H₆ that encodes for the following protein, called called Ub-MxeGyrA-ATEA-

H6:

MQIFVKTLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQQRLLIFAGKQLEDGRTLSDYN

IQKESTLHLVLRRLRGGCITGDALVALPEGESVRIADIVPGARPNSDNAIDLKVLDRHGNP

VLADRLFHSGEHPVYTVRTVEGLRVTGTANHPLLCLVDVAGVPTLLWKLIDEIKPGDYAV

IQRSAFSVDCAGFARGKPEFAPTTYTVGVPGLVRFLEAHRDPDAQIADELTDGRFYA

KVASVTDAGVQPVYSLRVDADHAFITNGFVSHATEAHHHHHH (SEQ ID NO: 764)

in which the intein sequence for MxeGyrA (N198A) is shown in bold, preceded by ubiquitin and followed by the endogenous local C-extein sequence (underlined) and a His₆-tag.

[0082] This plasmid was modified to replace the MxeGyrA intein with a fused Npu intein. First, the myc-KanR-NpuDnaE-Split plasmid was modified by QuikChange to remove the iRBS sequence separating the NpuN and NpuC genes. The resulting plasmid, myc-KanR-NpuDnaE-Fused, was then used as a template to amplify megaprimers bearing the fused Npu intein with overhangs homologous to the sequences surrounding MxeGyrA in the modified pTXB1 vector. The Npu gene with the N137A mutation was inserted in place of MxeGyrA using overlap-extension PCR with the Phusion polymerase. (39) Importantly, this construct was modified to include the native C-extein residues of Npu (CFN) instead of those for MxeGyrA (TEA). The resulting plasmid, pTXB1-Ub-NpuDnaE-ACFN-H₆ encoded for the following protein:

MQIFVKTLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQQRLLIFAGKQLEDGRTLSDYN

IQKESTLHLVLRRLRGGCLSYETEILTVEYGLLP~~IGKIVEKRIE~~CTVYSVDNNGNIYTQPVAQWHRGGEQEVFEYCLEDGSLIRATKDHKFMTVDGQMLPIDEIFERE~~LDLMRVDNLPNIK~~IATRKYLGKQNVYDIGVERDHN~~FAL~~KNGFIASACFNHHHHHH (SEQ ID NO: 765)

This fusion showed substantial *in vivo* hydrolysis of ubiquitin when expressed in *E. coli*. Thus, it was further modified using QuikChange mutagenesis by mutating the +1 cysteine to alanine, generating the plasmid pTXB1-Ub-NpuDnaE-AAFN-H₆. This plasmid encoded for the following protein (Ub-NpuDnaE-AAFN-H₆) that was used for *in vitro* thiolysis experiments:

MQIFVKTLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQQRLLIFAGKQLEDGRTLSDYN

IQKESTLHLVLRRLRGGCLSYETEILTVEYGLLP~~IGKIVEKRIE~~CTVYSVDNNGNIYTQPVAQWHRGGEQEVFEYCLEDGSLIRATKDHKFMTVDGQMLPIDEIFERE~~LDLMRVDNLPNIK~~IATRKYLGKQNVYDIGVERDHN~~FAL~~KNGFIASAAFNHHHHHH (SEQ ID NO: 766)

The pTXB1-Ub-AvaDnaE-AAFN-H₆ and pTXB1-Ub-MchtDnaE-AAFN-H₆ plasmids, encoding for the following protein sequences (Ub-AvaDnaE-AAFN-H₆ and Ub-MchtDnaE-AAFN-H₆, respectively), were cloned analogously by modifying the pTXB1-Ub-NpuDnaE-AAFN-H₆ plasmid.

Ub-AvaDnaE-AAFN-H₆

MQIFVKTLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQQRLLIFAGKQLEDGRTLSDYN

IQKESTLHLVLRRLRGGCLSYDTEVLTVEYGFVPIGEIVDKGIECSVFSIDSNGIVYTQPI

AQWHRGKQEVFEYCLEDGSIKATKDHKFMTQDGKMLPIDEIFEQE~~LDLLQVKGLPEIK~~

IASRKFLGVENVYDIGVGRDHNFFVKNGLIASAAFNHHHHHH (SEQ ID NO: 767)

Ub-MchtDnaE-AAFN-H₆

MQIFVKTLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQQRLLIFAGKQLEDGRTLSDYN

IQKESTLHLVLRRLRGGCLSYDTQILTVEYGAVAIGEIVEKQIECTVYSVDENGYVYTQPI
 AQWHNRGEQEVFEYLLLEDGATIRATKDHKFMTDEDQMLPIDQIFEQGLELKQVEVLQPVF
 VKIVRRQSLGVQNVYDIGVEKDNHFCCLASGEIASAAFNHHHHHH (SEQ ID NO: 768)

As a control for the removal of the +1 Cys residue in the DnaE intein constructs, the +1 Thr residue was mutated from the pTXB1-Ub-MxeGyrA-ATEA-H₆ plasmid by QuikChange mutagenesis to yield the plasmid pTXB1-Ub-MxeGyrA-AAEA-H₆, encoding for the protein Ub-MxeGyrA-AAEA-H₆.

MQIFVKTLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQQRLLIFAGKQLEDGRTLSDYN
 IQKESTLHLVLRRLRGGCITGDALVALPEGESVRIADIVPGARPNSDNAIDLKVLDRHGNP
 VLADRLFHSGEHPVYTVRTVEGLRVTGTANHPLLCCLVDVAGVPTLLWLKLIDEIKPGDYAV
 IQRSAFSVDCAGFARGKPEFAPTTYTVGVPGLVRFLEAHRDPDAQIADELTDGRFYA
 KVASVTDAGVQPVYSLRVDTADHAFTNGFVSHA^{AE}AHHHHHH (SEQ ID NO: 769)

[0083] Cloning of additional fusions to fused DnaE inteins: Several other proteins were fused to AvaDnaE or MchtDnaE to test the sequence dependence on thiolysis from these inteins. The proteins utilized were the N-terminal SH3 domain of human Grb2 (AAs 1-55 +/-an exogenous C-terminal Gly), the SH2 domain of human Abl kinase (AAs 122-217), eGFP, and the catalytic domain of human PARP1 (AAs 657-1015). All plasmids were cloned using the aforementioned methods to yield plasmids encoding the following proteins:

SH3-AvaDnaE-AAFN-H₆

MEAIKAYDFKATADDELSFKRGDILKVLNEECDQNWYKAELNGKDGFIKPNYIEMCLSYD
 TEVLTVEYGFVPIGEIVDKGIECSVFSIDSNGIVYTQPIAQWHHRGKQEVFEYCLEDGSI
 IKATKDHKFMTQDGKMLPIDEIFEQELDLLQVKGLPEIKIASRKFLGVENVYDIGVGRDH
 NFFVKNGLIASAAFNHHHHHH (SEQ ID NO: 770)

SH3-Gly-AvaDnaE-AAFN-H₆

MEAIKAYDFKATADDELSFKRGDILKVLNEECDQNWYKAELNGKDGFIKPNYIEMGCLSY
 DTEVLTVEYGFVPIGEIVDKGIECSVFSIDSNGIVYTQPIAQWHHRGKQEVFEYCLEDGS
 I IKATKDHKFMTQDGKMLPIDEIFEQELDLLQVKGLPEIKIASRKFLGVENVYDIGVGRD
 HNFFVKNGLIASAAFNHHHHHH (SEQ ID NO: 771)

SH3-MchtDnaE-AAFN-H₆

MEAIKAYDFKATADDELSFKRGDILKVLNEECDQNWYKAELNGKDGFIKPNYIEMCLSYD
 TQILTVEYGAVAIGEIVEKQIECTVYSVDENGYVYTQPIAQWHNRGEQEVFEYLLLEDGAT
 IRATKDHKFMTDEDQMLPIDQIFEQGLELKQVEVLQPVFVKIVRRQSLGVQNVYDIGVEK
 DNHFCCLASGEIASAAFNHHHHHH (SEQ ID NO: 772)

SH2-AvaDnaE-AAFN-H₆

MLEKHSWYHGPVSRNAAEYLLSSGINGSFLVRESESSPGQRSISLRYEGRVYHYRINTAS
 DGKLYVSSSRFNTLAELVHHHSTVADGLITTLHYPA^{CLSYD}TEVLTVEYGFVPIGEIVD
 KGIECSVFSIDSNGIVYTQPIAQWHHRGKQEVFEYCLEDGSI IKATKDHKFMTQDGKMLP
 IDEIFEQELDLLQVKGLPEIKIASRKFLGVENVYDIGVGRDHNFFVKNGLIASAAFNHHHH

HHH (SEQ ID NO: 773)

eGFP-AvaDnaE-AAFN-H₆

MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTTLKFICTTGKLPVPWPT
LVTTLTYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL
VNRIELKGIDFKEDGNILGHKLEYNNSHNVYIMADKQKNGIKVNFKIRHNIEDGSGVQLA
DHYQQNTPIGDGPVLLPDNHYLSTQSALS KDPNEKRDMVLLEFVTAAGITLGMDELYKC
LSYDTEVLTV EYGFVPIGEIVDKGIECSVFSIDSNGIVYTQPIAQWHHRGKQEVFEYCLE
DGSIIKATKDHKFM TQDGKMLPIDEIFEQELDLLQVKGLPEIKIASRKFLGVENVYDIGV
GRDHNFFVKNGLIASAAFNHHHHHH (SEQ ID NO: 774)

PARP_C-AvaDnaE-AAFN-H₆

MVNPGTKSKLPKPVQDLIKMIFDVESMKAMVEYEIDLQKMPLGKLSKRQIQAAYSILSE
VQQAVSQGSSDSQILDLSNRFYTLIPHDFGMKKPPLLNNADSVQAKAEMLDNLLDIEVAY
SLLRGGSDSSKDPIDVNYEKLKTDIKVVD RDSEAEIIRKYVKNTHATTHNAYDLEVID
IFKIEREGECQRYKPFKQLHNRRLWLHGSRTTNFAGILSQGLRIAPPEAPVTGYMFGKGI
YFADMVSKSANYCHTSQGDPIGLILLGEVALGNMYELKHASHISKLPKGKHSVKGLGKTT
PDPSANISLDGVDVPLGTGISSGVNDTSLLYNEYIVYDIAQVNLKYLLKLKFNFKTSLWC
LSYDTEVLTV EYGFVPIGEIVDKGIECSVFSIDSNGIVYTQPIAQWHHRGKQEVFEYCLE
DGSIIKATKDHKFM TQDGKMLPIDEIFEQELDLLQVKGLPEIKIASRKFLGVENVYDIGV
GRDHNFFVKNGLIASAAFNHHHHHH (SEQ ID NO: 775)

[0084] Purification of various Protein-Intein fusions: *E. coli* BL21(DE3) cells transformed with each Protein-Intein fusion plasmid were grown in 1 L of LB medium containing ampicillin (100 µg/mL) at 37 °C until OD₆₀₀ = 0.6. Then, expression was induced by addition of 0.5 mM IPTG and incubation for 3 hours at 37 °C or incubation for 16 hours at 18 °C. All Ub fusions were expressed at 37 °C, the eGFP fusion was expressed at 18 °C, and the SH3, SH2, and PARP_C fusions were expressed at both temperatures. After harvesting the cells by centrifugation (10,500 rcf, 30 min), the cell pellets were transferred to 50 mL conical tubes with 5 mL of lysis buffer (50 mM phosphate, 300 mM NaCl, 5 mM imidazole, No BME, pH 8.0) and stored at -80°C. The cell pellets were resuspended by adding an additional 15 mL of lysis buffer supplemented with Complete protein inhibitor cocktail. Cells were lysed by sonication (35% amplitude, 8x 20 second pulses separated by 30 seconds on ice). The soluble fraction was recovered by centrifugation (35,000 rcf, 30 min). The soluble fraction was mixed with 2 mL of Ni-NTA resin and incubated at 4°C for 30 minutes. After incubation, the slurry was loaded onto a fritted column. After discarding the flow-through, the column was washed with 5 column volumes (CV) of lysis buffer, 5 CV of wash buffer 1 (lysis buffer with 20 mM imidazole), and 3 CV of wash buffer 2 (lysis buffer with 50 mM imidazole). The protein was eluted with elution buffer (lysis buffer with 250 mM imidazole) in four 1.5 CV elution fractions. The wash and elution fractions were analyzed by SDS-PAGE with loading dye containing no thiols. The cleanest fractions were pooled and treated with 10 mM TCEP for 20 minutes on ice. Then, the solution was injected on an S75 or S200 10/300 gel filtration column (2× 1 mL injections), and eluted over 1.35 CV in thiolysis buffer (100 mM phosphates, 150 mM NaCl, 1 mM EDTA, 1mM

TCEP, pH 7.2). The FPLC fractions were analyzed by SDS-PAGE with loading dye containing no thiols, and the purest fractions were pooled and analyzed by analytical RP-HPLC and mass spectrometry. The concentration of pure protein was determined by UV $A_{280\text{nm}}$.

[0085] Thiolysis of Ub-Intein fusions and ligation of ubiquitin to a small fluorescent peptide: For each Ub-Intein fusion protein, four reactions were carried on a 100 μL scale at 30 °C. In the first reaction to monitor background hydrolysis, the fusion protein (50 μM) was incubated in thiolysis buffer (100 mM phosphate, 150 mM NaCl, 1 mM EDTA, 1mM TCEP, pH 7.2) supplemented with freshly added TCEP (an additional 5 mM). In the second and third reactions, the protein was incubated identically as for the first reaction, except that each reaction had either 100 mM MESNa or 1 mM CGK-Fluorescein. In the fourth reaction, both MESNa and the peptide were added. At various time points, 5 μL of reaction solution were removed and quenched in 30 μL 2 $\times$ SDS loading dye containing no thiols. As time points were collected, they were stored at -20 °C until the end of the reaction. After the reaction, the 35 μL quenched time points were thawed, treated with 1 μL of a 1 M TCEP stock solution, boiled for 10 minutes, and centrifuged at 17,000 rcf for 1 minute. Time points (5 μL) were loaded onto 12% Bis-Tris gels and run in MES-SDS running buffer. The gels were first imaged on a fluorescence imager to visualize the Ub-CGK-Fluorescein ligation product. Then the gels were coomassie-stained and imaged using the Licor Odyssey scanner. In addition, the reaction endpoints were quenched by 20-fold dilution in H_2O with 0.1% TFA and injected on an analytical C18 RP-HPLC column. The mixture was separated over a 2 minute isocratic phase in 0% B followed by a 0-73% B linear gradient in 30 minutes. The major peaks were collected and analyzed by MS.

[0086] Thiolysis of SH3-, SH2-, eGFP-, and PARPc-Intein fusions: Thiolysis reactions with several other proteins fused to the AvaDnaE and MchtDnaE fused inteins were carried out analogously to the ubiquitin reactions described above. In a typical reaction, carried out on a 300 μL scale at 30 °C, 10 μM fusion protein was treated with 5 mM TCEP in thiolysis buffer then incubated in the presence or absence of MESNa (either 100 mM or 200 mM) added from a pH-adjusted 1 M stock solution. At various time points, aliquots (15 μL) of the reaction solution were quenched in 30 μL of 2 $\times$ SDS gel loading dye containing no thiols and stored at -20 °C until the end of the reaction. After the reaction, the 45 μL quenched time points were thawed, treated with 1 μL of a 1 M TCEP stock solution, boiled for 10 minutes, and centrifuged at 17,000 rcf for 1 minute. Time points (15 μL) were loaded onto 12% Bis-Tris gels and run in MES-SDS running buffer. Then the gels were coomassie-stained and imaged using the Licor Odyssey scanner. In addition, the reaction endpoints were quenched by 4-fold dilution in H_2O with 0.1% TFA and injected on an analytical C18 RP-HPLC column. The mixture was separated over a 2 minute isocratic phase in 0% B followed by a 0-73% B linear gradient in 30 minutes. The product peaks were collected and analyzed by MS.

Observation of the Linear Thioester Intermediate in fused DnaE inteins

[0087] For Npu, Ava, and Mcht fusions to ubiquitin, three peaks were visible for the purified protein when directly injected onto a C18 RP-HPLC column from a neutral buffer. These peaks all had the same mass of the desired protein. When diluted 20-fold in H₂O containing 0.1% TFA (pH 2) and incubated for at least two hours at room temperature, the first two peaks merged into the third peak (Figure 4d). The same observation could not be made for MxeGyrA under identical conditions. To further confirm that an equilibrium between the precursor amide and linear thioester was occurring, the Ub-NpuDnaE-AAFN-H₆ protein was diluted 20-fold in thiolysis buffer containing 1% SDS. Before boiling, the two major peaks were visible. After boiling for 10 minutes, when the protein was unfolded, the first major peak partially converged into the second major peak, suggesting that the latter was the amide, which should be more stable in the unfolded intein. Additional evidence that the three peaks were in equilibrium came from pH titrations. The protein was diluted 20-fold into citric acid/phosphate buffers ranging from pH 2 to pH 8, incubated at room temperature for 3-4 hours, then analyzed by HPLC over a 30-73% B gradient in 30 minutes (Figure 4d). The relative abundance of the three species was modulated and showed a bell-shaped pH dependence, similar to the activities of enzymes containing multiple ionizable functional groups in their active sites.

[0088] In addition to observing the desired protein mass from all three observed HPLC peaks, the presence of a -18 Da species was observed in the first two peaks. This mass change is characteristic of a dehydration reaction, and such a reaction has been previously reported by Mootz *et. al.* for a mutant form of the SspDnaB intein that cannot efficiently catalyze the initial N-to-S acyl shift. (41) Specifically, the tetrahedral intermediate of the forward and reverse acylation reactions can undergo acid-catalyzed dehydration to yield a thiazoline side product. For Mootz and co-workers, this species was an irreversible side-product for their mutant intein under normal reaction conditions, and it lead to low yields. In the systems herein, where the DnaE inteins can react to completion, this species is either an artifact of acidification during RP-HPLC or it is fully reversible under normal reaction conditions. It is noteworthy that the observation of the thiazoline by MS further validates the presence of detectable levels of the tetrahedral intermediate in the present reaction mixtures.

[0089] For the DnaE intein fusions to proteins other than ubiquitin, similar HPLC profiles were observed with multiple peaks at neutral pH, however the ratios of the three peaks varied depending on the sequence. Additionally, for sequences more similar to the endogenous "A-E-Y" DnaE N-extein (such as the SH3 fusions with an "I-E-M" sequence), substantial accumulation of a dehydrated product (as much as 50% by HPLC/MS) was seen, similar to that observed by Mootz *et. al.* for the split SspDnaB intein. (41) For these constructs, this species appears to accumulate during protein expression resulting in a mixture of "trapped" (dehydrated) and "free" (native, hydrated) fusion protein. Upon addition of MESNa at neutral pH, the "free" protein rapidly undergoes thiolysis to yield the desired product, and the "trapped" protein slowly rehydrates and is also thiolized to yield the same desired product. Thus, in the reaction progress curves, a "burst" phase was observed followed by a slower phase. Importantly, the accumulation of dehydrated fusion protein could be reduced by expression at lower temperatures (18 °C instead of 37 °C), and these reactions could be driven faster and closer to completion by increasing the MESNa concentration from 100 mM to 200 mM MESNa.

In addition, it is noteworthy that for the SH3 thiolysis reaction, the MchtDnaE intein was substantially more efficient than the AvaDnaE intein, suggesting that different fused DnaE inteins may be preferable depending on the protein of interest.

References

[0090]

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<151> 2012-06-27

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Pro Ile Gly Lys Ile Val Glu Lys Arg Ile Glu Cys Thr Val Tyr Ser
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Val Asp Asn Asn Gly Asn Ile Tyr Thr Gln Pro Val Ala Gln Trp His
35 40 45

Asp Arg Gly Glu Gln Glu Val Phe Glu Tyr Cys Leu Glu Asp Gly Ser
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Leu Ile Arg Ala Thr Lys Asp His Lys Phe Met Thr Val Asp Gly Gln
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Val Asp Pro Glu Gly Arg Val Tyr Thr Gln Ala Ile Ala Gln Trp His
35 40 45

Asp Arg Gly Glu Gln Glu Val Leu Glu Tyr Glu Leu Glu Asp Gly Ser
50 55 60

Val Ile Arg Ala Thr Ser Asp His Arg Phe Leu Thr Thr Asp Tyr Gln
65 70 75 80

Leu Leu Ala Ile Glu Glu Ile Phe Ala Arg Gln Leu Asp Leu Leu Thr
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Pro Ile Gly Lys Ile Val Glu Glu Lys Ile Glu Cys Ser Val Tyr Thr
 20 25 30

Val Asp Glu Asn Gly Phe Val Tyr Thr Gln Pro Ile Ala Gln Trp His
 35 40 45

Pro Arg Gly Gln Gln Glu Ile Ile Glu Tyr Thr Leu Glu Asp Gly Arg
 50 55 60

Lys Ile Arg Ala Thr Lys Asp His Lys Met Met Thr Glu Ser Gly Glu
 65 70 75 80

Met Leu Pro Ile Glu Glu Ile Phe Gln Arg Glu Leu Asp Leu Lys Val
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Glu Thr Phe His Glu Met Ser Leu Leu Arg Arg Gly Ala Lys
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Pro Ile Gly Glu Ile Val Gly Lys Ala Ile Glu Cys Arg Val Tyr Ser
 20 25 30

Val Asp Gly Asn Gly Asn Ile Tyr Thr Gln Ser Ile Ala Gln Trp His
 35 40 45

Asn Arg Gly Glu Gln Glu Val Phe Glu Tyr Thr Leu Glu Asp Gly Ser
 50 55 60

Ile Ile Arg Ala Thr Lys Asp His Lys Phe Met Thr Thr Asp Gly Glu
 65 70 75 80

Met Leu Pro Ile Asp Glu Ile Phe Ala Arg Gln Leu Asp Leu Met Gln
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Val Gln Gly Leu His
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Pro Ile Gly Glu Ile Val Glu Lys Gly Ile Glu Cys Ser Val Phe Ser
 20 25 30

Ile Asn Asn Asn Gly Ile Val Tyr Thr Gln Pro Ile Ala Gln Trp His
 35 40 45

His Arg Gly Lys Gln Glu Val Phe Glu Tyr Cys Leu Glu Asp Gly Ser
 50 55 60

Ile Ile Lys Ala Thr Lys Asp His Lys Phe Met Thr Gln Asp Gly Lys
 65 70 75 80

Met Leu Pro Ile Asp Glu Ile Phe Glu Gln Glu Leu Asp Leu Leu Gln
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Val Lys Gly Leu Pro Glu
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 20 25 30

Ile Asp Ser Asn Gly Ile Val Tyr Thr Gln Pro Ile Ala Gln Trp His
 35 40 45

His Arg Gly Lys Gln Glu Val Phe Glu Tyr Cys Leu Glu Asp Gly Ser
 50 55 60

Ile Ile Lys Ala Thr Lys Asp His Lys Phe Met Thr Gln Asp Gly Lys
 65 70 75 80

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Val Lys Gly Leu Pro Glu
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<213> *Cylindrospermopsis raciborskii*

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20 25 30

Leu Asn Asp Ser Gly Asn Val Tyr Thr Gln Pro Ile Gly Gln Trp His
35 40 45

Asp Arg Gly Val Gln Asp Leu Tyr Glu Tyr Cys Leu Asp Asp Gly Ser
50 55 60

Thr Ile Arg Ala Thr Lys Asp His Lys Phe Met Thr Thr Gln Gly Glu
65 70 75 80

Met Val Pro Ile Asp Glu Ile Phe His Gln Gly Trp Glu Leu Val Gln
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Ile Val Asp Arg Lys Leu
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20 25 30

Val Asn Lys Asn Gly Phe Val Tyr Thr Gln Ser Ile Ala Gln Trp His
35 40 45

His Arg Gly Glu Gln Glu Val Phe Glu Tyr Tyr Leu Glu Asp Gly Glu
50 55 60

Thr Ile Arg Ala Thr Lys Asp His Lys Phe Met Thr Thr Glu Gly Lys
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Leu Thr Val

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25

30

Val Asp Lys Asn Gly Phe Val Tyr Thr Gln Asn Ile Ala Gln Trp His
35 40 45

Leu Arg Gly Gln Gln Glu Val Phe Glu Tyr Tyr Leu Asp Asp Gly Ser
50 55 60

Ile Leu Arg Ala Thr Lys Asp His Gln Phe Met Thr Leu Glu Gly Glu
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Ile Lys Ile

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Tyr Ile Gly Lys Ile Val Glu Glu Asn Ile Asn Cys Thr Val Tyr Thr
20 25 30

Val Asp Lys Asn Gly Phe Val Tyr Thr Gln Thr Ile Ala Gln Trp His
35 40 45

Asn Arg Gly Glu Gln Glu Ile Phe Glu Tyr Asp Leu Glu Asp Gly Ser
50 55 60

Lys Ile Lys Ala Thr Lys Asp His Lys Phe Met Thr Ile Asp Gly Glu
65 70 75 80

Met Leu Pro Ile Asp Glu Ile Phe Glu Lys Asn Leu Asp Leu Lys Gln
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Val Val Ser His Pro Asp Asp Tyr Leu Val

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Pro Ile Ala Lys Ile Val Ser Glu Glu Ile Asn Cys Thr Val Tyr Thr
          20          25          30

Val Asp Gln Asn Gly Phe Val Tyr Ser Gln Pro Ile Ser Gln Trp His
          35          40          45

Glu Arg Gly Leu Gln Glu Val Phe Glu Tyr Thr Leu Glu Asn Gly Gln
          50          55          60

Thr Ile Gln Ala Thr Lys Asp His Lys Phe Met Thr Ser Asp Gly Glu
65          70          75          80

Met Leu Ala Ile Asp Thr Ile Phe Glu Arg Gly Leu Asp Leu Lys Ser
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Ser Asp Phe Ser
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Val Asp Glu Asn Gly Tyr Val Tyr Thr Gln Pro Ile Ala Gln Trp His
          35          40          45

Asn Arg Gly Glu Gln Glu Val Phe Glu Tyr Leu Leu Glu Asp Gly Ala
          50          55          60

Thr Ile Arg Ala Thr Lys Asp His Lys Phe Met Thr Asp Glu Asp Gln
65          70          75          80

Met Leu Pro Ile Asp Gln Ile Phe Glu Gln Gly Leu Glu Leu Lys Gln
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20 25 30

Val Asp Glu Asn Gly Phe Val Tyr Thr Gln Ala Ile Ala Gln Trp His
35 40 45

Asp Arg Gly Tyr Gln Glu Ile Phe Ala Tyr Glu Leu Ala Asp Gly Ser
50 55 60

Val Ile Arg Ala Thr Lys Asp His Gln Phe Met Thr Glu Asp Gly Gln
65 70 75 80

Met Phe Pro Ile Asp Glu Ile Trp Glu Lys Gly Leu Asp Leu Lys Lys
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Leu Pro Thr Val Gln Asp Leu Pro Ala Ala Val Gly Tyr Thr Val Ser
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<210> 14

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Cys Asn Pro Asp Gly Tyr Ile Tyr Ser Gln Pro Ile Gly Gln Trp His
35 40 45

Gln Arg Gly Glu Gln Glu Val Ile Glu Tyr Glu Leu Ser Asp Gly Arg
50 55 60

Ile Ile Arg Ala Thr Ala Asp His Arg Phe Met Thr Glu Glu Gly Glu
65 70 75 80

Met Leu Ser Leu Asp Glu Ile Phe Glu Arg Ser Leu Glu Leu Lys Gln
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Pro Ile Gln Thr Ile Val Glu Gln Glu Leu Leu Cys His Val Tyr Ser
20 25 30

Val Asp Ala Gln Gly Leu Ile Tyr Ala Gln Leu Ile Glu Gln Trp His
35 40 45

Gln Arg Gly Asp Arg Leu Leu Tyr Glu Tyr Glu Leu Glu Asn Gly Gln
50 55 60

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

Leu Asp Gly Gln Gly His Leu Tyr Thr Gln Pro Ile Ala Gln Trp His
35 40 45

Phe Gln Gly Phe Arg Pro Val Tyr Glu Tyr Gln Leu Glu Asp Gly Ser
50 55 60

Thr Ile Cys Ala Thr Pro Asp His Arg Phe Met Thr Thr Arg Gly Gln
65 70 75 80

Met Leu Pro Ile Glu Gln Ile Phe Gln Glu Gly Leu Glu Leu Trp Gln
85 90 95

Val Ala Ile Ala Pro Arg Gln Ala Leu Leu Gln Gly Leu Lys Pro Ala

Val Ala Arg Ala Phe Arg Gln Ala Met Met Gln Gly Met Lys Phe Ala
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Val Gln Met Ser Gly
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Pro Ile Gly Lys Ile Val Glu Tyr Arg Ile Glu Cys Thr Val Tyr Thr
20 25 30

Val Asp Lys Asn Gly Tyr Ile Tyr Thr Gln Pro Ile Ala Gln Trp His
35 40 45

Asn Arg Gly Met Gln Glu Val Tyr Glu Tyr Ser Leu Glu Asp Gly Thr
50 55 60

Val Ile Arg Ala Thr Pro Glu His Lys Phe Met Thr Glu Asp Gly Gln
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20 25 30

Leu Asp Pro Gln Gly His Leu Tyr Thr Gln Pro Ile Ala Gln Trp His
35 40 45

Phe Gln Gly Phe Arg Pro Val Tyr Ala Tyr Gln Leu Glu Asp Gly Ser
50 55 60

Thr Ile Cys Ala Thr Pro Asp His Arg Phe Met Thr Thr Ser Gly Gln
65 70 75 80

Met Leu Pro Ile Glu Gln Ile Phe Arg Glu Gly Leu Glu Leu Trp Gln
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90

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Val Ala Ile Ala Pro Pro Gly Ala Leu Ala Gln Gly Leu Lys Pro Ala
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Val Gln Met Ser Cys
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Val Asp Glu Asn Gly Phe Val Tyr Thr Gln Pro Ile Ala Gln Trp His
 35 40 45

Asp Arg Gly Glu Gln Glu Val Phe Glu Tyr Cys Leu Glu Asp Gly Ser
 50 55 60

Thr Ile Arg Ala Thr Lys Asp His Lys Phe Met Thr Glu Asp Gly Glu
 65 70 75 80

Met Leu Pro Ile Asp Glu Ile Phe Glu Gln Gly Leu Asp Leu Lys Gln
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Val Lys Gly Leu Pro Asp
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Val Asp Asn Asn Gly Asn Ile Tyr Thr Gln Pro Val Ala Gln Trp His
 35 40 45

33 40 43
 Asp Arg Gly Glu Gln Glu Val Phe Glu Tyr Ser Leu Glu Asp Gly Ser
 50 55 60
 Leu Ile Arg Ala Thr Lys Asp His Lys Phe Met Thr Val Asp Gly Gln
 65 70 75 80
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 35 40 45
 Asp Arg Gly Glu Gln Glu Val Phe Glu Tyr Xaa Leu Glu Asp Gly Ser
 50 55 60
 Leu Ile Arg Ala Thr Lys Asp His Lys Phe Met Thr Val Asp Gly Gln
 65 70 75 80
 Met Leu Pro Ile Asp Glu Ile Phe Glu Arg Glu Leu Asp Leu Met Arg
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Pro	Ile	Gly	Lys	Ile	Val	Ser	Glu	Glu	Ile	Asn	Xaa	Ser	Val	Tyr	Ser
			20					25					30		

Val	Asp	Pro	Glu	Gly	Arg	Val	Tyr	Thr	Gln	Ala	Ile	Ala	Gln	Trp	His
		35					40					45			

Asp	Arg	Gly	Glu	Gln	Glu	Val	Leu	Glu	Tyr	Glu	Leu	Glu	Asp	Gly	Ser
	50					55					60				

Val	Ile	Arg	Ala	Thr	Ser	Asp	His	Arg	Phe	Leu	Thr	Thr	Asp	Tyr	Gln
65					70					75					80

Leu	Leu	Ala	Ile	Glu	Glu	Ile	Phe	Ala	Arg	Gln	Leu	Asp	Leu	Leu	Thr
			85						90					95	

Leu	Glu	Asn	Ile	Lys	Gln	Thr	Glu	Glu	Ala	Leu	Asp	Asn	His	Arg	Leu
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Pro	Phe	Pro	Leu	Leu	Asp	Ala	Gly	Thr	Ile	Lys
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Pro	Ile	Gly	Lys	Ile	Val	Glu	Glu	Lys	Ile	Glu	Xaa	Ser	Val	Tyr	Thr
			20					25					30		

Val	Asp	Glu	Asn	Gly	Phe	Val	Tyr	Thr	Gln	Pro	Ile	Ala	Gln	Trp	His
		35					40					45			

Pro Arg Gly Gln Gln Glu Ile Ile Glu Tyr Thr Leu Glu Asp Gly Arg
50 55 60

Lys Ile Arg Ala Thr Lys Asp His Lys Met Met Thr Glu Ser Gly Glu
65 70 75 80

Met Leu Pro Ile Glu Glu Ile Phe Gln Arg Glu Leu Asp Leu Lys Val
85 90 95

Glu Thr Phe His Glu Met Ser Leu Leu Arg Arg Gly Ala Lys
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Pro Ile Gly Glu Ile Val Gly Lys Ala Ile Glu Xaa Arg Val Tyr Ser
20 25 30

Val Asp Gly Asn Gly Asn Ile Tyr Thr Gln Ser Ile Ala Gln Trp His
35 40 45

Asn Arg Gly Glu Gln Glu Val Phe Glu Tyr Thr Leu Glu Asp Gly Ser
50 55 60

Ile Ile Arg Ala Thr Lys Asp His Lys Phe Met Thr Thr Asp Gly Glu
65 70 75 80

Met Leu Pro Ile Asp Glu Ile Phe Ala Arg Gln Leu Asp Leu Met Gln
85 90 95

Val Gln Gly Leu His
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Pro	Ile	Gly	Glu	Ile	Val	Glu	Lys	Gly	Ile	Glu	Xaa	Ser	Val	Phe	Ser
		20						25					30		

Ile	Asn	Asn	Asn	Gly	Ile	Val	Tyr	Thr	Gln	Pro	Ile	Ala	Gln	Trp	His
	35						40					45			

His	Arg	Gly	Lys	Gln	Glu	Val	Phe	Glu	Tyr	Xaa	Leu	Glu	Asp	Gly	Ser
	50						55					60			

Ile	Ile	Lys	Ala	Thr	Lys	Asp	His	Lys	Phe	Met	Thr	Gln	Asp	Gly	Lys
65					70					75				80	

Met	Leu	Pro	Ile	Asp	Glu	Ile	Phe	Glu	Gln	Glu	Leu	Asp	Leu	Leu	Gln
			85						90					95	

Val	Lys	Gly	Leu	Pro	Glu
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Pro	Ile	Gly	Glu	Ile	Val	Asp	Lys	Gly	Ile	Glu	Xaa	Ser	Val	Phe	Ser
		20						25					30		

Ile	Asp	Ser	Asn	Gly	Ile	Val	Tyr	Thr	Gln	Pro	Ile	Ala	Gln	Trp	His

35 40 45
 His Arg Gly Lys Gln Glu Val Phe Glu Tyr Xaa Leu Glu Asp Gly Ser
 50 55 60

 Ile Ile Lys Ala Thr Lys Asp His Lys Phe Met Thr Gln Asp Gly Lys
 65 70 75 80

 Met Leu Pro Ile Asp Glu Ile Phe Glu Gln Glu Leu Asp Leu Leu Gln
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 Val Lys Gly Leu Pro Glu
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 20 25 30

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 35 40 45

 Asp Arg Gly Val Gln Asp Leu Tyr Glu Tyr Xaa Leu Asp Asp Gly Ser
 50 55 60

 Thr Ile Arg Ala Thr Lys Asp His Lys Phe Met Thr Thr Gln Gly Glu
 65 70 75 80

 Met Val Pro Ile Asp Glu Ile Phe His Gln Gly Trp Glu Leu Val Gln
 85 90 95

 Val Ser Gly Ile Ser Lys Leu Val Gln Gln Arg Thr Leu Pro Phe Ile
 100 105 110

 Ile Val Asp Arg Lys Leu
 115

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 <223> Xaa is Ala or Ser

<400> 28
 Cys Leu Ser Tyr Asp Thr Glu Ile Leu Thr Val Glu Tyr Gly Pro Met
 1 5 10 15
 Pro Ile Gly Lys Ile Val Glu Glu Asn Ile Asn Xaa Ser Val Tyr Thr
 20 25 30
 Val Asn Lys Asn Gly Phe Val Tyr Thr Gln Ser Ile Ala Gln Trp His
 35 40 45
 His Arg Gly Glu Gln Glu Val Phe Glu Tyr Tyr Leu Glu Asp Gly Glu
 50 55 60
 Thr Ile Arg Ala Thr Lys Asp His Lys Phe Met Thr Thr Glu Gly Lys
 65 70 75 80
 Met Leu Pro Ile Asp Glu Ile Phe Glu Asn Asn Leu Asp Leu Lys Lys
 85 90 95
 Leu Thr Val

<210> 29
 <211> 99
 <212> PRT
 <213> Cyanothece PCC8801

<220>
 <221> MISC_FEATURE
 <222> (28)..(28)
 <223> Xaa is Ala or Ser

<400> 29
 Cys Leu Ser Tyr Asp Thr Glu Ile Leu Thr Val Glu Tyr Gly Ala Ile
 1 5 10 15
 Pro Ile Gly Lys Val Val Glu Glu Asn Ile Asp Xaa Thr Val Tyr Thr
 20 25 30
 Val Asp Lys Asn Gly Phe Val Tyr Thr Gln Asn Ile Ala Gln Trp His
 35 40 45
 Leu Arg Gly Gln Gln Glu Val Phe Glu Tyr Tyr Leu Asp Asp Gly Ser
 50 55 60

50

55

60

Ile Leu Arg Ala Thr Lys Asp His Gln Phe Met Thr Leu Glu Gly Glu
65 70 75 80

Met Leu Pro Ile His Glu Ile Phe Glu Arg Gly Leu Glu Leu Lys Lys
85 90 95

Ile Lys Ile

<210> 30

<211> 106

<212> PRT

<213> Crocosphaera watsonii

<220>

<221> MISC_FEATURE

<222> (28)..(28)

<223> Xaa is Ala or Ser

<400> 30

Cys Leu Ser Tyr Asp Thr Glu Ile Leu Thr Val Glu Tyr Gly Ala Met
1 5 10 15

Tyr Ile Gly Lys Ile Val Glu Glu Asn Ile Asn Xaa Thr Val Tyr Thr
20 25 30

Val Asp Lys Asn Gly Phe Val Tyr Thr Gln Thr Ile Ala Gln Trp His
35 40 45

Asn Arg Gly Glu Gln Glu Ile Phe Glu Tyr Asp Leu Glu Asp Gly Ser
50 55 60

Lys Ile Lys Ala Thr Lys Asp His Lys Phe Met Thr Ile Asp Gly Glu
65 70 75 80

Met Leu Pro Ile Asp Glu Ile Phe Glu Lys Asn Leu Asp Leu Lys Gln
85 90 95

Val Val Ser His Pro Asp Asp Tyr Leu Val
100 105

<210> 31

<211> 100

<212> PRT

<213> Microcystis aeruginosa

<220>

<221> MISC_FEATURE

<222> (28)..(28)

<223> Xaa is Ala or Ser

<400> 31

Cys Leu Gly Gly Glu Thr Leu Ile Leu Thr Glu Glu Tyr Gly Leu Leu
1 5 10 15

Pro Ile Ala Lys Ile Val Ser Glu Glu Ile Asn Xaa Thr Val Tyr Thr

20

25

30

Val Asp Gln Asn Gly Phe Val Tyr Ser Gln Pro Ile Ser Gln Trp His
35 40 45

Glu Arg Gly Leu Gln Glu Val Phe Glu Tyr Thr Leu Glu Asn Gly Gln
50 55 60

Thr Ile Gln Ala Thr Lys Asp His Lys Phe Met Thr Ser Asp Gly Glu
65 70 75 80

Met Leu Ala Ile Asp Thr Ile Phe Glu Arg Gly Leu Asp Leu Lys Ser
85 90 95

Ser Asp Phe Ser
100

<210> 32

<211> 104

<212> PRT

<213> Microcoleus chthonoplastes

<220>

<221> MISC_FEATURE

<222> (28)..(28)

<223> Xaa is Ala or Ser

<400> 32

Cys Leu Ser Tyr Asp Thr Gln Ile Leu Thr Val Glu Tyr Gly Ala Val
1 5 10 15

Ala Ile Gly Glu Ile Val Glu Lys Gln Ile Glu Xaa Thr Val Tyr Ser
20 25 30

Val Asp Glu Asn Gly Tyr Val Tyr Thr Gln Pro Ile Ala Gln Trp His
35 40 45

Asn Arg Gly Glu Gln Glu Val Phe Glu Tyr Leu Leu Glu Asp Gly Ala
50 55 60

Thr Ile Arg Ala Thr Lys Asp His Lys Phe Met Thr Asp Glu Asp Gln
65 70 75 80

Met Leu Pro Ile Asp Gln Ile Phe Glu Gln Gly Leu Glu Leu Lys Gln
85 90 95

Val Glu Val Leu Gln Pro Val Phe
100

<210> 33
 <211> 112
 <212> PRT
 <213> *Oscillatoria limnetica*

<220>
 <221> MISC_FEATURE
 <222> (28)..(28)
 <223> Xaa is Ala or Ser

<400> 33
 Cys Leu Ser Tyr Asn Thr Glu Val Leu Thr Val Glu Tyr Gly Pro Leu
 1 5 10 15
 Pro Ile Gly Lys Ile Val Asp Glu Gln Ile His Xaa Arg Val Tyr Ser
 20 25 30
 Val Asp Glu Asn Gly Phe Val Tyr Thr Gln Ala Ile Ala Gln Trp His
 35 40 45
 Asp Arg Gly Tyr Gln Glu Ile Phe Ala Tyr Glu Leu Ala Asp Gly Ser
 50 55 60
 Val Ile Arg Ala Thr Lys Asp His Gln Phe Met Thr Glu Asp Gly Gln
 65 70 75 80
 Met Phe Pro Ile Asp Glu Ile Trp Glu Lys Gly Leu Asp Leu Lys Lys
 85 90 95
 Leu Pro Thr Val Gln Asp Leu Pro Ala Ala Val Gly Tyr Thr Val Ser
 100 105 110

<210> 34
 <211> 113
 <212> PRT
 <213> *Synechococcus elongatus*

<220>
 <221> MISC_FEATURE
 <222> (28)..(28)
 <223> Xaa is Ala or Ser

<220>
 <221> MISC_FEATURE
 <222> (32)..(32)
 <223> Xaa is Ala or Ser

<220>
 <221> MISC_FEATURE
 <222> (33)..(33)

<223> Xaa is Ala or Ser

<400> 34

Cys Leu Ala Ala Asp Thr Glu Val Leu Thr Val Glu Tyr Gly Pro Ile
1 5 10 15

Ala Ile Gly Lys Leu Val Glu Glu Asn Ile Arg Xaa Gln Val Tyr Xaa
20 25 30

Xaa Asn Pro Asp Gly Tyr Ile Tyr Ser Gln Pro Ile Gly Gln Trp His
35 40 45

Gln Arg Gly Glu Gln Glu Val Ile Glu Tyr Glu Leu Ser Asp Gly Arg
50 55 60

Ile Ile Arg Ala Thr Ala Asp His Arg Phe Met Thr Glu Glu Gly Glu
65 70 75 80

Met Leu Ser Leu Asp Glu Ile Phe Glu Arg Ser Leu Glu Leu Lys Gln
85 90 95

Ile Pro Thr Pro Leu Leu Ala Ile Ala Gln Pro Ser Pro Leu Ala Thr
100 105 110

Ala

<210> 35

<211> 107

<212> PRT

<213> Synechococcus PCC7002

<220>

<221> MISC_FEATURE

<222> (28)..(28)

<223> Xaa is Ala or Ser

<400> 35

Cys Leu Ala Gly Gly Thr Pro Val Val Thr Val Glu Tyr Gly Val Leu
1 5 10 15

Pro Ile Gln Thr Ile Val Glu Gln Glu Leu Leu Xaa His Val Tyr Ser
20 25 30

Val Asp Ala Gln Gly Leu Ile Tyr Ala Gln Leu Ile Glu Gln Trp His
35 40 45

Gln Arg Gly Asp Arg Leu Leu Tyr Glu Tyr Glu Leu Glu Asn Gly Gln
50 55 60

Met Ile Arg Ala Thr Pro Asp His Arg Phe Leu Thr Thr Thr Gly Glu
65 70 75 80

Leu Leu Pro Ile Asp Glu Ile Phe Thr Gln Asn Leu Asp Leu Ala Ala
85 90 95

Trp Ala Val Pro Asp Ser Leu Pro Arg Thr Ala
 100 105

<210> 36

<211> 117

<212> PRT

<213> Thermosynechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (28)..(28)

<223> Xaa is Ala or Ser

<220>

<221> MISC_FEATURE

<222> (67)..(67)

<223> Xaa is Ala or Ser

<400> 36

Cys Leu Ser Gly Glu Thr Ala Val Met Thr Val Glu Tyr Gly Ala Val
 1 5 10 15

Pro Ile Arg Arg Leu Val Gln Glu Arg Leu Ser Xaa His Val Tyr Ser
 20 25 30

Leu Asp Gly Gln Gly His Leu Tyr Thr Gln Pro Ile Ala Gln Trp His
 35 40 45

Phe Gln Gly Phe Arg Pro Val Tyr Glu Tyr Gln Leu Glu Asp Gly Ser
 50 55 60

Thr Ile Xaa Ala Thr Pro Asp His Arg Phe Met Thr Thr Arg Gly Gln
 65 70 75 80

Met Leu Pro Ile Glu Gln Ile Phe Gln Glu Gly Leu Glu Leu Trp Gln
 85 90 95

Val Ala Ile Ala Pro Arg Gln Ala Leu Leu Gln Gly Leu Lys Pro Ala
 100 105 110

Val Gln Met Ser Gly
 115

<210> 37

<211> 101

<212> PRT

<213> Trichodesmium erythraeum

<220>

<221> MISC_FEATURE

<222> (28)..(28)

<223> Xaa is Ala or Ser

<220>

<221> MISC_FEATURE

<222> (96)..(96)

<223> Xaa is Ala or Ser

<400> 37

Cys Leu Thr Tyr Glu Thr Glu Ile Met Thr Val Glu Tyr Gly Pro Leu
1 5 10 15

Pro Ile Gly Lys Ile Val Glu Tyr Arg Ile Glu Xaa Thr Val Tyr Thr
20 25 30

Val Asp Lys Asn Gly Tyr Ile Tyr Thr Gln Pro Ile Ala Gln Trp His
35 40 45

Asn Arg Gly Met Gln Glu Val Tyr Glu Tyr Ser Leu Glu Asp Gly Thr
50 55 60

Val Ile Arg Ala Thr Pro Glu His Lys Phe Met Thr Glu Asp Gly Gln
65 70 75 80

Met Leu Pro Ile Asp Glu Ile Phe Glu Arg Asn Leu Asp Leu Lys Xaa
85 90 95

Leu Gly Thr Leu Glu
100

<210> 38

<211> 117

<212> PRT

<213> Thermosynechococcus vulcanus

<220>

<221> MISC_FEATURE

<222> (28)..(28)

<223> Xaa is Ala or Ser

<220>

<221> MISC_FEATURE

<222> (67)..(67)

<223> Xaa is Ala or Ser

<220>

<221> MISC_FEATURE

<222> (117)..(117)

<223> Xaa is Ala or Ser

<400> 38

Cys Leu Ser Gly Glu Thr Ala Val Met Thr Val Glu Tyr Gly Ala Ile
1 5 10 15

Pro Ile Arg Arg Leu Val Gln Glu Arg Leu Ile Xaa Gln Val Tyr Ser
20 25 30

Leu Asp Pro Gln Gly His Leu Tyr Thr Gln Pro Ile Ala Gln Trp His
35 40 45

Phe Gln Gly Phe Arg Pro Val Tyr Ala Tyr Gln Leu Glu Asp Gly Ser
50 55 60

Thr Ile Xaa Ala Thr Pro Asp His Arg Phe Met Thr Thr Ser Gly Gln
65 70 75 80

Met Leu Pro Ile Glu Gln Ile Phe Arg Glu Gly Leu Glu Leu Trp Gln
85 90 95

Val Ala Ile Ala Pro Pro Gly Ala Leu Ala Gln Gly Leu Lys Pro Ala
100 105 110

Val Gln Met Ser Xaa
115

<210> 39

<211> 36

<212> PRT

<213> Nostoc punctiforme

<400> 39

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

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

Ile Ala Ser Asn
35

<210> 40

<211> 36

<212> PRT

<213> Synechocystis PCC6803

<400> 40

Met Val Lys Val Ile Gly Arg Arg Ser Leu Gly Val Gln Arg Ile Phe
1 5 10 15

Asp Ile Gly Leu Pro Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ala
20 25 30

Ile Ala Ala Asn
35

<210> 41

<211> 36

<212> PRT

<213> Aphanothece halophytica

<400> 41

Met	Val	Lys	Ile	Ile	Lys	Arg	Gln	Ser	Leu	Gly	Arg	Gln	Asn	Val	Tyr
1				5					10					15	

Asp	Val	Cys	Val	Glu	Thr	Asp	His	Asn	Phe	Val	Leu	Ala	Asn	Gly	Cys
			20					25					30		

Val	Ala	Ser	Asn
			35

<210> 42

<211> 36

<212> PRT

<213> Aphanizomenon ovalisporum

<400> 42

Met	Val	Lys	Ile	Thr	Ala	Arg	Lys	Phe	Val	Gly	Arg	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	His	His	His	Asn	Phe	Ala	Ile	Lys	Asn	Gly	Leu
			20					25					30		

Ile	Ala	Ser	Asn
			35

<210> 43

<211> 36

<212> PRT

<213> Anabaena PCC7120

<400> 43

Met	Ile	Lys	Ile	Ala	Ser	Arg	Lys	Phe	Leu	Gly	Val	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Arg	Arg	Asp	His	Asn	Phe	Phe	Ile	Lys	Asn	Gly	Leu
			20					25					30		

Ile	Ala	Ser	Asn
			35

<210> 44

<211> 36

<212> PRT

<213> Anabaena variabilis

<400> 44

Met	Ile	Lys	Ile	Ala	Ser	Arg	Lys	Phe	Leu	Gly	Val	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Gly	Arg	Asp	His	Asn	Phe	Phe	Val	Lys	Asn	Gly	Leu
			20					25					30		

Ile Ala Ser Asn
35

<210> 45

<211> 36

<212> PRT

<213> *Cylindrospermopsis raciborskii*

<400> 45

Met Val Lys Ile Val Ser Arg Arg Tyr Leu Gly Lys Ala Asp Val Tyr
1 5 10 15

Asp Ile Gly Val Ala Lys Asp His Asn Phe Ile Ile Lys Asn Gly Leu
20 25 30

Val Ala Ser Asn
35

<210> 46

<211> 36

<212> PRT

<213> *Cyanothece CCY0110*

<400> 46

Met Val Lys Ile Ile Glu Arg Arg Ser Leu Gly Lys Gln Asn Val Tyr
1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ser Asn Asn Leu
20 25 30

Ile Ala Ser Asn
35

<210> 47

<211> 36

<212> PRT

<213> *Cyanothece PCC8801*

<400> 47

Met Val Lys Ile Val Ser Tyr Arg Ser Leu Gly Lys Gln Phe Val Tyr
1 5 10 15

Asp Ile Gly Val Ala Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ser
20 25 30

Ile Ala Ser Asn
35

<210> 48

<211> 36

<212> PRT

<213> *Crocospaera watsonii*

<400> 48

Met Val Lys Ile Ile Gly Cys Arg Ser Leu Gly Thr Gln Lys Val Tyr
 1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Ser
 20 25 30

Ile Ala Ser Asn
 35

<210> 49

<211> 36

<212> PRT

<213> *Microcystis aeruginosa*

<400> 49

Met Val Lys Ile Ile Gly Arg Gln Ser Leu Gly Arg Lys Pro Val Tyr
 1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Gly Asn Gly Leu
 20 25 30

Ile Ala Ser Asn
 35

<210> 50

<211> 36

<212> PRT

<213> *Microcoleus chthonoplastes*

<400> 50

Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
 20 25 30

Ile Ala Ser Asn
 35

<210> 51

<211> 36

<212> PRT

<213> *Oscillatoria limnetica*

<400> 51

Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
 20 25 30

Ile Ala Ser Asn

35

<210> 52

<211> 36

<212> PRT

<213> *Synechococcus elongatus*

<400> 52

Met Val Lys Ile Val Arg Arg Arg Ser Leu Gly Val Gln Pro Val Tyr
 1 5 10 15

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

Val Ala Ser Asn
 35

<210> 53

<211> 36

<212> PRT

<213> *Synechococcus PCC7002*

<400> 53

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

Asp Ile Gly Leu Ser Gln Asp His Asn Phe Leu Leu Gly Gln Gly Leu
 20 25 30

Ile Ala Ala Asn
 35

<210> 54

<211> 35

<212> PRT

<213> *Thermosynechococcus elongatus*

<400> 54

Met Lys Ile Val Gly Arg Arg Leu Met Gly Trp Gln Ala Val Tyr Asp
 1 5 10 15

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

Ala Ala Asn
 35

<210> 55

<211> 36

<212> PRT

<213> *Trichodesmium erythraeum*

<400> 55

Met Val Lys Ile Val Ser Arg Lys Leu Ala Lys Thr Glu Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Thr Lys Asp His Asn Phe Val Leu Ala Asn Gly Leu
 20 25 30

Ile Ala Ser Asn
 35

<210> 56

<211> 35

<212> PRT

<213> Thermosynechococcus vulcanus

<400> 56

Met Lys Ile Val Gly Arg Arg Leu Val Gly Trp Gln Ala Val Tyr Asp
 1 5 10 15

Ile Gly Leu Ala Gly Asp His Asn Phe Leu Leu Ala Asn Gly Ala Ile
 20 25 30

Ala Ala Asn
 35

<210> 57

<211> 36

<212> PRT

<213> Nostoc punctiforme

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 57

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

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

Ile Ala Ser Xaa
 35

<210> 58

<211> 36

<212> PRT

<213> Synechocystis PCC6803

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 58

```
Met Val Lys Val Ile Gly Arg Arg Ser Leu Gly Val Gln Arg Ile Phe
1           5           10          15
```

```
Asp Ile Gly Leu Pro Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ala
          20           25          30
```

```
Ile Ala Ala Xaa
          35
```

<210> 59

<211> 36

<212> PRT

<213> Aphanothece halophytica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 59

```
Met Val Lys Ile Ile Lys Arg Gln Ser Leu Gly Arg Gln Asn Val Tyr
1           5           10          15
```

```
Asp Val Cys Val Glu Thr Asp His Asn Phe Val Leu Ala Asn Gly Cys
          20           25          30
```

```
Val Ala Ser Xaa
          35
```

<210> 60

<211> 36

<212> PRT

<213> Aphanizomenon ovalisporum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 60

```
Met Val Lys Ile Thr Ala Arg Lys Phe Val Gly Arg Glu Asn Val Tyr
1           5           10          15
```

```
Asp Ile Gly Val Glu His His His Asn Phe Ala Ile Lys Asn Gly Leu
          20           25          30
```

```
Ile Ala Ser Xaa
          35
```

<210> 61
 <211> 36
 <212> PRT
 <213> Anabaena PCC7120

<220>
 <221> MISC_FEATURE
 <222> (36)..(36)
 <223> Xaa is any amino acid excluding Asn and/or Gln

<400> 61
 Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
 1 5 10 15
 Asp Ile Gly Val Arg Arg Asp His Asn Phe Phe Ile Lys Asn Gly Leu
 20 25 30
 Ile Ala Ser Xaa
 35

<210> 62
 <211> 36
 <212> PRT
 <213> Anabaena variabilis

<220>
 <221> MISC_FEATURE
 <222> (36)..(36)
 <223> Xaa is any amino acid excluding Asn and/or Gln

<400> 62
 Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
 1 5 10 15
 Asp Ile Gly Val Gly Arg Asp His Asn Phe Phe Val Lys Asn Gly Leu
 20 25 30
 Ile Ala Ser Xaa
 35

<210> 63
 <211> 36
 <212> PRT
 <213> Cyindrospermopsis raciborskii

<220>
 <221> MISC_FEATURE
 <222> (36)..(36)
 <223> Xaa is any amino acid excluding Asn and/or Gln

<400> 63

Met	Val	Lys	Ile	Val	Ser	Arg	Arg	Tyr	Leu	Gly	Lys	Ala	Asp	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Ala	Lys	Asp	His	Asn	Phe	Ile	Ile	Lys	Asn	Gly	Leu
			20					25					30		

Val	Ala	Ser	Xaa
			35

<210> 64

<211> 36

<212> PRT

<213> Cyanothece CCY0110

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 64

Met	Val	Lys	Ile	Ile	Glu	Arg	Arg	Ser	Leu	Gly	Lys	Gln	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ser	Asn	Asn	Leu
			20					25					30		

Ile	Ala	Ser	Xaa
			35

<210> 65

<211> 36

<212> PRT

<213> Cyanothece PCC8801

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 65

Met	Val	Lys	Ile	Val	Ser	Tyr	Arg	Ser	Leu	Gly	Lys	Gln	Phe	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Ala	Gln	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Ser
			20					25					30		

Ile	Ala	Ser	Xaa
			35

<210> 66

<211> 36

<212> PRT

<213> Crocosphaera watsonii

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 66

Met	Val	Lys	Ile	Ile	Gly	Cys	Arg	Ser	Leu	Gly	Thr	Gln	Lys	Val	Tyr
1			5					10					15		

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Ser
		20						25					30		

Ile	Ala	Ser	Xaa
			35

<210> 67

<211> 36

<212> PRT

<213> Microcystis aeruginosa

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 67

Met	Val	Lys	Ile	Ile	Gly	Arg	Gln	Ser	Leu	Gly	Arg	Lys	Pro	Val	Tyr
1			5					10					15		

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Gly	Asn	Gly	Leu
		20						25					30		

Ile	Ala	Ser	Xaa
			35

<210> 68

<211> 36

<212> PRT

<213> Microcoleus chthonoplastes

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 68

Met	Val	Lys	Ile	Val	Arg	Arg	Gln	Ser	Leu	Gly	Val	Gln	Asn	Val	Tyr
1			5					10					15		

Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
 20 25 30

Ile Ala Ser Xaa
 35

<210> 69

<211> 36

<212> PRT

<213> *Oscillatoria limnetica*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 69

Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr

1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
 20 25 30

Ile Ala Ser Xaa
 35

<210> 70

<211> 36

<212> PRT

<213> *Synechococcus elongatus*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 70

Met Val Lys Ile Val Arg Arg Arg Ser Leu Gly Val Gln Pro Val Tyr
 1 5 10 15

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

Val Ala Ser Xaa
 35

<210> 71

<211> 36

<212> PRT

<213> *Synechococcus PCC7002*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 71

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

Asp	Ile	Gly	Leu	Ser	Gln	Asp	His	Asn	Phe	Leu	Leu	Gly	Gln	Gly	Leu
			20					25					30		

Ile	Ala	Ala	Xaa
			35

<210> 72

<211> 35

<212> PRT

<213> Thermosynechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 72

Met	Lys	Ile	Val	Gly	Arg	Arg	Leu	Met	Gly	Trp	Gln	Ala	Val	Tyr	Asp
1				5					10					15	

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

Ala	Ala	Xaa
		35

<210> 73

<211> 36

<212> PRT

<213> Trichodesmium erythraeum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 73

Met	Val	Lys	Ile	Val	Ser	Arg	Lys	Leu	Ala	Lys	Thr	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Thr	Lys	Asp	His	Asn	Phe	Val	Leu	Ala	Asn	Gly	Leu
			20					25					30		

Ile Ala Ser Xaa
35

<210> 74

<211> 35

<212> PRT

<213> Thermosynechococcus vulcanus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 74

Met Lys Ile Val Gly Arg Arg Leu Val Gly Trp Gln Ala Val Tyr Asp
1 5 10 15

Ile Gly Leu Ala Gly Asp His Asn Phe Leu Leu Ala Asn Gly Ala Ile
20 25 30

Ala Ala Xaa
35

<210> 75

<211> 36

<212> PRT

<213> Nostoc punctiforme

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 75

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

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

Ile Ala Ser Xaa
35

<210> 76

<211> 36

<212> PRT

<213> Synechocystis PCC6803

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 76

Met Val Lys Val Ile Gly Arg Arg Ser Leu Gly Val Gln Arg Ile Phe
1 5 10 15

Asp Ile Gly Leu Pro Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ala
20 25 30

Ile Ala Ala Xaa

35

<210> 77

<211> 36

<212> PRT

<213> Aphanothece halophytica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 77

Met Val Lys Ile Ile Lys Arg Gln Ser Leu Gly Arg Gln Asn Val Tyr
1 5 10 15

Asp Val Cys Val Glu Thr Asp His Asn Phe Val Leu Ala Asn Gly Cys
20 25 30

Val Ala Ser Xaa
35

<210> 78

<211> 36

<212> PRT

<213> Aphanizomenon ovalisporum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 78

```

Met Val Lys Ile Thr Ala Arg Lys Phe Val Gly Arg Glu Asn Val Tyr
1           5           10           15

```

```

Asp Ile Gly Val Glu His His His Asn Phe Ala Ile Lys Asn Gly Leu
          20           25           30

```

```

Ile Ala Ser Xaa
          35

```

<210> 79

<211> 36

<212> PRT

<213> Anabaena PCC7120

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexaanoic acid

<400> 79

```

Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
1           5           10           15

```

```

Asp Ile Gly Val Arg Arg Asp His Asn Phe Phe Ile Lys Asn Gly Leu
          20           25           30

```

```

Ile Ala Ser Xaa
          35

```

<210> 80

<211> 36

<212> PRT

<213> Anabaena variabilis

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexaanoic acid

<400> 80

```

Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
1           5           10           15

```

```

Asp Ile Gly Val Gly Arg Asp His Asn Phe Phe Val Lys Asn Gly Leu
          20           25           30

```

Ile Ala Ser Xaa
35

<210> 81

<211> 36

<212> PRT

<213> *Cylindrospermopsis raciborskii*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 81

Met	Val	Lys	Ile	Val	Ser	Arg	Arg	Tyr	Leu	Gly	Lys	Ala	Asp	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Ala	Lys	Asp	His	Asn	Phe	Ile	Ile	Lys	Asn	Gly	Leu
			20					25					30		

Val Ala Ser Xaa
35

<210> 82

<211> 36

<212> PRT

<213> *Cyanothece CCY0110*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 82

Met	Val	Lys	Ile	Ile	Glu	Arg	Arg	Ser	Leu	Gly	Lys	Gln	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ser	Asn	Asn	Leu
			20					25					30		

Ile Ala Ser Xaa
35

<210> 83

<211> 36

<212> PRT

<213> *Cyanothece PCC8801*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 83

```
Met Val Lys Ile Val Ser Tyr Arg Ser Leu Gly Lys Gln Phe Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Ala Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ser
          20           25           30
```

```
Ile Ala Ser Xaa
          35
```

<210> 84

<211> 36

<212> PRT

<213> *Crocospaera watsonii*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 84

```
Met Val Lys Ile Ile Gly Cys Arg Ser Leu Gly Thr Gln Lys Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Ser
          20           25           30
```

```
Ile Ala Ser Xaa
          35
```

<210> 85

<211> 36

<212> PRT

<213> *Microcystis aeruginosa*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-

aminopentonic acid, or 2-aminohexanoic acid

<400> 85

```
Met Val Lys Ile Ile Gly Arg Gln Ser Leu Gly Arg Lys Pro Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Gly Asn Gly Leu
          20           25           30
```

```
Ile Ala Ser Xaa
```

35

<210> 86

<211> 36

<212> PRT

<213> Microcoleus chthonoplastes

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 86

```
Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
          20           25           30
```

```
Ile Ala Ser Xaa
          35
```

<210> 87

<211> 36

<212> PRT

<213> Oscillatoria limnetica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 87

```
Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
1           5           10           15
```

Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
 20 25 30

Ile Ala Ser Xaa
 35

<210> 88

<211> 36

<212> PRT

<213> Synechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 88

Met Val Lys Ile Val Arg Arg Arg Ser Leu Gly Val Gln Pro Val Tyr
 1 5 10 15

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

Val Ala Ser Xaa
 35

<210> 89

<211> 36

<212> PRT

<213> Synechococcus PCC7002

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 89

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

Asp Ile Gly Leu Ser Gln Asp His Asn Phe Leu Leu Gly Gln Gly Leu
 20 25 30

Ile Ala Ala Xaa
 35

<210> 90

<211> 35

<212> PRT

<213> Thermosynechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 90

Met	Lys	Ile	Val	Gly	Arg	Arg	Leu	Met	Gly	Trp	Gln	Ala	Val	Tyr	Asp
1				5					10					15	

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

Ala	Ala	Xaa
		35

<210> 91

<211> 36

<212> PRT

<213> Trichodesmium erythraeum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 91

Met	Val	Lys	Ile	Val	Ser	Arg	Lys	Leu	Ala	Lys	Thr	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Thr	Lys	Asp	His	Asn	Phe	Val	Leu	Ala	Asn	Gly	Leu
		20						25					30		

Ile	Ala	Ser	Xaa
			35

<210> 92

<211> 35

<212> PRT

<213> Thermosynechococcus vulcanus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 92

```
Met Lys Ile Val Gly Arg Arg Leu Val Gly Trp Gln Ala Val Tyr Asp
1           5           10           15
```

```
Ile Gly Leu Ala Gly Asp His Asn Phe Leu Leu Ala Asn Gly Ala Ile
          20           25           30
```

```
Ala Ala Xaa
          35
```

<210> 93

<211> 36

<212> PRT

<213> Nostoc punctiforme

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 93

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

```
Asp Ile Gly Val Glu Arg Asp His Asn Phe Ala Leu Lys Asn Gly Phe
          20           25           30
```

```
Ile Ala Ser Xaa
          35
```

<210> 94

<211> 36

<212> PRT

<213> Synechocystis PCC6803

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 94

```
Met Val Lys Val Ile Gly Arg Arg Ser Leu Gly Val Gln Arg Ile Phe
1           5           10           15
```

```
Asp Ile Gly Leu Pro Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ala
          20           25           30
```

Ile Ala Ala Xaa
35

<210> 95

<211> 36

<212> PRT

<213> Aphanothece halophytica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 95

Met	Val	Lys	Ile	Ile	Lys	Arg	Gln	Ser	Leu	Gly	Arg	Gln	Asn	Val	Tyr
1				5					10					15	

Asp	Val	Cys	Val	Glu	Thr	Asp	His	Asn	Phe	Val	Leu	Ala	Asn	Gly	Cys
			20					25					30		

Val Ala Ser Xaa
35

<210> 96

<211> 36

<212> PRT

<213> Aphanizomenon ovalisporum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 96

Met	Val	Lys	Ile	Thr	Ala	Arg	Lys	Phe	Val	Gly	Arg	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	His	His	His	Asn	Phe	Ala	Ile	Lys	Asn	Gly	Leu
			20					25					30		

Ile Ala Ser Xaa
35

<210> 97

<211> 36

<212> PRT

<213> Anabaena PCC7120

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 97

```
Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Arg Arg Asp His Asn Phe Phe Ile Lys Asn Gly Leu
          20           25           30
```

```
Ile Ala Ser Xaa
          35
```

<210> 98

<211> 36

<212> PRT

<213> Anabaena variabilis

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 98

```
Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Gly Arg Asp His Asn Phe Phe Val Lys Asn Gly Leu
          20           25           30
```

```
Ile Ala Ser Xaa
          35
```

<210> 99

<211> 36

<212> PRT

<213> Cylindrospermopsis raciborskii

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 99

```
Met Val Lys Ile Val Ser Arg Arg Tyr Leu Gly Lys Ala Asp Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Ala Lys Asp His Asn Phe Ile Ile Lys Asn Gly Leu
          20           25           30
```

```
Val Ala Ser Xaa
          35
```

<210> 100

<211> 36

<212> PRT

<213> Cyanothece CCY0110

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 100

Met	Val	Lys	Ile	Ile	Glu	Arg	Arg	Ser	Leu	Gly	Lys	Gln	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ser	Asn	Asn	Leu
			20					25					30		

Ile	Ala	Ser	Xaa
			35

<210> 101

<211> 36

<212> PRT

<213> Cyanothece PCC8801

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 101

Met	Val	Lys	Ile	Val	Ser	Tyr	Arg	Ser	Leu	Gly	Lys	Gln	Phe	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Ala	Gln	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Ser
			20					25					30		

Ile	Ala	Ser	Xaa
			35

<210> 102

<211> 36

<212> PRT

<213> Crocosphaera watsonii

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 102

Met	Val	Lys	Ile	Ile	Gly	Cys	Arg	Ser	Leu	Gly	Thr	Gln	Lys	Val	Tyr
1				5					10					15	

1 3 10 13
 Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Ser
 20 25 30

Ile Ala Ser Xaa
 35

<210> 103

<211> 36

<212> PRT

<213> Microcystis aeruginosa

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 103

Met Val Lys Ile Ile Gly Arg Gln Ser Leu Gly Arg Lys Pro Val Tyr
 1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Gly Asn Gly Leu
 20 25 30

Ile Ala Ser Xaa
 35

<210> 104

<211> 36

<212> PRT

<213> Microcoleus chthonoplastes

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 104

Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
 20 25 30

Ile Ala Ser Xaa
 35

<210> 105

<211> 36

<212> PRT

<213> Oscillatoria limnetica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 105

Met	Val	Lys	Ile	Val	Arg	Arg	Gln	Ser	Leu	Gly	Val	Gln	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Cys	Leu	Ala	Ser	Gly	Glu
			20					25					30		

Ile	Ala	Ser	Xaa
			35

<210> 106

<211> 36

<212> PRT

<213> Synechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 106

Met	Val	Lys	Ile	Val	Arg	Arg	Arg	Ser	Leu	Gly	Val	Gln	Pro	Val	Tyr
1				5					10					15	

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

Val	Ala	Ser	Xaa
			35

<210> 107

<211> 36

<212> PRT

<213> Synechococcus PCC7002

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 107

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

Asp	Ile	Gly	Leu	Ser	Gln	Asp	His	Asn	Phe	Leu	Leu	Gly	Gln	Gly	Leu

20

25

30

Ile Ala Ala Xaa
35

<210> 108

<211> 35

<212> PRT

<213> Thermosynechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 108

Met Lys Ile Val Gly Arg Arg Leu Met Gly Trp Gln Ala Val Tyr Asp
1 5 10 15

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

Ala Ala Xaa
35

<210> 109

<211> 36

<212> PRT

<213> Trichodesmium erythraeum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 109

Met Val Lys Ile Val Ser Arg Lys Leu Ala Lys Thr Glu Asn Val Tyr
1 5 10 15

Asp Ile Gly Val Thr Lys Asp His Asn Phe Val Leu Ala Asn Gly Leu
20 25 30

Ile Ala Ser Xaa
35

<210> 110

<211> 35

<212> PRT

<213> Thermosynechococcus vulcanus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 110

```
Met Lys Ile Val Gly Arg Arg Leu Val Gly Trp Gln Ala Val Tyr Asp
1           5           10           15
```

```
Ile Gly Leu Ala Gly Asp His Asn Phe Leu Leu Ala Asn Gly Ala Ile
          20           25           30
```

```
Ala Ala Xaa
          35
```

<210> 111

<211> 36

<212> PRT

<213> Nostoc punctiforme

<400> 111

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

```
Asp Ile Gly Val Glu Arg Asp His Asn Phe Ala Leu Lys Asn Gly Phe
          20           25           30
```

```
Ile Ala Ser Ala
          35
```

<210> 112

<211> 36

<212> PRT

<213> Synechocystis PCC6803

<400> 112

```
Met Val Lys Val Ile Gly Arg Arg Ser Leu Gly Val Gln Arg Ile Phe
1           5           10           15
```

```
Asp Ile Gly Leu Pro Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ala
          20           25           30
```

```
Ile Ala Ala Ala
          35
```

<210> 113

<211> 36

<212> PRT

<213> Aphanothece halophytica

<400> 113

```
Met Val Lys Ile Ile Lys Arg Gln Ser Leu Gly Arg Gln Asn Val Tyr
1           5           10           15
```

```
Asp Val Cys Val Glu Thr Asp His Asn Phe Val Leu Ala Asn Gly Cys
          20           25           30
```

Val Ala Ser Ala
35

<210> 114

<211> 36

<212> PRT

<213> Aphanizomenon ovalisporum

<400> 114

Met Val Lys Ile Thr Ala Arg Lys Phe Val Gly Arg Glu Asn Val Tyr
1 5 10 15

Asp Ile Gly Val Glu His His His Asn Phe Ala Ile Lys Asn Gly Leu
20 25 30

Ile Ala Ser Ala
35

<210> 115

<211> 36

<212> PRT

<213> Anabaena PCC7120

<400> 115

Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
1 5 10 15

Asp Ile Gly Val Arg Arg Asp His Asn Phe Phe Ile Lys Asn Gly Leu
20 25 30

Ile Ala Ser Ala
35

<210> 116

<211> 36

<212> PRT

<213> Anabaena variabilis

<400> 116

Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
1 5 10 15

Asp Ile Gly Val Gly Arg Asp His Asn Phe Phe Val Lys Asn Gly Leu

20

25

30

Ile Ala Ser Ala
35

<210> 117

<211> 36

<212> PRT

<213> *Cylindrospermopsis raciborskii*

<400> 117

Met Val Lys Ile Val Ser Arg Arg Tyr Leu Gly Lys Ala Asp Val Tyr
1 5 10 15

Asp Ile Gly Val Ala Lys Asp His Asn Phe Ile Ile Lys Asn Gly Leu
20 25 30

Val Ala Ser Ala
35

<210> 118

<211> 36

<212> PRT

<213> *Cyanothece* CCY0110

<400> 118

Met Val Lys Ile Ile Glu Arg Arg Ser Leu Gly Lys Gln Asn Val Tyr
1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ser Asn Asn Leu
20 25 30

Ile Ala Ser Ala
35

<210> 119

<211> 36

<212> PRT

<213> *Cyanothece* PCC8801

<400> 119

Met Val Lys Ile Val Ser Tyr Arg Ser Leu Gly Lys Gln Phe Val Tyr
1 5 10 15

Asp Ile Gly Val Ala Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ser
20 25 30

Ile Ala Ser Ala
35

<210> 120

<211> 36

<212> PRT

<213> *Crocospaera watsonii*

<400> 120

Met Val Lys Ile Ile Gly Cys Arg Ser Leu Gly Thr Gln Lys Val Tyr
1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Ser
20 25 30

Ile Ala Ser Ala
35

<210> 121

<211> 36

<212> PRT

<213> Microcystis aeruginosa

<400> 121

Met Val Lys Ile Ile Gly Arg Gln Ser Leu Gly Arg Lys Pro Val Tyr
1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Gly Asn Gly Leu
20 25 30

Ile Ala Ser Ala
35

<210> 122

<211> 36

<212> PRT

<213> Microcoleus chthonoplastes

<400> 122

Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
20 25 30

Ile Ala Ser Ala
35

<210> 123

<211> 36

<212> PRT

<213> Oscillatoria limnetica

<400> 123

Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
20 25 30

Ile Ala Ser Ala
35

<210> 124

<211> 36

<212> PRT

<213> Synechococcus elongatus

<400> 124

Met Val Lys Ile Val Arg Arg Arg Ser Leu Gly Val Gln Pro Val Tyr
 1 5 10 15

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

Val Ala Ser Ala
 35

<210> 125

<211> 36

<212> PRT

<213> Synechococcus PCC7002

<400> 125

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

Asp Ile Gly Leu Ser Gln Asp His Asn Phe Leu Leu Gly Gln Gly Leu
 20 25 30

Ile Ala Ala Ala
 35

<210> 126

<211> 35

<212> PRT

<213> Thermosynechococcus elongatus

<400> 126

Met Lys Ile Val Gly Arg Arg Leu Met Gly Trp Gln Ala Val Tyr Asp
 1 5 10 15

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

Ala Ala Ala
 35

<210> 127

<211> 36

<212> PRT

<213> Trichodesmium erythraeum

<400> 127

Met Val Lys Ile Val Ser Arg Lys Leu Ala Lys Thr Glu Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Thr Lys Asp His Asn Phe Val Leu Ala Asn Gly Leu
 20 25 30

Ile Ala Ser Ala
 35

<210> 128

<211> 35

<212> PRT

<213> Thermosynechococcus vulcanus

<400> 128

```

Met Lys Ile Val Gly Arg Arg Leu Val Gly Trp Gln Ala Val Tyr Asp
1           5           10           15

```

```

Ile Gly Leu Ala Gly Asp His Asn Phe Leu Leu Ala Asn Gly Ala Ile
          20           25           30

```

```

Ala Ala Ala
          35

```

<210> 129

<211> 39

<212> PRT

<213> Nostoc punctiforme

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 129

```

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

```

```

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

```

```

Ile Ala Ser Xaa Xaa Phe Asn
          35

```

<210> 130

<211> 39

<212> PRT

<213> Synechocystis PCC6803

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 130

Met	Val	Lys	Val	Ile	Gly	Arg	Arg	Ser	Leu	Gly	Val	Gln	Arg	Ile	Phe
1				5					10					15	

Asp	Ile	Gly	Leu	Pro	Gln	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Ala
			20					25					30		

Ile	Ala	Ala	Xaa	Xaa	Phe	Asn
			35			

<210> 131

<211> 39

<212> PRT

<213> Aphanothece halophytica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 131

Met	Val	Lys	Ile	Ile	Lys	Arg	Gln	Ser	Leu	Gly	Arg	Gln	Asn	Val	Tyr
1				5					10					15	

Asp	Val	Cys	Val	Glu	Thr	Asp	His	Asn	Phe	Val	Leu	Ala	Asn	Gly	Cys
			20					25					30		

Val	Ala	Ser	Xaa	Xaa	Phe	Asn
			35			

<210> 132

<211> 39

<212> PRT

<213> Aphanizomenon ovalisporum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 132

```
Met Val Lys Ile Thr Ala Arg Lys Phe Val Gly Arg Glu Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu His His His Asn Phe Ala Ile Lys Asn Gly Leu
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 133

<211> 39

<212> PRT

<213> Anabaena PCC7120

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 133

```
Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Arg Arg Asp His Asn Phe Phe Ile Lys Asn Gly Leu
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 134

<211> 39

<212> PRT

<213> Anabaena variabilis

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 134

Met	Ile	Lys	Ile	Ala	Ser	Arg	Lys	Phe	Leu	Gly	Val	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Gly	Arg	Asp	His	Asn	Phe	Phe	Val	Lys	Asn	Gly	Leu
		20						25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn
			35			

<210> 135

<211> 39

<212> PRT

<213> *Cylindrospermopsis raciborskii*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 135

Met	Val	Lys	Ile	Val	Ser	Arg	Arg	Tyr	Leu	Gly	Lys	Ala	Asp	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Ala	Lys	Asp	His	Asn	Phe	Ile	Ile	Lys	Asn	Gly	Leu
			20					25					30		

Val	Ala	Ser	Xaa	Xaa	Phe	Asn
			35			

<210> 136

<211> 39

<212> PRT

<213> *Cyanothece CCY0110*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 136

```
Met Val Lys Ile Ile Glu Arg Arg Ser Leu Gly Lys Gln Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ser Asn Asn Leu
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 137

<211> 39

<212> PRT

<213> Cyanothecce PCC8801

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 137

```
Met Val Lys Ile Val Ser Tyr Arg Ser Leu Gly Lys Gln Phe Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Ala Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ser
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 138

<211> 39

<212> PRT

<213> Crocosphaera watsonii

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 138

```
Met Val Lys Ile Ile Gly Cys Arg Ser Leu Gly Thr Gln Lys Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Ser
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 139

<211> 39

<212> PRT

<213> Microcystis aeruginosa

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 139

```
Met Val Lys Ile Ile Gly Arg Gln Ser Leu Gly Arg Lys Pro Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Gly Asn Gly Leu
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 140

<211> 39

<212> PRT

<213> Microcoleus chthonoplastes

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 140

```
Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 141

<211> 39

<212> PRT

<213> *Oscillatoria limnetica*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 141

```
Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 142

<211> 39

<212> PRT

<213> *Synechococcus elongatus*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 142

```
Met Val Lys Ile Val Arg Arg Arg Ser Leu Gly Val Gln Pro Val Tyr
1           5           10           15
```

```
Asp Leu Gly Val Ala Thr Val His Asn Phe Val Leu Ala Asn Gly Leu
          20           25           30
```

```
Val Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 143

<211> 39

<212> PRT

<213> Synechococcus PCC7002

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 143

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

```
Asp Ile Gly Leu Ser Gln Asp His Asn Phe Leu Leu Gly Gln Gly Leu
          20           25           30
```

```
Ile Ala Ala Xaa Xaa Phe Asn
          35
```

<210> 144

<211> 38

<212> PRT

<213> Thermosynechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Cys

<400> 144

```
Met Lys Ile Val Gly Arg Arg Leu Met Gly Trp Gln Ala Val Tyr Asp
1           5           10           15
```

```
Ile Gly Leu Ala Ala Asp His Asn Phe Val Leu Ala Asn Gly Ala Ile
          20           25           30
```

```
Ala Ala Xaa Xaa Phe Asn
          35
```

<210> 145

<211> 39

<212> PRT

<213> Trichodesmium erythraeum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Asn

<400> 145

```
Met Val Lys Ile Val Ser Arg Lys Leu Ala Lys Thr Glu Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Thr Lys Asp His Asn Phe Val Leu Ala Asn Gly Leu
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 146

<211> 38

<212> PRT

<213> Thermosynechococcus vulcanus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Cys

<400> 146

Met Lys Ile Val Gly Arg Arg Leu Val Gly Trp Gln Ala Val Tyr Asp
 1 5 10 15

Ile Gly Leu Ala Gly Asp His Asn Phe Leu Leu Ala Asn Gly Ala Ile
 20 25 30

Ala Ala Xaa Xaa Phe Asn
 35

<210> 147

<211> 39

<212> PRT

<213> Nostoc punctiforme

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural
 aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-
 aminopentonic acid, or 2-aminohexanoic acid

<400> 147

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

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

Ile Ala Ser Xaa Xaa Phe Asn
 35

<210> 148

<211> 39

<212> PRT

<213> Synechocystis PCC6803

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 148

```
Met Val Lys Val Ile Gly Arg Arg Ser Leu Gly Val Gln Arg Ile Phe
 1           5           10          15
```

```
Asp Ile Gly Leu Pro Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ala
      20           25           30
```

```
Ile Ala Ala Xaa Xaa Phe Asn
      35
```

<210> 149

<211> 39

<212> PRT

<213> Aphanothece halophytica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 149

```
Met Val Lys Ile Ile Lys Arg Gln Ser Leu Gly Arg Gln Asn Val Tyr
 1           5           10          15
```

```
Asp Val Cys Val Glu Thr Asp His Asn Phe Val Leu Ala Asn Gly Cys
      20           25           30
```

```
Val Ala Ser Xaa Xaa Phe Asn
      35
```

<210> 150

<211> 39

<212> PRT

<213> Aphanizomenon ovalisporum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 150

Met	Val	Lys	Ile	Thr	Ala	Arg	Lys	Phe	Val	Gly	Arg	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	His	His	His	Asn	Phe	Ala	Ile	Lys	Asn	Gly	Leu
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn
			35			

<210> 151

<211> 39

<212> PRT

<213> Anabaena PCC7120

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 151

Met	Ile	Lys	Ile	Ala	Ser	Arg	Lys	Phe	Leu	Gly	Val	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Arg	Arg	Asp	His	Asn	Phe	Phe	Ile	Lys	Asn	Gly	Leu
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn
			35			

<210> 152

<211> 39

<212> PRT

<213> Anabaena variabilis

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 152

```
Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Gly Arg Asp His Asn Phe Phe Val Lys Asn Gly Leu
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 153

<211> 39

<212> PRT

<213> Cylindrospermopsis raciborskii

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 153

```
Met Val Lys Ile Val Ser Arg Arg Tyr Leu Gly Lys Ala Asp Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Ala Lys Asp His Asn Phe Ile Ile Lys Asn Gly Leu
          20           25           30
```

```
Val Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 154

<211> 39

<212> PRT

<213> Cyanothece CCY0110

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 154

Met	Val	Lys	Ile	Ile	Glu	Arg	Arg	Ser	Leu	Gly	Lys	Gln	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ser	Asn	Asn	Leu
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn
			35			

<210> 155

<211> 39

<212> PRT

<213> Cyanothece PCC8801

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 155

Met	Val	Lys	Ile	Val	Ser	Tyr	Arg	Ser	Leu	Gly	Lys	Gln	Phe	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Ala	Gln	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Ser
			20					25					30		

Ile Ala Ser Xaa Xaa Phe Asn
35

<210> 156

<211> 39

<212> PRT

<213> Crocosphaera watsonii

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 156

Met	Val	Lys	Ile	Ile	Gly	Cys	Arg	Ser	Leu	Gly	Thr	Gln	Lys	Val	Tyr
1			5						10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Ser
			20					25					30		

Ile Ala Ser Xaa Xaa Phe Asn
35

<210> 157

<211> 39

<212> PRT

<213> Microcystis aeruginosa

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 157

Met	Val	Lys	Ile	Ile	Gly	Arg	Gln	Ser	Leu	Gly	Arg	Lys	Pro	Val	Tyr
1			5						10					15	

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Gly Asn Gly Leu
 20 25 30

Ile Ala Ser Xaa Xaa Phe Asn
 35

<210> 158

<211> 39

<212> PRT

<213> Microcoleus chthonoplastes

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 158

Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
 20 25 30

Ile Ala Ser Xaa Xaa Phe Asn
 35

<210> 159

<211> 39

<212> PRT

<213> Oscillatoria limnetica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 159

Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu

20

25

30

Ile Ala Ser Xaa Xaa Phe Asn
 35

<210> 160

<211> 39

<212> PRT

<213> Synechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 160

Met Val Lys Ile Val Arg Arg Arg Ser Leu Gly Val Gln Pro Val Tyr
 1 5 10 15

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

Val Ala Ser Xaa Xaa Phe Asn
 35

<210> 161

<211> 39

<212> PRT

<213> Synechococcus PCC7002

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 161

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

```
Asp Ile Gly Leu Ser Gln Asp His Asn Phe Leu Leu Gly Gln Gly Leu
          20           25          30
```

```
Ile Ala Ala Xaa Xaa Phe Asn
          35
```

<210> 162

<211> 38

<212> PRT

<213> Thermosynechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 162

```
Met Lys Ile Val Gly Arg Arg Leu Met Gly Trp Gln Ala Val Tyr Asp
1           5           10          15
```

```
Ile Gly Leu Ala Ala Asp His Asn Phe Val Leu Ala Asn Gly Ala Ile
          20           25          30
```

```
Ala Ala Xaa Xaa Phe Asn
          35
```

<210> 163

<211> 39

<212> PRT

<213> Trichodesmium erythraeum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 163

Met	Val	Lys	Ile	Val	Ser	Arg	Lys	Leu	Ala	Lys	Thr	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Thr	Lys	Asp	His	Asn	Phe	Val	Leu	Ala	Asn	Gly	Leu
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn
			35			

<210> 164

<211> 38

<212> PRT

<213> Thermosynechococcus vulcanus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 164

Met	Lys	Ile	Val	Gly	Arg	Arg	Leu	Val	Gly	Trp	Gln	Ala	Val	Tyr	Asp
1				5					10					15	

Ile	Gly	Leu	Ala	Gly	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Ala	Ile
			20					25					30		

Ala	Ala	Xaa	Xaa	Phe	Asn
			35		

<210> 165

<211> 39

<212> PRT

<213> Nostoc punctiforme

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 165

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

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

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn
						35

<210> 166

<211> 39

<212> PRT

<213> Synechocystis PCC6803

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 166

Met	Val	Lys	Val	Ile	Gly	Arg	Arg	Ser	Leu	Gly	Val	Gln	Arg	Ile	Phe
1				5					10					15	

Asp	Ile	Gly	Leu	Pro	Gln	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Ala
			20					25					30		

Ile	Ala	Ala	Xaa	Xaa	Phe	Asn
						35

<210> 167

<211> 39

<212> PRT

<213> Aphanothece halophytica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 167

Met	Val	Lys	Ile	Ile	Lys	Arg	Gln	Ser	Leu	Gly	Arg	Gln	Asn	Val	Tyr
1				5					10					15	

Asp	Val	Cys	Val	Glu	Thr	Asp	His	Asn	Phe	Val	Leu	Ala	Asn	Gly	Cys
			20					25					30		

Val	Ala	Ser	Xaa	Xaa	Phe	Asn
			35			

<210> 168

<211> 39

<212> PRT

<213> Aphanizomenon ovalisporum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 168

Met	Val	Lys	Ile	Thr	Ala	Arg	Lys	Phe	Val	Gly	Arg	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	His	His	His	Asn	Phe	Ala	Ile	Lys	Asn	Gly	Leu
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn
			35			

<210> 169

<211> 39

<212> PRT

<213> Anabaena PCC7120

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 169

```
Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Arg Arg Asp His Asn Phe Phe Ile Lys Asn Gly Leu
                20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
                35
```

<210> 170

<211> 39

<212> PRT

<213> Anabaena variabilis

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 170

```
Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Gly Arg Asp His Asn Phe Phe Val Lys Asn Gly Leu
                20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
                35
```

<210> 171

<211> 39

<212> PRT

<213> Cylindrospermopsis raciborskii

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 171

Met	Val	Lys	Ile	Val	Ser	Arg	Arg	Tyr	Leu	Gly	Lys	Ala	Asp	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Ala	Lys	Asp	His	Asn	Phe	Ile	Ile	Lys	Asn	Gly	Leu
			20					25					30		

Val	Ala	Ser	Xaa	Xaa	Phe	Asn
			35			

<210> 172

<211> 39

<212> PRT

<213> Cyanothecce CCY0110

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 172

Met	Val	Lys	Ile	Ile	Glu	Arg	Arg	Ser	Leu	Gly	Lys	Gln	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ser	Asn	Asn	Leu
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn
			35			

<210> 173

<211> 39

<212> PRT

<213> Cyanothecce PCC8801

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 173

Met	Val	Lys	Ile	Val	Ser	Tyr	Arg	Ser	Leu	Gly	Lys	Gln	Phe	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Ala	Gln	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Ser
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn
			35			

<210> 174

<211> 39

<212> PRT

<213> Crocosphaera watsonii

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 174

Met	Val	Lys	Ile	Ile	Gly	Cys	Arg	Ser	Leu	Gly	Thr	Gln	Lys	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Ser
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn
			35			

<210> 175

<211> 39

<212> PRT

<213> Microcystis aeruginosa

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 175

Met	Val	Lys	Ile	Ile	Gly	Arg	Gln	Ser	Leu	Gly	Arg	Lys	Pro	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Gly	Asn	Gly	Leu
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn
						35

<210> 176

<211> 39

<212> PRT

<213> Microcoleus chthonoplastes

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 176

Met	Val	Lys	Ile	Val	Arg	Arg	Gln	Ser	Leu	Gly	Val	Gln	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Cys	Leu	Ala	Ser	Gly	Glu
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn
						35

<210> 177

<211> 39

<212> PRT

<213> Oscillatoria limnetica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 177

```
Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 178

<211> 39

<212> PRT

<213> Synechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 178

```
Met Val Lys Ile Val Arg Arg Arg Ser Leu Gly Val Gln Pro Val Tyr
1           5           10           15
```

```
Asp Leu Gly Val Ala Thr Val His Asn Phe Val Leu Ala Asn Gly Leu
          20           25           30
```

```
Val Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 179

<211> 39

<212> PRT

<213> Synechococcus PCC7002

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 179

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

```
Asp Ile Gly Leu Ser Gln Asp His Asn Phe Leu Leu Gly Gln Gly Leu
          20           25           30
```

```
Ile Ala Ala Xaa Xaa Phe Asn
          35
```

<210> 180

<211> 38

<212> PRT

<213> Thermosynechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 180

```
Met Lys Ile Val Gly Arg Arg Leu Met Gly Trp Gln Ala Val Tyr Asp
1           5           10           15
```

```
Ile Gly Leu Ala Ala Asp His Asn Phe Val Leu Ala Asn Gly Ala Ile
          20           25           30
```

```
Ala Ala Xaa Xaa Phe Asn
          35
```

<210> 181

<211> 39

<212> PRT

<213> Trichodesmium erythraeum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 181

```
Met Val Lys Ile Val Ser Arg Lys Leu Ala Lys Thr Glu Asn Val Tyr
1          5          10          15
```

```
Asp Ile Gly Val Thr Lys Asp His Asn Phe Val Leu Ala Asn Gly Leu
          20          25          30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 182

<211> 38

<212> PRT

<213> Thermosynechococcus vulcanus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 182

```
Met Lys Ile Val Gly Arg Arg Leu Val Gly Trp Gln Ala Val Tyr Asp
1          5          10          15
```

```
Ile Gly Leu Ala Gly Asp His Asn Phe Leu Leu Ala Asn Gly Ala Ile
          20          25          30
```

```
Ala Ala Xaa Xaa Phe Asn
          35
```

<210> 183

<211> 39

<212> PRT

<213> Nostoc punctiforme

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 183

```

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

```

```

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

```

```

Ile Ala Ser Xaa Ala Phe Asn
          35

```

<210> 184

<211> 39

<212> PRT

<213> Synechocystis PCC6803

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 184

```

Met Val Lys Val Ile Gly Arg Arg Ser Leu Gly Val Gln Arg Ile Phe
1           5           10           15

```

```

Asp Ile Gly Leu Pro Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ala
          20           25           30

```

```

Ile Ala Ala Xaa Ala Phe Asn
          35

```

<210> 185

<211> 39

<212> PRT

<213> Aphanothece halophytica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 185

```

Met Val Lys Ile Ile Lys Arg Gln Ser Leu Gly Arg Gln Asn Val Tyr
1           5           10           15

```

```

Asp Val Cys Val Glu Thr Asp His Asn Phe Val Leu Ala Asn Gly Cys
          20           25           30

```

```

Val Ala Ser Xaa Ala Phe Asn
          35

```

<210> 186

<211> 39

<212> PRT

<213> Aphanizomenon ovalisporum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 186

Met	Val	Lys	Ile	Thr	Ala	Arg	Lys	Phe	Val	Gly	Arg	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	His	His	His	Asn	Phe	Ala	Ile	Lys	Asn	Gly	Leu
			20					25					30		

Ile	Ala	Ser	Xaa	Ala	Phe	Asn
			35			

<210> 187

<211> 39

<212> PRT

<213> Anabaena PCC7120

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 187

Met	Ile	Lys	Ile	Ala	Ser	Arg	Lys	Phe	Leu	Gly	Val	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Arg	Arg	Asp	His	Asn	Phe	Phe	Ile	Lys	Asn	Gly	Leu
			20					25					30		

Ile	Ala	Ser	Xaa	Ala	Phe	Asn
			35			

<210> 188

<211> 39

<212> PRT

<213> Anabaena variabilis

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 188

Met	Ile	Lys	Ile	Ala	Ser	Arg	Lys	Phe	Leu	Gly	Val	Glu	Asn	Val	Tyr
1				5					10					15	

Asp Ile Gly Val Gly Arg Asp His Asn Phe Phe Val Lys Asn Gly Leu
 20 25 30

Ile Ala Ser Xaa Ala Phe Asn
 35

<210> 189

<211> 39

<212> PRT

<213> *Cylindrospermopsis raciborskii*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 189

Met Val Lys Ile Val Ser Arg Arg Tyr Leu Gly Lys Ala Asp Val Tyr
 1 5 10 15

Asp Ile Gly Val Ala Lys Asp His Asn Phe Ile Ile Lys Asn Gly Leu
 20 25 30

Val Ala Ser Xaa Ala Phe Asn
 35

<210> 190

<211> 39

<212> PRT

<213> *Cyanothece CCY0110*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 190

Met Val Lys Ile Ile Glu Arg Arg Ser Leu Gly Lys Gln Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ser Asn Asn Leu
 20 25 30

Ile Ala Ser Xaa Ala Phe Asn
 35

<210> 191

<211> 39

<212> PRT

<213> *Cyanothece PCC8801*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 191

Met	Val	Lys	Ile	Val	Ser	Tyr	Arg	Ser	Leu	Gly	Lys	Gln	Phe	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Ala	Gln	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Ser
			20					25					30		

Ile	Ala	Ser	Xaa	Ala	Phe	Asn
			35			

<210> 192

<211> 39

<212> PRT

<213> Crocosphaera watsonii

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 192

Met	Val	Lys	Ile	Ile	Gly	Cys	Arg	Ser	Leu	Gly	Thr	Gln	Lys	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Ser
			20					25					30		

Ile	Ala	Ser	Xaa	Ala	Phe	Asn
			35			

<210> 193

<211> 39

<212> PRT

<213> Microcystis aeruginosa

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 193

Met	Val	Lys	Ile	Ile	Gly	Arg	Gln	Ser	Leu	Gly	Arg	Lys	Pro	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Gly	Asn	Gly	Leu
			20					25					30		

Ile	Ala	Ser	Xaa	Ala	Phe	Asn

35

<210> 194

<211> 39

<212> PRT

<213> Microcoleus chthonoplastes

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 194

Met	Val	Lys	Ile	Val	Arg	Arg	Gln	Ser	Leu	Gly	Val	Gln	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Cys	Leu	Ala	Ser	Gly	Glu
			20					25					30		

Ile	Ala	Ser	Xaa	Ala	Phe	Asn
			35			

<210> 195

<211> 39

<212> PRT

<213> Oscillatoria limnetica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 195

Met	Val	Lys	Ile	Val	Arg	Arg	Gln	Ser	Leu	Gly	Val	Gln	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Cys	Leu	Ala	Ser	Gly	Glu
			20					25					30		

Ile	Ala	Ser	Xaa	Ala	Phe	Asn
			35			

<210> 196

<211> 39

<212> PRT

<213> Synechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 196

Met Val Lys Ile Val Arg Arg Arg Ser Leu Gly Val Gln Pro Val Tyr
 1 5 10 15

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

Val Ala Ser Xaa Ala Phe Asn
 35

<210> 197

<211> 39

<212> PRT

<213> Synechococcus PCC7002

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 197

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

Asp Ile Gly Leu Ser Gln Asp His Asn Phe Leu Leu Gly Gln Gly Leu
 20 25 30

Ile Ala Ala Xaa Ala Phe Asn
 35

<210> 198

<211> 38

<212> PRT

<213> Thermosynechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 198

Met Lys Ile Val Gly Arg Arg Leu Met Gly Trp Gln Ala Val Tyr Asp
 1 5 10 15

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

Ala Ala Xaa Ala Phe Asn
 35

<210> 199

<211> 39

<212> PRT

<213> Trichodesmium erythraeum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 199

```
Met Val Lys Ile Val Ser Arg Lys Leu Ala Lys Thr Glu Asn Val Tyr
 1           5           10          15
```

```
Asp Ile Gly Val Thr Lys Asp His Asn Phe Val Leu Ala Asn Gly Leu
          20           25          30
```

```
Ile Ala Ser Xaa Ala Phe Asn
```

35

<210> 200

<211> 38

<212> PRT

<213> Thermosynechococcus vulcanus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 200

```
Met Lys Ile Val Gly Arg Arg Leu Val Gly Trp Gln Ala Val Tyr Asp
 1           5           10          15
```

```
Ile Gly Leu Ala Gly Asp His Asn Phe Leu Leu Ala Asn Gly Ala Ile
          20           25          30
```

```
Ala Ala Xaa Ala Phe Asn
          35
```

<210> 201

<211> 39

<212> PRT

<213> Nostoc punctiforme

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 201

```

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

```

```

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

```

```

Ile Ala Ser Xaa Xaa Phe Asn
          35

```

<210> 202

<211> 39

<212> PRT

<213> Synechocystis PCC6803

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 202

```

Met Val Lys Val Ile Gly Arg Arg Ser Leu Gly Val Gln Arg Ile Phe
1           5           10           15

```

```

Asp Ile Gly Leu Pro Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ala
          20           25           30

```

```

Ile Ala Ala Xaa Xaa Phe Asn
          35

```

<210> 203

<211> 39

<212> PRT

<213> Aphanothece halophytica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 203

```
Met Val Lys Ile Ile Lys Arg Gln Ser Leu Gly Arg Gln Asn Val Tyr
1           5           10           15
```

```
Asp Val Cys Val Glu Thr Asp His Asn Phe Val Leu Ala Asn Gly Cys
          20           25           30
```

```
Val Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 204

<211> 39

<212> PRT

<213> Aphanizomenon ovalisporum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 204

```
Met Val Lys Ile Thr Ala Arg Lys Phe Val Gly Arg Glu Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu His His His Asn Phe Ala Ile Lys Asn Gly Leu
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 205

<211> 39

<212> PRT

<213> Anabaena PCC7120

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 205

Met	Ile	Lys	Ile	Ala	Ser	Arg	Lys	Phe	Leu	Gly	Val	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Arg	Arg	Asp	His	Asn	Phe	Phe	Ile	Lys	Asn	Gly	Leu
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn
						35

<210> 206

<211> 39

<212> PRT

<213> Anabaena variabilis

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 206

Met	Ile	Lys	Ile	Ala	Ser	Arg	Lys	Phe	Leu	Gly	Val	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Gly	Arg	Asp	His	Asn	Phe	Phe	Val	Lys	Asn	Gly	Leu
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn
						35

<210> 207

<211> 39

<212> PRT

<213> *Cylindrospermopsis raciborskii*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 207

Met	Val	Lys	Ile	Val	Ser	Arg	Arg	Tyr	Leu	Gly	Lys	Ala	Asp	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Ala	Lys	Asp	His	Asn	Phe	Ile	Ile	Lys	Asn	Gly	Leu

20

25

30

Val	Ala	Ser	Xaa	Xaa	Phe	Asn
						35

<210> 208

<211> 39

<212> PRT

<213> *Cyanothece CCY0110*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 208

Met	Val	Lys	Ile	Ile	Glu	Arg	Arg	Ser	Leu	Gly	Lys	Gln	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ser	Asn	Asn	Leu
			20					25						30	

Ile Ala Ser Xaa Xaa Phe Asn
35

<210> 209

<211> 39

<212> PRT

<213> Cyanotheca PCC8801

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 209

Met	Val	Lys	Ile	Val	Ser	Tyr	Arg	Ser	Leu	Gly	Lys	Gln	Phe	Val	Tyr
1			5						10					15	

Asp	Ile	Gly	Val	Ala	Gln	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Ser
		20						25					30		

Ile Ala Ser Xaa Xaa Phe Asn
35

<210> 210

<211> 39

<212> PRT

<213> Crocosphaera watsonii

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 210

Met	Val	Lys	Ile	Ile	Gly	Cys	Arg	Ser	Leu	Gly	Thr	Gln	Lys	Val	Tyr

1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Ser
20 25 30

Ile Ala Ser Xaa Xaa Phe Asn
35

$\langle 210 \rangle$ 211

<211> 39

<212> PRT

<213> *Microcystis aeruginosa*

$\langle 220 \rangle$

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

$\langle 400 \rangle$ 211

Met Val Lys Ile Ile Gly Arg Gln Ser Leu Gly Arg Lys Pro Val Tyr
1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Gly Asn Gly Leu
20 25 30

Ile Ala Ser Xaa Xaa Phe Asn
35

<210> 212

<211> 39

<212> PRT

<213> Microcoleus chthonoplastes

$\langle 220 \rangle$

<221> MISC FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexanoic acid

$\langle 220 \rangle$

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 212

```
Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 213

<211> 39

<212> PRT

<213> *Oscillatoria limnetica*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 213

```
Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 214

<211> 39

<212> PRT

<213> *Synechococcus elongatus*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 214

Met	Val	Lys	Ile	Val	Arg	Arg	Arg	Ser	Leu	Gly	Val	Gln	Pro	Val	Tyr
1				5					10					15	

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

Val	Ala	Ser	Xaa	Xaa	Phe	Asn
			35			

<210> 215

<211> 39

<212> PRT

<213> Synechococcus PCC7002

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 215

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

Asp	Ile	Gly	Leu	Ser	Gln	Asp	His	Asn	Phe	Leu	Leu	Gly	Gln	Gly	Leu
			20					25					30		

Ile	Ala	Ala	Xaa	Xaa	Phe	Asn
			35			

<210> 216

<211> 38

<212> PRT

<213> Thermosynechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Cys

<400> 216

```
Met Lys Ile Val Gly Arg Arg Leu Met Gly Trp Gln Ala Val Tyr Asp
1          5          10          15
```

```
Ile Gly Leu Ala Ala Asp His Asn Phe Val Leu Ala Asn Gly Ala Ile
          20          25          30
```

```
Ala Ala Xaa Xaa Phe Asn
          35
```

<210> 217

<211> 39

<212> PRT

<213> Trichodesmium erythraeum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Asn

<400> 217

```
Met Val Lys Ile Val Ser Arg Lys Leu Ala Lys Thr Glu Asn Val Tyr
1          5          10          15
```

```
Asp Ile Gly Val Thr Lys Asp His Asn Phe Val Leu Ala Asn Gly Leu
          20          25          30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 218

<211> 38

<212> PRT

<213> Thermosynechococcus vulcanus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Cys

<400> 218

```
Met Lys Ile Val Gly Arg Arg Leu Val Gly Trp Gln Ala Val Tyr Asp
1           5           10           15
```

```
Ile Gly Leu Ala Gly Asp His Asn Phe Leu Leu Ala Asn Gly Ala Ile
          20           25           30
```

```
Ala Ala Xaa Xaa Phe Asn
          35
```

<210> 219

<211> 39

<212> PRT

<213> Nostoc punctiforme

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexaanoic acid

<400> 219

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

```
Asp Ile Gly Val Glu Arg Asp His Asn Phe Ala Leu Lys Asn Gly Phe
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 220

<211> 39

<212> PRT

<213> Synechocystis PCC6803

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 220

Met	Val	Lys	Val	Ile	Gly	Arg	Arg	Ser	Leu	Gly	Val	Gln	Arg	Ile	Phe
1				5					10					15	

Asp	Ile	Gly	Leu	Pro	Gln	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Ala
			20					25					30		

Ile	Ala	Ala	Xaa	Xaa	Phe	Asn
						35

<210> 221

<211> 39

<212> PRT

<213> Aphanothece halophytica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 221

```
Met Val Lys Ile Ile Lys Arg Gln Ser Leu Gly Arg Gln Asn Val Tyr
1           5           10           15
```

```
Asp Val Cys Val Glu Thr Asp His Asn Phe Val Leu Ala Asn Gly Cys
          20           25           30
```

```
Val Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 222

<211> 39

<212> PRT

<213> Aphanizomenon ovalisporum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 222

```
Met Val Lys Ile Thr Ala Arg Lys Phe Val Gly Arg Glu Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu His His His Asn Phe Ala Ile Lys Asn Gly Leu
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 223

<211> 39

<212> PRT

<213> Anabaena PCC7120

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexaanoic acid

<400> 223

```
Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
1           5           10          15
```

```
Asp Ile Gly Val Arg Arg Asp His Asn Phe Phe Ile Lys Asn Gly Leu
          20          25          30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 224

<211> 39

<212> PRT

<213> Anabaena variabilis

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexaanoic acid

<400> 224

```
Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
1           5           10          15
```

```
Asp Ile Gly Val Gly Arg Asp His Asn Phe Phe Val Lys Asn Gly Leu
          20          25          30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 225

<211> 39

<212> PRT

<213> Cylandropermopsis raciborskii

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 225

Met	Val	Lys	Ile	Val	Ser	Arg	Arg	Tyr	Leu	Gly	Lys	Ala	Asp	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Ala	Lys	Asp	His	Asn	Phe	Ile	Ile	Lys	Asn	Gly	Leu
			20					25					30		

Val	Ala	Ser	Xaa	Xaa	Phe	Asn
			35			

<210> 226

<211> 39

<212> PRT

<213> Cyanothece CCY0110

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 226

Met	Val	Lys	Ile	Ile	Glu	Arg	Arg	Ser	Leu	Gly	Lys	Gln	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ser	Asn	Asn	Leu
			20					25					30		

Ile Ala Ser Xaa Xaa Phe Asn
35

<210> 227

<211> 39

<212> PRT

<213> Cyanotheca PCC8801

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 227

Met	Val	Lys	Ile	Val	Ser	Tyr	Arg	Ser	Leu	Gly	Lys	Gln	Phe	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Ala	Gln	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Ser
			20					25					30		

Ile Ala Ser Xaa Xaa Phe Asn
35

<210> 228

<211> 39

<212> PRT

<213> Crocosphaera watsonii

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural

aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexanoic acid

<400> 228

```
Met Val Lys Ile Ile Gly Cys Arg Ser Leu Gly Thr Gln Lys Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Ser
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 229

<211> 39

<212> PRT

<213> Microcystis aeruginosa

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexanoic acid

<400> 229

```
Met Val Lys Ile Ile Gly Arg Gln Ser Leu Gly Arg Lys Pro Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Gly Asn Gly Leu
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 230

<211> 39

<212> PRT

<213> Microcoleus chthonoplastes

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural

aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopantoic acid, or 2-aminohexanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopantoic acid, or 2-aminohexanoic acid

<400> 230

```
Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 231

<211> 39

<212> PRT

<213> Oscillatoria limnetica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopantoic acid, or 2-aminohexanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopantoic acid, or 2-aminohexanoic acid

<400> 231

```
Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 232

<211> 39

<212> PRT

<213> Synechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 232

Met	Val	Lys	Ile	Val	Arg	Arg	Arg	Ser	Leu	Gly	Val	Gln	Pro	Val	Tyr
1				5					10					15	

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

Val	Ala	Ser	Xaa	Xaa	Phe	Asn
			35			

<210> 233

<211> 39

<212> PRT

<213> Synechococcus PCC7002

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 233

Met	Val	Lys	Ile	Ile	Arg	Arg	Lys	Phe	Ile	Gly	His	Ala	Pro	Thr	Tyr

1 5 10 15

Asp Ile Gly Leu Ser Gln Asp His Asn Phe Leu Leu Gly Gln Gly Leu
 20 25 30

Ile Ala Ala Xaa Xaa Phe Asn
 35

<210> 234

<211> 38

<212> PRT

<213> Thermosynechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 234

Met Lys Ile Val Gly Arg Arg Leu Met Gly Trp Gln Ala Val Tyr Asp
 1 5 10 15

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

Ala Ala Xaa Xaa Phe Asn
 35

<210> 235

<211> 39

<212> PRT

<213> Trichodesmium erythraeum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 235

```
Met Val Lys Ile Val Ser Arg Lys Leu Ala Lys Thr Glu Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Thr Lys Asp His Asn Phe Val Leu Ala Asn Gly Leu
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 236

<211> 38

<212> PRT

<213> Thermosynechococcus vulcanus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 236

```
Met Lys Ile Val Gly Arg Arg Leu Val Gly Trp Gln Ala Val Tyr Asp
1           5           10           15
```

```
Ile Gly Leu Ala Gly Asp His Asn Phe Leu Leu Ala Asn Gly Ala Ile
          20           25           30
```

```
Ala Ala Xaa Xaa Phe Asn
          35
```

<210> 237

<211> 39

<212> PRT

<213> Nostoc punctiforme

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 237

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

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

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn
						35

<210> 238

<211> 39

<212> PRT

<213> Synechocystis PCC6803

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 238

Met	Val	Lys	Val	Ile	Gly	Arg	Arg	Ser	Leu	Gly	Val	Gln	Arg	Ile	Phe
1				5					10					15	

Asp	Ile	Gly	Leu	Pro	Gln	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Ala
			20					25					30		

Ile	Ala	Ala	Xaa	Xaa	Phe	Asn
						35

<210> 239

<211> 39

<212> PRT

<213> Aphanothece halophytica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 239

Met	Val	Lys	Ile	Ile	Lys	Arg	Gln	Ser	Leu	Gly	Arg	Gln	Asn	Val	Tyr
1				5					10					15	

Asp	Val	Cys	Val	Glu	Thr	Asp	His	Asn	Phe	Val	Leu	Ala	Asn	Gly	Cys
			20					25					30		

Val	Ala	Ser	Xaa	Xaa	Phe	Asn
			35			

<210> 240

<211> 39

<212> PRT

<213> Aphanizomenon ovalisporum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 240

Met	Val	Lys	Ile	Thr	Ala	Arg	Lys	Phe	Val	Gly	Arg	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	His	His	His	Asn	Phe	Ala	Ile	Lys	Asn	Gly	Leu
			20					25					30		

Ile Ala Ser Xaa Xaa Phe Asn 35

<210> 241

<211> 39

<212> PRT

<213> Anabaena PCC7120

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 241

Met	Ile	Lys	Ile	Ala	Ser	Arg	Lys	Phe	Leu	Gly	Val	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Arg	Arg	Asp	His	Asn	Phe	Phe	Ile	Lys	Asn	Gly	Leu
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn
			35			

<210> 242

<211> 39

<212> PRT

<213> Anabaena variabilis

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 242

Met	Ile	Lys	Ile	Ala	Ser	Arg	Lys	Phe	Leu	Gly	Val	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Gly	Arg	Asp	His	Asn	Phe	Phe	Val	Lys	Asn	Gly	Leu
			20					25					30		

Ile Ala Ser Xaa Xaa Phe Asn
35

<210> 243

<211> 39

<212> PRT

<213> Cylindrospermopsis raciborskii

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopantoic acid, or 2-aminohexanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 243

Met	Val	Lys	Ile	Val	Ser	Arg	Arg	Tyr	Leu	Gly	Lys	Ala	Asp	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Ala	Lys	Asp	His	Asn	Phe	Ile	Ile	Lys	Asn	Gly	Leu
			20					25					30		

Val Ala Ser Xaa Xaa Phe Asn
35

<210> 244

<211> 39

<212> PRT

<213> Cyanotheca CCY0110

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopantoic acid, or 2-aminohexanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 244

Met	Val	Lys	Ile	Ile	Glu	Arg	Arg	Ser	Leu	Gly	Lys	Gln	Asn	Val	Tyr

1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ser Asn Asn Leu
 20 25 30

Ile Ala Ser Xaa Xaa Phe Asn
 35

<210> 245

<211> 39

<212> PRT

<213> Cyanotheca PCC8801

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 245

Met Val Lys Ile Val Ser Tyr Arg Ser Leu Gly Lys Gln Phe Val Tyr
 1 5 10 15

Asp Ile Gly Val Ala Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ser
 20 25 30

Ile Ala Ser Xaa Xaa Phe Asn
 35

<210> 246

<211> 39

<212> PRT

<213> Crocosphaera watsonii

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 246

```
Met Val Lys Ile Ile Gly Cys Arg Ser Leu Gly Thr Gln Lys Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Ser
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 247

<211> 39

<212> PRT

<213> Microcystis aeruginosa

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 247

```
Met Val Lys Ile Ile Gly Arg Gln Ser Leu Gly Arg Lys Pro Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Gly Asn Gly Leu
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 248

<211> 39

<212> PRT

<213> Microcoleus chthonoplastes

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 248

Met	Val	Lys	Ile	Val	Arg	Arg	Gln	Ser	Leu	Gly	Val	Gln	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Cys	Leu	Ala	Ser	Gly	Glu
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn
						35

<210> 249

<211> 39

<212> PRT

<213> *Oscillatoria limnetica*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 249

Met	Val	Lys	Ile	Val	Arg	Arg	Gln	Ser	Leu	Gly	Val	Gln	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Cys	Leu	Ala	Ser	Gly	Glu
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn
						35

<210> 250

<211> 39

<212> PRT

<213> *Synechococcus elongatus*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 250

```
Met Val Lys Ile Val Arg Arg Arg Ser Leu Gly Val Gln Pro Val Tyr
1           5           10           15
```

```
Asp Leu Gly Val Ala Thr Val His Asn Phe Val Leu Ala Asn Gly Leu
          20           25           30
```

```
Val Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 251

<211> 39

<212> PRT

<213> Synechococcus PCC7002

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 251

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

```
Asp Ile Gly Leu Ser Gln Asp His Asn Phe Leu Leu Gly Gln Gly Leu
          20           25           30
```

```
Ile Ala Ala Xaa Xaa Phe Asn
          35
```

<210> 252

<211> 38

<212> PRT

<213> Thermosynechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopantoic acid, or 2-aminohexanoic acid

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 252

Met	Lys	Ile	Val	Gly	Arg	Arg	Leu	Met	Gly	Trp	Gln	Ala	Val	Tyr	Asp
1				5					10					15	

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

Ala	Ala	Xaa	Xaa	Phe	Asn
					35

<210> 253

<211> 39

<212> PRT

<213> Trichodesmium erythraeum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopantoic acid, or 2-aminohexanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 253

Met	Val	Lys	Ile	Val	Ser	Arg	Lys	Leu	Ala	Lys	Thr	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Thr	Lys	Asp	His	Asn	Phe	Val	Leu	Ala	Asn	Gly	Leu
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn
						35

<210> 254

<211> 38

<212> PRT

<213> Thermosynechococcus vulcanus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 254

Met	Lys	Ile	Val	Gly	Arg	Arg	Leu	Val	Gly	Trp	Gln	Ala	Val	Tyr	Asp
1				5					10					15	

Ile	Gly	Leu	Ala	Gly	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Ala	Ile
			20					25					30		

Ala	Ala	Xaa	Xaa	Phe	Asn
					35

<210> 255

<211> 39

<212> PRT

<213> Nostoc punctiforme

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 255

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

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

Ile	Ala	Ser	Xaa	Ala	Phe	Asn
						35

<210> 256

<211> 39

<212> PRT

<213> Synechocystis PCC6803

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 256

```
Met Val Lys Val Ile Gly Arg Arg Ser Leu Gly Val Gln Arg Ile Phe
 1              5              10              15

Asp Ile Gly Leu Pro Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ala
      20              25              30

Ile Ala Ala Xaa Ala Phe Asn
      35
```

<210> 257

<211> 39

<212> PRT

<213> Aphanothece halophytica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 257

```
Met Val Lys Ile Ile Lys Arg Gln Ser Leu Gly Arg Gln Asn Val Tyr
 1              5              10              15

Asp Val Cys Val Glu Thr Asp His Asn Phe Val Leu Ala Asn Gly Cys
      20              25              30

Val Ala Ser Xaa Ala Phe Asn
      35
```

<210> 258

<211> 39

<212> PRT

<213> Aphanizomenon ovalisporum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 258

```
Met Val Lys Ile Thr Ala Arg Lys Phe Val Gly Arg Glu Asn Val Tyr
1           5           10          15
```

```
Asp Ile Gly Val Glu His His His Asn Phe Ala Ile Lys Asn Gly Leu
          20          25          30
```

```
Ile Ala Ser Xaa Ala Phe Asn
          35
```

<210> 259

<211> 39

<212> PRT

<213> Anabaena PCC7120

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 259

```
Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
1           5           10          15
```

```
Asp Ile Gly Val Arg Arg Asp His Asn Phe Phe Ile Lys Asn Gly Leu
          20          25          30
```

```
Ile Ala Ser Xaa Ala Phe Asn
          35
```

<210> 260

<211> 39

<212> PRT

<213> Anabaena variabilis

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 260

```
Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
1           5           10          15
```

Asp Ile Gly Val Gly Arg Asp His Asn Phe Phe Val Lys Asn Gly Leu
 20 25 30

Ile Ala Ser Xaa Ala Phe Asn
 35

<210> 261

<211> 39

<212> PRT

<213> Cylindrospermopsis raciborskii

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 261

Met Val Lys Ile Val Ser Arg Arg Tyr Leu Gly Lys Ala Asp Val Tyr
 1 5 10 15

Asp Ile Gly Val Ala Lys Asp His Asn Phe Ile Ile Lys Asn Gly Leu
 20 25 30

Val Ala Ser Xaa Ala Phe Asn
 35

<210> 262

<211> 39

<212> PRT

<213> Cyanotheca CCY0110

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 262

Met Val Lys Ile Ile Glu Arg Arg Ser Leu Gly Lys Gln Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ser Asn Asn Leu
 20 25 30

Ile Ala Ser Xaa Ala Phe Asn
 35

<210> 263

<211> 39

<212> PRT

<213> Cyanothecce PCC8801

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 263

Met	Val	Lys	Ile	Val	Ser	Tyr	Arg	Ser	Leu	Gly	Lys	Gln	Phe	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Ala	Gln	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Ser
			20					25					30		

Ile	Ala	Ser	Xaa	Ala	Phe	Asn
						35

<210> 264

<211> 39

<212> PRT

<213> Crocosphaera watsonii

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 264

Met	Val	Lys	Ile	Ile	Gly	Cys	Arg	Ser	Leu	Gly	Thr	Gln	Lys	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Ser
			20					25					30		

Ile	Ala	Ser	Xaa	Ala	Phe	Asn
						35

<210> 265

<211> 39

<212> PRT

<213> Microcystis aeruginosa

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 265

```
Met Val Lys Ile Ile Gly Arg Gln Ser Leu Gly Arg Lys Pro Val Tyr
1           5           10          15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Gly Asn Gly Leu
          20           25          30
```

```
Ile Ala Ser Xaa Ala Phe Asn
          35
```

<210> 266

<211> 39

<212> PRT

<213> Microcoleus chthonoplastes

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 266

```
Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
1           5           10          15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
          20           25          30
```

```
Ile Ala Ser Xaa Ala Phe Asn
          35
```

<210> 267

<211> 39

<212> PRT

<213> Oscillatoria limnetica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 267

```
Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
```

1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
 20 25 30

Ile Ala Ser Xaa Ala Phe Asn
 35

<210> 268

<211> 39

<212> PRT

<213> Synechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 268

Met Val Lys Ile Val Arg Arg Arg Ser Leu Gly Val Gln Pro Val Tyr
 1 5 10 15

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

Val Ala Ser Xaa Ala Phe Asn
 35

<210> 269

<211> 39

<212> PRT

<213> Synechococcus PCC7002

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 269

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

Asp Ile Gly Leu Ser Gln Asp His Asn Phe Leu Leu Gly Gln Gly Leu
 20 25 30

Ile Ala Ala Xaa Ala Phe Asn
 35

<210> 270

<211> 38

<212> PRT

<213> Thermosynechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexaanoic acid

<400> 270

Met	Lys	Ile	Val	Gly	Arg	Arg	Leu	Met	Gly	Trp	Gln	Ala	Val	Tyr	Asp
1				5					10					15	

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

Ala	Ala	Xaa	Ala	Phe	Asn
			35		

<210> 271

<211> 39

<212> PRT

<213> Trichodesmium erythraeum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexaanoic acid

<400> 271

Met	Val	Lys	Ile	Val	Ser	Arg	Lys	Leu	Ala	Lys	Thr	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Thr	Lys	Asp	His	Asn	Phe	Val	Leu	Ala	Asn	Gly	Leu
			20					25					30		

Ile	Ala	Ser	Xaa	Ala	Phe	Asn
			35			

<210> 272

<211> 38

<212> PRT

<213> Thermosynechococcus vulcanus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 272

```
Met Lys Ile Val Gly Arg Arg Leu Val Gly Trp Gln Ala Val Tyr Asp
1           5           10          15
```

```
Ile Gly Leu Ala Gly Asp His Asn Phe Leu Leu Ala Asn Gly Ala Ile
          20           25           30
```

```
Ala Ala Xaa Ala Phe Asn
          35
```

<210> 273

<211> 39

<212> PRT

<213> Nostoc punctiforme

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 273

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

```
Asp Ile Gly Val Glu Arg Asp His Asn Phe Ala Leu Lys Asn Gly Phe
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 274

<211> 39

<212> PRT

<213> Synechocystis PCC6803

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 274

```
Met Val Lys Val Ile Gly Arg Arg Ser Leu Gly Val Gln Arg Ile Phe
 1           5           10          15
```

```
Asp Ile Gly Leu Pro Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ala
      20           25          30
```

```
Ile Ala Ala Xaa Xaa Phe Asn
      35
```

<210> 275

<211> 39

<212> PRT

<213> Aphanothece halophytica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 275

```
Met Val Lys Ile Ile Lys Arg Gln Ser Leu Gly Arg Gln Asn Val Tyr
 1           5           10          15
```

```
Asp Val Cys Val Glu Thr Asp His Asn Phe Val Leu Ala Asn Gly Cys
      20           25          30
```

```
Val Ala Ser Xaa Xaa Phe Asn
      35
```

<210> 276

<211> 39

<212> PRT

<213> Aphanizomenon ovalisporum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 276

```
Met Val Lys Ile Thr Ala Arg Lys Phe Val Gly Arg Glu Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu His His His Asn Phe Ala Ile Lys Asn Gly Leu
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 277

<211> 39

<212> PRT

<213> Anabaena PCC7120

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 277

```
Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Arg Arg Asp His Asn Phe Phe Ile Lys Asn Gly Leu
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 278

<211> 39

<212> PRT

<213> Anabaena variabilis

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 278

```
Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
 1           5           10           15
```

```
Asp Ile Gly Val Gly Arg Asp His Asn Phe Phe Val Lys Asn Gly Leu
      20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
      35
```

<210> 279

<211> 39

<212> PRT

<213> *Cylindrospermopsis raciborskii*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 279

```
Met Val Lys Ile Val Ser Arg Arg Tyr Leu Gly Lys Ala Asp Val Tyr
 1           5           10           15
```

```
Asp Ile Gly Val Ala Lys Asp His Asn Phe Ile Ile Lys Asn Gly Leu
      20           25           30
```

```
Val Ala Ser Xaa Xaa Phe Asn
      35
```

<210> 280

<211> 39

<212> PRT

<213> *Cyanothece CCY0110*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

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<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 280

```
Met Val Lys Ile Ile Glu Arg Arg Ser Leu Gly Lys Gln Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ser Asn Asn Leu
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 281

<211> 39

<212> PRT

<213> Cyanothecce PCC8801

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 281

```
Met Val Lys Ile Val Ser Tyr Arg Ser Leu Gly Lys Gln Phe Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Ala Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ser
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 282

<211> 39

<212> PRT

<213> Crocosphaera watsonii

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 282

```
Met Val Lys Ile Ile Gly Cys Arg Ser Leu Gly Thr Gln Lys Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Ser
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 283

<211> 39

<212> PRT

<213> Microcystis aeruginosa

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 283

```
Met Val Lys Ile Ile Gly Arg Gln Ser Leu Gly Arg Lys Pro Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Gly Asn Gly Leu
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 284

<211> 39

<212> PRT

<213> Microcoleus chthonoplastes

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 284

```
Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 285

<211> 39

<212> PRT

<213> *Oscillatoria limnetica*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 285

```
Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 286

<211> 39

<212> PRT

<213> *Synechococcus elongatus*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 286

Met	Val	Lys	Ile	Val	Arg	Arg	Arg	Ser	Leu	Gly	Val	Gln	Pro	Val	Tyr
1				5					10					15	

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

Val	Ala	Ser	Xaa	Xaa	Phe	Asn
			35			

<210> 287

<211> 39

<212> PRT

<213> Synechococcus PCC7002

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 287

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

Asp	Ile	Gly	Leu	Ser	Gln	Asp	His	Asn	Phe	Leu	Leu	Gly	Gln	Gly	Leu
			20					25					30		

Ile	Ala	Ala	Xaa	Xaa	Phe	Asn
			35			

<210> 288

<211> 38

<212> PRT

<213> Thermosynechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Cys

<400> 288

Met	Lys	Ile	Val	Gly	Arg	Arg	Leu	Met	Gly	Trp	Gln	Ala	Val	Tyr	Asp
1				5					10					15	

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

Ala	Ala	Xaa	Xaa	Phe	Asn
					35

<210> 289

<211> 39

<212> PRT

<213> Trichodesmium erythraeum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 289

Met	Val	Lys	Ile	Val	Ser	Arg	Lys	Leu	Ala	Lys	Thr	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Thr	Lys	Asp	His	Asn	Phe	Val	Leu	Ala	Asn	Gly	Leu
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn
						35

<210> 290

<211> 38

<212> PRT

<213> Thermosynechococcus vulcanus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Cys

<400> 290

Met Lys Ile Val Gly Arg Arg Leu Val Gly Trp Gln Ala Val Tyr Asp
 1 5 10 15

Ile Gly Leu Ala Gly Asp His Asn Phe Leu Leu Ala Asn Gly Ala Ile
 20 25 30

Ala Ala Xaa Xaa Phe Asn
 35

<210> 291

<211> 39

<212> PRT

<213> Nostoc punctiforme

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 291

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

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

Ile Ala Ser Xaa Xaa Phe Asn
 35

<210> 292

<211> 39

<212> PRT

<213> Synechocystis PCC6803

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural

aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexanoic acid

<400> 292

```
Met Val Lys Val Ile Gly Arg Arg Ser Leu Gly Val Gln Arg Ile Phe
1           5           10           15
```

```
Asp Ile Gly Leu Pro Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ala
          20           25           30
```

```
Ile Ala Ala Xaa Xaa Phe Asn
          35
```

<210> 293

<211> 39

<212> PRT

<213> Aphanothece halophytica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexanoic acid

<400> 293

```
Met Val Lys Ile Ile Lys Arg Gln Ser Leu Gly Arg Gln Asn Val Tyr
1           5           10           15
```

```
Asp Val Cys Val Glu Thr Asp His Asn Phe Val Leu Ala Asn Gly Cys
          20           25           30
```

```
Val Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 294

<211> 39

<212> PRT

<213> Aphanizomenon ovalisporum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 294

```
Met Val Lys Ile Thr Ala Arg Lys Phe Val Gly Arg Glu Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu His His His Asn Phe Ala Ile Lys Asn Gly Leu
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 295

<211> 39

<212> PRT

<213> Anabaena PCC7120

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 295

```
Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Arg Arg Asp His Asn Phe Phe Ile Lys Asn Gly Leu
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 296

<211> 39

<212> PRT

<213> Anabaena variabilis

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 296

```
Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
1           5           10           15

Asp Ile Gly Val Gly Arg Asp His Asn Phe Phe Val Lys Asn Gly Leu
          20           25           30

Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 297

<211> 39

<212> PRT

<213> Cylindrospermopsis raciborskii

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 297

```
Met Val Lys Ile Val Ser Arg Arg Tyr Leu Gly Lys Ala Asp Val Tyr
1           5           10           15

Asp Ile Gly Val Ala Lys Asp His Asn Phe Ile Ile Lys Asn Gly Leu
          20           25           30

Val Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 298

<211> 39

<212> PRT

<213> Cyanothece CCY0110

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopantoic acid, or 2-aminohexanoic acid

<400> 298

```
Met Val Lys Ile Ile Glu Arg Arg Ser Leu Gly Lys Gln Asn Val Tyr
 1              5              10              15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ser Asn Asn Leu
      20              25              30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
      35
```

<210> 299

<211> 39

<212> PRT

<213> Cyanothece PCC8801

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopantoic acid, or 2-aminohexanoic acid

<400> 299

```
Met Val Lys Ile Val Ser Tyr Arg Ser Leu Gly Lys Gln Phe Val Tyr
 1              5              10              15
```

```
Asp Ile Gly Val Ala Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ser
      20              25              30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
      35
```

<210> 300

<211> 39

<212> PRT

<213> *Crocospaera watsonii*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 300

Met	Val	Lys	Ile	Ile	Gly	Cys	Arg	Ser	Leu	Gly	Thr	Gln	Lys	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Ser
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn
			35			

<210> 301

<211> 39

<212> PRT

<213> *Microcystis aeruginosa*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 301

Met	Val	Lys	Ile	Ile	Gly	Arg	Gln	Ser	Leu	Gly	Arg	Lys	Pro	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Gly	Asn	Gly	Leu
			20					25					30		

Ile Ala Ser Xaa Xaa Phe Asn
35

<210> 302

<211> 39

<212> PRT

<213> Microcoleus chthonoplastes

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopantoic acid, or 2-aminohexanoic acid

<400> 302

Met	Val	Lys	Ile	Val	Arg	Arg	Gln	Ser	Leu	Gly	Val	Gln	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Cys	Leu	Ala	Ser	Gly	Glu
			20					25					30		

Ile Ala Ser Xaa Xaa Phe Asn
35

<210> 303

<211> 39

<212> PRT

<213> Oscillatoria limnetica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopantoic acid, or 2-aminohexanoic acid

<400> 303

Met	Val	Lys	Ile	Val	Arg	Arg	Gln	Ser	Leu	Gly	Val	Gln	Asn	Val	Tyr


```

1         5         10        15
Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
      20              25              30

```

```

Ile Ala Ser Xaa Xaa Phe Asn
      35

```

<210> 304

<211> 39

<212> PRT

<213> Synechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 304

```

Met Val Lys Ile Val Arg Arg Arg Ser Leu Gly Val Gln Pro Val Tyr
1         5         10        15

```

```

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

```

```

Val Ala Ser Xaa Xaa Phe Asn
      35

```

<210> 305

<211> 39

<212> PRT

<213> Synechococcus PCC7002

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-

aminopentoic acid, or 2-aminohexaanoic acid

<400> 305

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

```
Asp Ile Gly Leu Ser Gln Asp His Asn Phe Leu Leu Gly Gln Gly Leu
          20           25           30
```

```
Ile Ala Ala Xaa Xaa Phe Asn
          35
```

<210> 306

<211> 38

<212> PRT

<213> Thermosynechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 306

```
Met Lys Ile Val Gly Arg Arg Leu Met Gly Trp Gln Ala Val Tyr Asp
1           5           10           15
```

```
Ile Gly Leu Ala Ala Asp His Asn Phe Val Leu Ala Asn Gly Ala Ile
          20           25           30
```

```
Ala Ala Xaa Xaa Phe Asn
          35
```

<210> 307

<211> 39

<212> PRT

<213> Trichodesmium erythraeum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 307

```
Met Val Lys Ile Val Ser Arg Lys Leu Ala Lys Thr Glu Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Thr Lys Asp His Asn Phe Val Leu Ala Asn Gly Leu
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 308

<211> 38

<212> PRT

<213> Thermosynechococcus vulcanus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 308

```
Met Lys Ile Val Gly Arg Arg Leu Val Gly Trp Gln Ala Val Tyr Asp
1           5           10           15
```

```
Ile Gly Leu Ala Gly Asp His Asn Phe Leu Leu Ala Asn Gly Ala Ile
          20           25           30
```

```
Ala Ala Xaa Xaa Phe Asn
          35
```

<210> 309

<211> 39

<212> PRT

<213> Nostoc punctiforme

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 309

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

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

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn
			35			

<210> 310

<211> 39

<212> PRT

<213> Synechocystis PCC6803

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 310

Met	Val	Lys	Val	Ile	Gly	Arg	Arg	Ser	Leu	Gly	Val	Gln	Arg	Ile	Phe
1			5					10					15		

Asp	Ile	Gly	Leu	Pro	Gln	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Ala
		20					25						30		

Ile	Ala	Ala	Xaa	Xaa	Phe	Asn
			35			

<210> 311

<211> 39

<212> PRT

<213> Aphanothece halophytica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 311

Met	Val	Lys	Ile	Ile	Lys	Arg	Gln	Ser	Leu	Gly	Arg	Gln	Asn	Val	Tyr
1			5						10					15	

Asp	Val	Cys	Val	Glu	Thr	Asp	His	Asn	Phe	Val	Leu	Ala	Asn	Gly	Cys
			20					25					30		

Val	Ala	Ser	Xaa	Xaa	Phe	Asn
			35			

<210> 312

<211> 39

<212> PRT

<213> Aphanizomenon ovalisporum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 312

Met	Val	Lys	Ile	Thr	Ala	Arg	Lys	Phe	Val	Gly	Arg	Glu	Asn	Val	Tyr
1			5						10					15	

Asp	Ile	Gly	Val	Glu	His	His	His	Asn	Phe	Ala	Ile	Lys	Asn	Gly	Leu
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn
			35			

<210> 313

<211> 39

<212> PRT

<213> Anabaena PCC7120

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 313

Met	Ile	Lys	Ile	Ala	Ser	Arg	Lys	Phe	Leu	Gly	Val	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Arg	Arg	Asp	His	Asn	Phe	Phe	Ile	Lys	Asn	Gly	Leu
		20					25						30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn
			35			

<210> 314

<211> 39

<212> PRT

<213> Anabaena variabilis

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 314

Met	Ile	Lys	Ile	Ala	Ser	Arg	Lys	Phe	Leu	Gly	Val	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Gly	Arg	Asp	His	Asn	Phe	Phe	Val	Lys	Asn	Gly	Leu
		20					25						30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn
			35			

<210> 315

<211> 39

<212> PRT

<213> Cylindrospermopsis raciborskii

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 315

```
Met Val Lys Ile Val Ser Arg Arg Tyr Leu Gly Lys Ala Asp Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Ala Lys Asp His Asn Phe Ile Ile Lys Asn Gly Leu
          20           25           30
```

```
Val Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 316

<211> 39

<212> PRT

<213> Cyanothecce CCY0110

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 316

```
Met Val Lys Ile Ile Glu Arg Arg Ser Leu Gly Lys Gln Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ser Asn Asn Leu
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 317

<211> 39

<212> PRT

<213> Cyanothecce PCC8801

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 317

Met Val Lys Ile Val Ser Tyr Arg Ser Leu Gly Lys Gln Phe Val Tyr
1 5 10 15

Asp Ile Gly Val Ala Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ser
20 25 30

Ile Ala Ser Xaa Xaa Phe Asn
35

<210> 318

<211> 39

<212> PRT

<213> Crocosphaera watsonii

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 318

Met Val Lys Ile Ile Gly Cys Arg Ser Leu Gly Thr Gln Lys Val Tyr
1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Ser
20 25 30

Ile Ala Ser Xaa Xaa Phe Asn
35

<210> 319

<211> 39

<212> PRT

<213> Microcystis aeruginosa

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 319

```
Met Val Lys Ile Ile Gly Arg Gln Ser Leu Gly Arg Lys Pro Val Tyr
 1           5           10           15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Gly Asn Gly Leu
      20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
      35
```

<210> 320

<211> 39

<212> PRT

<213> Microcoleus chthonoplastes

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 320

```
Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
 1           5           10           15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
      20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
      35
```

<210> 321

<211> 39

<212> PRT

<213> Oscillatoria limnetica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 321

```
Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 322

<211> 39

<212> PRT

<213> Synechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 322

```
Met Val Lys Ile Val Arg Arg Arg Ser Leu Gly Val Gln Pro Val Tyr
1           5           10           15
```

```
Asp Leu Gly Val Ala Thr Val His Asn Phe Val Leu Ala Asn Gly Leu
          20           25           30
```

```
Val Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 323

<211> 39

<212> PRT

<213> Synechococcus PCC7002

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 323

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

```
Asp Ile Gly Leu Ser Gln Asp His Asn Phe Leu Leu Gly Gln Gly Leu
          20           25          30
```

```
Ile Ala Ala Xaa Xaa Phe Asn
          35
```

<210> 324

<211> 38

<212> PRT

<213> Thermosynechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 324

```
Met Lys Ile Val Gly Arg Arg Leu Met Gly Trp Gln Ala Val Tyr Asp
1           5           10          15
```

```
Ile Gly Leu Ala Ala Asp His Asn Phe Val Leu Ala Asn Gly Ala Ile
          20           25          30
```

```
Ala Ala Xaa Xaa Phe Asn
          35
```

<210> 325

<211> 39

<212> PRT

<213> Trichodesmium erythraeum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 325

```
Met Val Lys Ile Val Ser Arg Lys Leu Ala Lys Thr Glu Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Thr Lys Asp His Asn Phe Val Leu Ala Asn Gly Leu
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn
          35
```

<210> 326

<211> 38

<212> PRT

<213> Thermosynechococcus vulcanus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 326

```
Met Lys Ile Val Gly Arg Arg Leu Val Gly Trp Gln Ala Val Tyr Asp
1           5           10           15
```

```
Ile Gly Leu Ala Gly Asp His Asn Phe Leu Leu Ala Asn Gly Ala Ile
          20           25           30
```

```
Ala Ala Xaa Xaa Phe Asn
          35
```

<210> 327

<211> 39

<212> PRT

<213> Nostoc punctiforme

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 327

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

```
Asp Ile Gly Val Glu Arg Asp His Asn Phe Ala Leu Lys Asn Gly Phe
          --          --          --
```

20

25

30

Ile Ala Ser Xaa Ala Phe Asn
35

<210> 328

<211> 39

<212> PRT

<213> Synechocystis PCC6803

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 328

Met Val Lys Val Ile Gly Arg Arg Ser Leu Gly Val Gln Arg Ile Phe
1 5 10 15

Asp Ile Gly Leu Pro Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ala
20 25 30

Ile Ala Ala Xaa Ala Phe Asn
35

<210> 329

<211> 39

<212> PRT

<213> Aphanothece halophytica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 329

Met Val Lys Ile Ile Lys Arg Gln Ser Leu Gly Arg Gln Asn Val Tyr
1 5 10 15

Asp Val Cys Val Glu Thr Asp His Asn Phe Val Leu Ala Asn Gly Cys
20 25 30

Val Ala Ser Xaa Ala Phe Asn
35

<210> 330

<211> 39

<212> PRT

<213> Aphanizomenon ovalisporum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 330

```
Met Val Lys Ile Thr Ala Arg Lys Phe Val Gly Arg Glu Asn Val Tyr
 1           5           10          15
```

```
Asp Ile Gly Val Glu His His His Asn Phe Ala Ile Lys Asn Gly Leu
      20           25          30
```

```
Ile Ala Ser Xaa Ala Phe Asn
      35
```

<210> 331

<211> 39

<212> PRT

<213> Anabaena PCC7120

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 331

```
Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
 1           5           10          15
```

```
Asp Ile Gly Val Arg Arg Asp His Asn Phe Phe Ile Lys Asn Gly Leu
      20           25          30
```

```
Ile Ala Ser Xaa Ala Phe Asn
      35
```

<210> 332

<211> 39

<212> PRT

<213> Anabaena variabilis

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 332

```
Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
 1           5           10          15
```

```
Asp Ile Gly Val Gly Arg Asp His Asn Phe Phe Val Lys Asn Gly Leu
      20           25          30
```

```
Ile Ala Ser Xaa Ala Phe Asn
      35
```

<210> 333
 <211> 39
 <212> PRT
 <213> *Cylindrospermopsis raciborskii*

<220>
 <221> MISC_FEATURE
 <222> (36)..(36)
 <223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 333
 Met Val Lys Ile Val Ser Arg Arg Tyr Leu Gly Lys Ala Asp Val Tyr
 1 5 10 15
 Asp Ile Gly Val Ala Lys Asp His Asn Phe Ile Ile Lys Asn Gly Leu
 20 25 30
 Val Ala Ser Xaa Ala Phe Asn
 35

<210> 334
 <211> 39
 <212> PRT
 <213> *Cyanothece CCY0110*

<220>
 <221> MISC_FEATURE
 <222> (36)..(36)
 <223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 334
 Met Val Lys Ile Ile Glu Arg Arg Ser Leu Gly Lys Gln Asn Val Tyr
 1 5 10 15
 Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ser Asn Asn Leu
 20 25 30
 Ile Ala Ser Xaa Ala Phe Asn
 35

<210> 335
 <211> 39
 <212> PRT
 <213> *Cyanothece PCC8801*

<220>
 <221> MISC_FEATURE
 <222> (36)..(36)
 <223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 335

Met Val Lys Ile Val Ser Tyr Arg Ser Leu Gly Lys Gln Phe Val Tyr
 1 5 10 15

Asp Ile Gly Val Ala Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ser
 20 25 30

Ile Ala Ser Xaa Ala Phe Asn
 35

<210> 336

<211> 39

<212> PRT

<213> Crocosphaera watsonii

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 336

Met Val Lys Ile Ile Gly Cys Arg Ser Leu Gly Thr Gln Lys Val Tyr
 1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Ser
 20 25 30

Ile Ala Ser Xaa Ala Phe Asn
 35

<210> 337

<211> 39

<212> PRT

<213> Microcystis aeruginosa

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 337

Met Val Lys Ile Ile Gly Arg Gln Ser Leu Gly Arg Lys Pro Val Tyr
 1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Gly Asn Gly Leu
 20 25 30

Ile Ala Ser Xaa Ala Phe Asn
 35

<210> 338

<211> 39

<212> PRT

<213> Microcoleus chthonoplastes

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 338

Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
20 25 30

Ile Ala Ser Xaa Ala Phe Asn
35

<210> 339

<211> 39

<212> PRT

<213> Oscillatoria limnetica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 339

Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
20 25 30

Ile Ala Ser Xaa Ala Phe Asn
35

<210> 340

<211> 39

<212> PRT

<213> Synechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 340

Met Val Lys Ile Val Arg Arg Arg Ser Leu Gly Val Gln Pro Val Tyr
1 5 10 15

Asp Leu Gly Val Ala Thr Val His Asn Phe Val Leu Ala Asn Gly Leu

- - 20 25 30 -

Val Ala Ser Xaa Ala Phe Asn
35

<210> 341
<211> 39
<212> PRT
<213> Synechococcus PCC7002

<220>
<221> MISC_FEATURE
<222> (36)..(36)
<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 341
Met Val Lys Ile Ile Arg Arg Lys Phe Ile Gly His Ala Pro Thr Tyr
1 5 10 15

Asp Ile Gly Leu Ser Gln Asp His Asn Phe Leu Leu Gly Gln Gly Leu
20 25 30

Ile Ala Ala Xaa Ala Phe Asn
35

<210> 342
<211> 38
<212> PRT
<213> Thermosynechococcus elongatus

<220>
<221> MISC_FEATURE
<222> (35)..(35)
<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 342
Met Lys Ile Val Gly Arg Arg Leu Met Gly Trp Gln Ala Val Tyr Asp
1 5 10 15

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

Ala Ala Xaa Ala Phe Asn
35

<210> 343
<211> 39
<212> PRT
<213> Trichodesmium erythraeum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 343

Met	Val	Lys	Ile	Val	Ser	Arg	Lys	Leu	Ala	Lys	Thr	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Thr	Lys	Asp	His	Asn	Phe	Val	Leu	Ala	Asn	Gly	Leu
			20					25					30		

Ile	Ala	Ser	Xaa	Ala	Phe	Asn
			35			

<210> 344

<211> 38

<212> PRT

<213> Thermosynechococcus vulcanus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 344

Met	Lys	Ile	Val	Gly	Arg	Arg	Leu	Val	Gly	Trp	Gln	Ala	Val	Tyr	Asp
1				5					10					15	

Ile	Gly	Leu	Ala	Gly	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Ala	Ile
			20					25					30		

Ala	Ala	Xaa	Ala	Phe	Asn
			35		

<210> 345

<211> 39

<212> PRT

<213> Nostoc punctiforme

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 345

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

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

Ile Ala Ser Ala Xaa Phe Asn
35

<210> 346

<211> 39

<212> PRT

<213> Synechocystis PCC6803

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 346

Met Val Lys Val Ile Gly Arg Arg Ser Leu Gly Val Gln Arg Ile Phe
1 5 10 15

Asp Ile Gly Leu Pro Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ala
20 25 30

Ile Ala Ala Ala Xaa Phe Asn
35

<210> 347

<211> 39

<212> PRT

<213> Aphanothece halophytica

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 347

Met Val Lys Ile Ile Lys Arg Gln Ser Leu Gly Arg Gln Asn Val Tyr
1 5 10 15

Asp Val Cys Val Glu Thr Asp His Asn Phe Val Leu Ala Asn Gly Cys
20 25 30

Val Ala Ser Ala Xaa Phe Asn
35

<210> 348

<211> 39

<212> PRT

<213> Aphanizomenon ovalisporum

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 348

```
Met Val Lys Ile Thr Ala Arg Lys Phe Val Gly Arg Glu Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu His His His Asn Phe Ala Ile Lys Asn Gly Leu
          20           25           30
```

```
Ile Ala Ser Ala Xaa Phe Asn
          35
```

<210> 349

<211> 39

<212> PRT

<213> Anabaena PCC7120

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 349

```
Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Arg Arg Asp His Asn Phe Phe Ile Lys Asn Gly Leu
          20           25           30
```

```
Ile Ala Ser Ala Xaa Phe Asn
          35
```

<210> 350

<211> 39

<212> PRT

<213> Anabaena variabilis

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 350

```
Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Gly Arg Asp His Asn Phe Phe Val Lys Asn Gly Leu
          20           25           30
```

```
Ile Ala Ser Ala Xaa Phe Asn
          35
```

<210> 351

<211> 39
 <212> PRT
 <213> Cylindrospermopsis raciborskii

<220>
 <221> MISC_FEATURE
 <222> (37)..(37)
 <223> Xaa is any amino acid excluding Cys

<400> 351
 Met Val Lys Ile Val Ser Arg Arg Tyr Leu Gly Lys Ala Asp Val Tyr
 1 5 10 15
 Asp Ile Gly Val Ala Lys Asp His Asn Phe Ile Ile Lys Asn Gly Leu
 20 25 30
 Val Ala Ser Ala Xaa Phe Asn
 35

<210> 352
 <211> 39
 <212> PRT
 <213> Cyanothece CCY0110

<220>
 <221> MISC_FEATURE
 <222> (37)..(37)
 <223> Xaa is any amino acid excluding Cys

<400> 352
 Met Val Lys Ile Ile Glu Arg Arg Ser Leu Gly Lys Gln Asn Val Tyr
 1 5 10 15
 Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ser Asn Asn Leu
 20 25 30
 Ile Ala Ser Ala Xaa Phe Asn
 35

<210> 353
 <211> 39
 <212> PRT
 <213> Cyanothece PCC8801

<220>
 <221> MISC_FEATURE
 <222> (37)..(37)
 <223> Xaa is any amino acid excluding Cys

<400> 353
 Met Val Lys Ile Val Ser Tyr Arg Ser Leu Gly Lys Gln Phe Val Tyr
 1 5 10 15

- - - - -

Asp Ile Gly Val Ala Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ser
 20 25 30

Ile Ala Ser Ala Xaa Phe Asn
 35

<210> 354

<211> 39

<212> PRT

<213> Crocosphaera watsonii

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 354

Met Val Lys Ile Ile Gly Cys Arg Ser Leu Gly Thr Gln Lys Val Tyr
 1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Ser
 20 25 30

Ile Ala Ser Ala Xaa Phe Asn
 35

<210> 355

<211> 39

<212> PRT

<213> Microcystis aeruginosa

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 355

Met Val Lys Ile Ile Gly Arg Gln Ser Leu Gly Arg Lys Pro Val Tyr
 1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Gly Asn Gly Leu
 20 25 30

Ile Ala Ser Ala Xaa Phe Asn
 35

<210> 356

<211> 39

<212> PRT

<213> Microcoleus chthonoplastes

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 356

Met	Val	Lys	Ile	Val	Arg	Arg	Gln	Ser	Leu	Gly	Val	Gln	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Cys	Leu	Ala	Ser	Gly	Glu
			20					25					30		

Ile	Ala	Ser	Ala	Xaa	Phe	Asn
				35		

<210> 357

<211> 39

<212> PRT

<213> Oscillatoria limnetica

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 357

Met	Val	Lys	Ile	Val	Arg	Arg	Gln	Ser	Leu	Gly	Val	Gln	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Cys	Leu	Ala	Ser	Gly	Glu
			20					25					30		

Ile	Ala	Ser	Ala	Xaa	Phe	Asn
				35		

<210> 358

<211> 39

<212> PRT

<213> Synechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 358

Met	Val	Lys	Ile	Val	Arg	Arg	Arg	Ser	Leu	Gly	Val	Gln	Pro	Val	Tyr
1				5					10					15	

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

Val Ala Ser Ala Xaa Phe Asn
35

<210> 359

<211> 39

<212> PRT

<213> Synechococcus PCC7002

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 359

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

Asp Ile Gly Leu Ser Gln Asp His Asn Phe Leu Leu Gly Gln Gly Leu
20 25 30

Ile Ala Ala Ala Xaa Phe Asn
35

<210> 360

<211> 38

<212> PRT

<213> Thermosynechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Cys

<400> 360

Met Lys Ile Val Gly Arg Arg Leu Met Gly Trp Gln Ala Val Tyr Asp
1 5 10 15

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

Ala Ala Ala Xaa Phe Asn
35

<210> 361

<211> 39

<212> PRT

<213> Trichodesmium erythraeum

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 361

```
Met Val Lys Ile Val Ser Arg Lys Leu Ala Lys Thr Glu Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Thr Lys Asp His Asn Phe Val Leu Ala Asn Gly Leu
20           25           30
```

```
Ile Ala Ser Ala Xaa Phe Asn
```

35

<210> 362

<211> 38

<212> PRT

<213> Thermosynechococcus vulcanus

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Cys

<400> 362

```
Met Lys Ile Val Gly Arg Arg Leu Val Gly Trp Gln Ala Val Tyr Asp
1           5           10           15
```

```
Ile Gly Leu Ala Gly Asp His Asn Phe Leu Leu Ala Asn Gly Ala Ile
20           25           30
```

```
Ala Ala Ala Xaa Phe Asn
35
```

<210> 363

<211> 39

<212> PRT

<213> Nostoc punctiforme

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 363

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

```
Asp Ile Gly Val Glu Arg Asp His Asn Phe Ala Leu Lys Asn Gly Phe
20           25           30
```

Ile Ala Ser Ala Xaa Phe Asn
35

<210> 364

<211> 39

<212> PRT

<213> Synechocystis PCC6803

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 364

Met	Val	Lys	Val	Ile	Gly	Arg	Arg	Ser	Leu	Gly	Val	Gln	Arg	Ile	Phe
1				5					10					15	

Asp	Ile	Gly	Leu	Pro	Gln	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Ala
			20					25					30		

Ile Ala Ala Ala Xaa Phe Asn
35

<210> 365

<211> 39

<212> PRT

<213> Aphanothece halophytica

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 365

Met	Val	Lys	Ile	Ile	Lys	Arg	Gln	Ser	Leu	Gly	Arg	Gln	Asn	Val	Tyr
1			5						10				15		

Asp	Val	Cys	Val	Glu	Thr	Asp	His	Asn	Phe	Val	Leu	Ala	Asn	Gly	Cys
			20					25					30		

Val Ala Ser Ala Xaa Phe Asn
35

<210> 366

<211> 39

<212> PRT

<213> Aphanizomenon ovalisporum

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 366

```
Met Val Lys Ile Thr Ala Arg Lys Phe Val Gly Arg Glu Asn Val Tyr
1           5           10          15
```

```
Asp Ile Gly Val Glu His His His Asn Phe Ala Ile Lys Asn Gly Leu
          20           25          30
```

```
Ile Ala Ser Ala Xaa Phe Asn
          35
```

<210> 367

<211> 39

<212> PRT

<213> Anabaena PCC7120

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 367

```
Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
1           5           10          15
```

```
Asp Ile Gly Val Arg Arg Asp His Asn Phe Phe Ile Lys Asn Gly Leu
          20           25          30
```

```
Ile Ala Ser Ala Xaa Phe Asn
          35
```

<210> 368

<211> 39

<212> PRT

<213> Anabaena variabilis

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural

aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexanoic acid

<400> 368

```
Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
 1             5             10             15
```

```
Asp Ile Gly Val Gly Arg Asp His Asn Phe Phe Val Lys Asn Gly Leu
```

20

25

30

```
Ile Ala Ser Ala Xaa Phe Asn
      35
```

<210> 369

<211> 39

<212> PRT

<213> *Cylindrospermopsis raciborskii*

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexanoic acid

<400> 369

```
Met Val Lys Ile Val Ser Arg Arg Tyr Leu Gly Lys Ala Asp Val Tyr
 1             5             10             15
```

```
Asp Ile Gly Val Ala Lys Asp His Asn Phe Ile Ile Lys Asn Gly Leu
      20             25             30
```

```
Val Ala Ser Ala Xaa Phe Asn
      35
```

<210> 370

<211> 39

<212> PRT

<213> *Cyanothece* CCY0110

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexanoic acid

<400> 370

```
Met Val Lys Ile Ile Glu Arg Arg Ser Leu Gly Lys Gln Asn Val Tyr
 1             5             10             15
```

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ser Asn Asn Leu
 20 25 30

Ile Ala Ser Ala Xaa Phe Asn
 35

<210> 371

<211> 39

<212> PRT

<213> Cyanotheca PCC8801

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 371

Met Val Lys Ile Val Ser Tyr Arg Ser Leu Gly Lys Gln Phe Val Tyr
 1 5 10 15

Asp Ile Gly Val Ala Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ser
 20 25 30

Ile Ala Ser Ala Xaa Phe Asn
 35

<210> 372

<211> 39

<212> PRT

<213> Crocosphaera watsonii

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 372

Met Val Lys Ile Ile Gly Cys Arg Ser Leu Gly Thr Gln Lys Val Tyr
 1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Ser
 20 25 30

Ile Ala Ser Ala Xaa Phe Asn
 35

<210> 373

<211> 39

<212> PRT

<213> Microcystis aeruginosa

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 373

Met	Val	Lys	Ile	Ile	Gly	Arg	Gln	Ser	Leu	Gly	Arg	Lys	Pro	Val	Tyr
1			5						10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Gly	Asn	Gly	Leu
			20					25					30		

Ile	Ala	Ser	Ala	Xaa	Phe	Asn
						35

<210> 374

<211> 39

<212> PRT

<213> Microcoleus chthonoplastes

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 374

Met	Val	Lys	Ile	Val	Arg	Arg	Gln	Ser	Leu	Gly	Val	Gln	Asn	Val	Tyr
1			5						10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Cys	Leu	Ala	Ser	Gly	Glu
			20					25					30		

Ile	Ala	Ser	Ala	Xaa	Phe	Asn
						35

<210> 375

<211> 39

<212> PRT

<213> Oscillatoria limnetica

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 375

```
Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
 1             5             10             15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
      20             25             30
```

```
Ile Ala Ser Ala Xaa Phe Asn
      35
```

<210> 376

<211> 39

<212> PRT

<213> Synechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 376

```
Met Val Lys Ile Val Arg Arg Arg Ser Leu Gly Val Gln Pro Val Tyr
 1             5             10             15
```

```
Asp Leu Gly Val Ala Thr Val His Asn Phe Val Leu Ala Asn Gly Leu
      20             25             30
```

```
Val Ala Ser Ala Xaa Phe Asn
      35
```

<210> 377

<211> 39

<212> PRT

<213> Synechococcus PCC7002

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 377

```
Met Val Lys Ile Ile Arg Arg Lys Phe Ile Gly His Ala Pro Thr Tyr
```


1 5 10 15
 Asp Ile Gly Leu Ser Gln Asp His Asn Phe Leu Leu Gly Gln Gly Leu

20 25 30

Ile Ala Ala Ala Xaa Phe Asn
 35

<210> 378

<211> 38

<212> PRT

<213> Thermosynechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 378

Met Lys Ile Val Gly Arg Arg Leu Met Gly Trp Gln Ala Val Tyr Asp
 1 5 10 15

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

Ala Ala Ala Xaa Phe Asn
 35

<210> 379

<211> 39

<212> PRT

<213> Trichodesmium erythraeum

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 379

Met Val Lys Ile Val Ser Arg Lys Leu Ala Lys Thr Glu Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Thr Lys Asp His Asn Phe Val Leu Ala Asn Gly Leu
 20 25 30

Ile Ala Ser Ala Xaa Phe Asn
 --

35

<210> 380

<211> 38

<212> PRT

<213> Thermosynechococcus vulcanus

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 380

```
Met Lys Ile Val Gly Arg Arg Leu Val Gly Trp Gln Ala Val Tyr Asp
1           5           10           15
```

```
Ile Gly Leu Ala Gly Asp His Asn Phe Leu Leu Ala Asn Gly Ala Ile
                20           25           30
```

```
Ala Ala Ala Xaa Phe Asn
                35
```

<210> 381

<211> 39

<212> PRT

<213> Nostoc punctiforme

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 381

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

```
Asp Ile Gly Val Glu Arg Asp His Asn Phe Ala Leu Lys Asn Gly Phe
                20           25           30
```

```
Ile Ala Ser Ala Xaa Phe Asn
                35
```

<210> 382

<211> 39

<212> PRT

<213> Synechocystis PCC6803

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 382

```
Met Val Lys Val Ile Gly Arg Arg Ser Leu Gly Val Gln Arg Ile Phe
1           5           10           15
```

```
Asp Ile Gly Leu Pro Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ala
          20           25           30
```

```
Ile Ala Ala Ala Xaa Phe Asn
          35
```

<210> 383

<211> 39

<212> PRT

<213> Aphanothece halophytica

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 383

```
Met Val Lys Ile Ile Lys Arg Gln Ser Leu Gly Arg Gln Asn Val Tyr
1           5           10           15
```

```
Asp Val Cys Val Glu Thr Asp His Asn Phe Val Leu Ala Asn Gly Cys
          20           25           30
```

```
Val Ala Ser Ala Xaa Phe Asn
          35
```

<210> 384

<211> 39

<212> PRT

<213> Aphanizomenon ovalisporum

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 384

```
Met Val Lys Ile Thr Ala Arg Lys Phe Val Gly Arg Glu Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu His His His Asn Phe Ala Ile Lys Asn Gly Leu
          20           25           30
```

```
Ile Ala Ser Ala Xaa Phe Asn
          35
```

<210> 385

<211> 39

<212> PRT

<213> Anabaena PCC7120

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 385

Met	Ile	Lys	Ile	Ala	Ser	Arg	Lys	Phe	Leu	Gly	Val	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Arg	Arg	Asp	His	Asn	Phe	Phe	Ile	Lys	Asn	Gly	Leu
			20					25					30		

Ile	Ala	Ser	Ala	Xaa	Phe	Asn
						35

<210> 386

<211> 39

<212> PRT

<213> Anabaena variabilis

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 386

Met	Ile	Lys	Ile	Ala	Ser	Arg	Lys	Phe	Leu	Gly	Val	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Gly	Arg	Asp	His	Asn	Phe	Phe	Val	Lys	Asn	Gly	Leu
			20					25					30		

Ile	Ala	Ser	Ala	Xaa	Phe	Asn
						35

<210> 387

<211> 39

<212> PRT

<213> Cylindrospermopsis raciborskii

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 387

```

Met Val Lys Ile Val Ser Arg Arg Tyr Leu Gly Lys Ala Asp Val Tyr
1           5           10           15

```

```

Asp Ile Gly Val Ala Lys Asp His Asn Phe Ile Ile Lys Asn Gly Leu
          20           25           30

```

```

Val Ala Ser Ala Xaa Phe Asn
          35

```

<210> 388

<211> 39

<212> PRT

<213> Cyanothece CCY0110

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 388

```

Met Val Lys Ile Ile Glu Arg Arg Ser Leu Gly Lys Gln Asn Val Tyr
1           5           10           15

```

```

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ser Asn Asn Leu
          20           25           30

```

```

Ile Ala Ser Ala Xaa Phe Asn
          35

```

<210> 389

<211> 39

<212> PRT

<213> Cyanothece PCC8801

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 389

```

Met Val Lys Ile Val Ser Tyr Arg Ser Leu Gly Lys Gln Phe Val Tyr
1           5           10           15

```

```

Asp Ile Gly Val Ala Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ser
          20           25           30

```

```

Ile Ala Ser Ala Xaa Phe Asn
          35

```

<210> 390

<211> 39

<212> PRT

<213> Crocosphaera watsonii

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 390

Met	Val	Lys	Ile	Ile	Gly	Cys	Arg	Ser	Leu	Gly	Thr	Gln	Lys	Val	Tyr
1			5					10					15		

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Ser
		20					25						30		

Ile	Ala	Ser	Ala	Xaa	Phe	Asn
		35				

<210> 391

<211> 39

<212> PRT

<213> Microcystis aeruginosa

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 391

Met	Val	Lys	Ile	Ile	Gly	Arg	Gln	Ser	Leu	Gly	Arg	Lys	Pro	Val	Tyr
1			5					10					15		

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Gly	Asn	Gly	Leu
		20					25						30		

Ile	Ala	Ser	Ala	Xaa	Phe	Asn
		35				

<210> 392

<211> 39

<212> PRT

<213> Microcoleus chthonoplastes

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 392

Met	Val	Lys	Ile	Val	Arg	Arg	Gln	Ser	Leu	Gly	Val	Gln	Asn	Val	Tyr
1			5					10					15		

Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
 20 25 30

Ile Ala Ser Ala Xaa Phe Asn
 35

<210> 393

<211> 39

<212> PRT

<213> *Oscillatoria limnetica*

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 393

Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
 20 25 30

Ile Ala Ser Ala Xaa Phe Asn
 35

<210> 394

<211> 39

<212> PRT

<213> *Synechococcus elongatus*

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 394

Met Val Lys Ile Val Arg Arg Arg Ser Leu Gly Val Gln Pro Val Tyr
 1 5 10 15

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

Val Ala Ser Ala Xaa Phe Asn
 35

<210> 395

<211> 39

<212> PRT

<213> *Synechococcus PCC7002*

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 395

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

Asp	Ile	Gly	Leu	Ser	Gln	Asp	His	Asn	Phe	Leu	Leu	Gly	Gln	Gly	Leu
		20						25					30		

Ile	Ala	Ala	Ala	Xaa	Phe	Asn
				35		

<210> 396

<211> 38

<212> PRT

<213> Thermosynechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 396

Met	Lys	Ile	Val	Gly	Arg	Arg	Leu	Met	Gly	Trp	Gln	Ala	Val	Tyr	Asp
1				5					10					15	

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

Ala	Ala	Ala	Xaa	Phe	Asn
				35	

<210> 397

<211> 39

<212> PRT

<213> Trichodesmium erythraeum

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 397

Met	Val	Lys	Ile	Val	Ser	Arg	Lys	Leu	Ala	Lys	Thr	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Thr	Lys	Asp	His	Asn	Phe	Val	Leu	Ala	Asn	Gly	Leu
		20						25					30		

Ile Ala Ser Ala Xaa Phe Asn
35

<210> 398

<211> 38

<212> PRT

<213> Thermosynechococcus vulcanus

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 398

Met Lys Ile Val Gly Arg Arg Leu Val Gly Trp Gln Ala Val Tyr Asp
1 5 10 15

Ile Gly Leu Ala Gly Asp His Asn Phe Leu Leu Ala Asn Gly Ala Ile
20 25 30

Ala Ala Ala Xaa Phe Asn
35

<210> 399

<211> 39

<212> PRT

<213> Nostoc punctiforme

<400> 399

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

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

Ile Ala Ser Ala Ala Phe Asn
35

<210> 400

<211> 39

<212> PRT

<213> Synechocystis PCC6803

<400> 400

Met Val Lys Val Ile Gly Arg Arg Ser Leu Gly Val Gln Arg Ile Phe
1 5 10 15

Asp Ile Gly Leu Pro Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ala
20 25 30

Ile Ala Ala Ala Ala Phe Asn
35

<210> 401

<211> 39

<212> PRT

<213> *Aphanothece halophytica*

<400> 401

Met	Val	Lys	Ile	Ile	Lys	Arg	Gln	Ser	Leu	Gly	Arg	Gln	Asn	Val	Tyr
1			5						10				15		

Asp	Val	Cys	Val	Glu	Thr	Asp	His	Asn	Phe	Val	Leu	Ala	Asn	Gly	Cys
			20					25					30		

Val	Ala	Ser	Ala	Ala	Phe	Asn
						35

<210> 402

<211> 39

<212> PRT

<213> *Aphanizomenon ovalisporum*

<400> 402

Met	Val	Lys	Ile	Thr	Ala	Arg	Lys	Phe	Val	Gly	Arg	Glu	Asn	Val	Tyr
1			5						10				15		

Asp	Ile	Gly	Val	Glu	His	His	His	Asn	Phe	Ala	Ile	Lys	Asn	Gly	Leu
			20					25					30		

Ile	Ala	Ser	Ala	Ala	Phe	Asn
						35

<210> 403

<211> 39

<212> PRT

<213> *Anabaena PCC7120*

<400> 403

Met	Ile	Lys	Ile	Ala	Ser	Arg	Lys	Phe	Leu	Gly	Val	Glu	Asn	Val	Tyr
1			5						10				15		

Asp	Ile	Gly	Val	Arg	Arg	Asp	His	Asn	Phe	Phe	Ile	Lys	Asn	Gly	Leu
			20					25					30		

Ile	Ala	Ser	Ala	Ala	Phe	Asn
						35

<210> 404

<211> 39

<212> PRT

<213> *Anabaena variabilis*

<400> 404

Met	Ile	Lys	Ile	Ala	Ser	Arg	Lys	Phe	Leu	Gly	Val	Glu	Asn	Val	Tyr
1			5						10				15		

Asp Ile Gly Val Gly Arg Asp His Asn Phe Phe Val Lys Asn Gly Leu
 20 25 30

Ile Ala Ser Ala Ala Phe Asn
 35

<210> 405

<211> 39

<212> PRT

<213> *Cylindrospermopsis raciborskii*

<400> 405

Met Val Lys Ile Val Ser Arg Arg Tyr Leu Gly Lys Ala Asp Val Tyr
 1 5 10 15

Asp Ile Gly Val Ala Lys Asp His Asn Phe Ile Ile Lys Asn Gly Leu
 20 25 30

Val Ala Ser Ala Ala Phe Asn
 35

<210> 406

<211> 39

<212> PRT

<213> *Cyanothece CCY0110*

<400> 406

Met Val Lys Ile Ile Glu Arg Arg Ser Leu Gly Lys Gln Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ser Asn Asn Leu
 20 25 30

Ile Ala Ser Ala Ala Phe Asn
 35

<210> 407

<211> 39

<212> PRT

<213> *Cyanothece PCC8801*

<400> 407

Met Val Lys Ile Val Ser Tyr Arg Ser Leu Gly Lys Gln Phe Val Tyr
 1 5 10 15

Asp Ile Gly Val Ala Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ser
 20 25 30

Ile Ala Ser Ala Ala Phe Asn
 35

<210> 408

<211> 39

<212> PRT

<213> *Crocospaera watsonii*

<400> 408

```

Met Val Lys Ile Ile Gly Cys Arg Ser Leu Gly Thr Gln Lys Val Tyr
1           5           10           15

```

```

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Ser
          20           25           30

```

```

Ile Ala Ser Ala Ala Phe Asn
          35

```

<210> 409

<211> 39

<212> PRT

<213> *Microcystis aeruginosa*

<400> 409

```

Met Val Lys Ile Ile Gly Arg Gln Ser Leu Gly Arg Lys Pro Val Tyr
1           5           10           15

```

```

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Gly Asn Gly Leu
          20           25           30

```

```

Ile Ala Ser Ala Ala Phe Asn
          35

```

<210> 410

<211> 39

<212> PRT

<213> *Microcoleus chthonoplastes*

<400> 410

```

Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
1           5           10           15

```

```

Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
          20           25           30

```

```

Ile Ala Ser Ala Ala Phe Asn
          35

```

<210> 411

<211> 39

<212> PRT

<213> *Oscillatoria limnetica*

<400> 411

```

Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
1           5           10           15

```

```

Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
          20           25           30

```

Ile Ala Ser Ala Ala Phe Asn
35

<210> 412

<211> 39

<212> PRT

<213> Synechococcus elongatus

<400> 412

Met Val Lys Ile Val Arg Arg Arg Ser Leu Gly Val Gln Pro Val Tyr
1 5 10 15

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

Val Ala Ser Ala Ala Phe Asn
35

<210> 413

<211> 39

<212> PRT

<213> Synechococcus PCC7002

<400> 413

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

Asp Ile Gly Leu Ser Gln Asp His Asn Phe Leu Leu Gly Gln Gly Leu
20 25 30

Ile Ala Ala Ala Ala Phe Asn
35

<210> 414

<211> 38

<212> PRT

<213> Thermosynechococcus elongatus

<400> 414

Met Lys Ile Val Gly Arg Arg Leu Met Gly Trp Gln Ala Val Tyr Asp
1 5 10 15

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

Ala Ala Ala Ala Phe Asn
35

<210> 415

<211> 39

<212> PRT

<213> Trichodesmium erythraeum

<400> 415

Met Val Lys Ile Val Ser Arg Lys Leu Ala Lys Thr Glu Asn Val Tyr
1 5 10 15

Asp Ile Gly Val Thr Lys Asp His Asn Phe Val Leu Ala Asn Gly Leu
20 25 30

Ile Ala Ser Ala Ala Phe Asn
35

<210> 416

<211> 38

<212> PRT

<213> Thermosynechococcus vulcanus

<400> 416

Met Lys Ile Val Gly Arg Arg Leu Val Gly Trp Gln Ala Val Tyr Asp
1 5 10 15

Ile Gly Leu Ala Gly Asp His Asn Phe Leu Leu Ala Asn Gly Ala Ile
20 25 30

Ala Ala Ala Ala Phe Asn
35

<210> 417

<211> 43

<212> PRT

<213> Nostoc punctiforme

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 417

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

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

Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
35 40

<210> 418

<211> 43

<212> PRT

<213> Synechocystis PCC6803

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 418

Met	Val	Lys	Val	Ile	Gly	Arg	Arg	Ser	Leu	Gly	Val	Gln	Arg	Ile	Phe
1				5					10					15	

Asp	Ile	Gly	Leu	Pro	Gln	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Ala
			20					25					30		

Ile	Ala	Ala	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 419

<211> 43

<212> PRT

<213> Aphanothece halophytica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 419

Met	Val	Lys	Ile	Ile	Lys	Arg	Gln	Ser	Leu	Gly	Arg	Gln	Asn	Val	Tyr
1				5					10					15	

Asp	Val	Cys	Val	Glu	Thr	Asp	His	Asn	Phe	Val	Leu	Ala	Asn	Gly	Cys
			20					25					30		

Val	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 420

<211> 43

<212> PRT

<213> Aphanizomenon ovalisporum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 420

Met	Val	Lys	Ile	Thr	Ala	Arg	Lys	Phe	Val	Gly	Arg	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	His	His	His	Asn	Phe	Ala	Ile	Lys	Asn	Gly	Leu
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 421

<211> 43

<212> PRT

<213> Anabaena PCC7120

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 421

Met	Ile	Lys	Ile	Ala	Ser	Arg	Lys	Phe	Leu	Gly	Val	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Arg	Arg	Asp	His	Asn	Phe	Phe	Ile	Lys	Asn	Gly	Leu
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 422

<211> 43

<212> PRT

<213> *Anabaena variabilis*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 422

Met	Ile	Lys	Ile	Ala	Ser	Arg	Lys	Phe	Leu	Gly	Val	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Gly	Arg	Asp	His	Asn	Phe	Phe	Val	Lys	Asn	Gly	Leu
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 423

<211> 43

<212> PRT

<213> *Cylindrospermopsis raciborskii*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 423

Met	Val	Lys	Ile	Val	Ser	Arg	Arg	Tyr	Leu	Gly	Lys	Ala	Asp	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Ala	Lys	Asp	His	Asn	Phe	Ile	Ile	Lys	Asn	Gly	Leu
			20					25					30		

Val	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 424

<211> 43

<212> PRT

<213> Cyanothece CCY0110

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 424

Met	Val	Lys	Ile	Ile	Glu	Arg	Arg	Ser	Leu	Gly	Lys	Gln	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ser	Asn	Asn	Leu
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 425

<211> 43

<212> PRT

<213> Cyanothece PCC8801

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 425

Met	Val	Lys	Ile	Val	Ser	Tyr	Arg	Ser	Leu	Gly	Lys	Gln	Phe	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Ala	Gln	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Ser
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 426

<211> 43

<212> PRT

<213> Crocosphaera watsonii

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 426

Met	Val	Lys	Ile	Ile	Gly	Cys	Arg	Ser	Leu	Gly	Thr	Gln	Lys	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Ser
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 427

<211> 43

<212> PRT

<213> Microcystis aeruginosa

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 427

Met	Val	Lys	Ile	Ile	Gly	Arg	Gln	Ser	Leu	Gly	Arg	Lys	Pro	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Gly	Asn	Gly	Leu
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 428

<211> 43

<212> PRT

<213> Microcoleus chthonoplastes

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 428

Met	Val	Lys	Ile	Val	Arg	Arg	Gln	Ser	Leu	Gly	Val	Gln	Asn	Val	Tyr
1				5					10				15		

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Cys	Leu	Ala	Ser	Gly	Glu
		20						25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 429

<211> 43

<212> PRT

<213> Oscillatoria limnetica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 429

Met	Val	Lys	Ile	Val	Arg	Arg	Gln	Ser	Leu	Gly	Val	Gln	Asn	Val	Tyr
1				5					10				15		

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Cys	Leu	Ala	Ser	Gly	Glu
		20						25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 430

<211> 43

<212> PRT

<213> Synechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 430

Met	Val	Lys	Ile	Val	Arg	Arg	Arg	Ser	Leu	Gly	Val	Gln	Pro	Val	Tyr
1				5					10					15	

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

Val	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 431

<211> 43

<212> PRT

<213> Synechococcus PCC7002

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 431

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

Asp	Ile	Gly	Leu	Ser	Gln	Asp	His	Asn	Phe	Leu	Leu	Gly	Gln	Gly	Leu
			20					25					30		

Ile	Ala	Ala	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
			35				40			

<210> 432

<211> 42

<212> PRT

<213> Thermosynechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Cys

<400> 432

Met	Lys	Ile	Val	Gly	Arg	Arg	Leu	Met	Gly	Trp	Gln	Ala	Val	Tyr	Asp
1				5					10					15	

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

Ala	Ala	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40		

<210> 433

<211> 43

<212> PRT

<213> Trichodesmium erythraeum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Asn

<400> 433

Met	Val	Lys	Ile	Val	Ser	Arg	Lys	Leu	Ala	Lys	Thr	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Thr	Lys	Asp	His	Asn	Phe	Val	Leu	Ala	Asn	Gly	Leu
			20					25						30	

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 434

<211> 42

<212> PRT

<213> Thermosynechococcus vulcanus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Cys

<400> 434

Met	Lys	Ile	Val	Gly	Arg	Arg	Leu	Val	Gly	Trp	Gln	Ala	Val	Tyr	Asp
1				5					10					15	

Ile	Gly	Leu	Ala	Gly	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Ala	Ile
			20					25					30		

Ala	Ala	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40		

<210> 435

<211> 43

<212> PRT

<213> Nostoc punctiforme

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexanoic acid

<400> 435

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

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

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
			35				40			

<210> 436

<211> 43

<212> PRT

<213> Synechocystis PCC6803

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 436

Met	Val	Lys	Val	Ile	Gly	Arg	Arg	Ser	Leu	Gly	Val	Gln	Arg	Ile	Phe
1				5					10					15	

Asp	Ile	Gly	Leu	Pro	Gln	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Ala
			20					25					30		

Ile	Ala	Ala	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
			35				40			

<210> 437

<211> 43

<212> PRT

<213> Aphanothece halophytica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 437

Met	Val	Lys	Ile	Ile	Lys	Arg	Gln	Ser	Leu	Gly	Arg	Gln	Asn	Val	Tyr
1				5					10					15	

Asp	Val	Cys	Val	Glu	Thr	Asp	His	Asn	Phe	Val	Leu	Ala	Asn	Gly	Cys
			20					25					30		

Val Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 438

<211> 43

<212> PRT

<213> Aphanizomenon ovalisporum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 438

Met Val Lys Ile Thr Ala Arg Lys Phe Val Gly Arg Glu Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Glu His His His Asn Phe Ala Ile Lys Asn Gly Leu
 20 25 30

Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 439

<211> 43

<212> PRT

<213> Anabaena PCC7120

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 439

Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Arg Arg Asp His Asn Phe Phe Ile Lys Asn Gly Leu
 20 25 30

Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 440

<211> 43

<212> PRT

<213> *Anabaena variabilis*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 440

Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Gly Arg Asp His Asn Phe Phe Val Lys Asn Gly Leu
 20 25 30

Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 441

<211> 43

<212> PRT

<213> *Cylindrospermopsis raciborskii*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 441

Met Val Lys Ile Val Ser Arg Arg Tyr Leu Gly Lys Ala Asp Val Tyr
 1 5 10 15

Asp Ile Gly Val Ala Lys Asp His Asn Phe Ile Ile Lys Asn Gly Leu
 20 25 30

Val Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 442

<211> 43

<212> PRT

<213> Cyanothece CCY0110

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 442

Met Val Lys Ile Ile Glu Arg Arg Ser Leu Gly Lys Gln Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ser Asn Asn Leu
 20 25 30

Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 443

<211> 43

<212> PRT

<213> Cyanothece PCC8801

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 443

```
Met Val Lys Ile Val Ser Tyr Arg Ser Leu Gly Lys Gln Phe Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Ala Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ser
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
          35           40
```

<210> 444

<211> 43

<212> PRT

<213> *Crocospaera watsonii*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 444

```
Met Val Lys Ile Ile Gly Cys Arg Ser Leu Gly Thr Gln Lys Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Ser
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
          35           40
```

<210> 445

<211> 43

<212> PRT

<213> *Microcystis aeruginosa*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 445

```
Met Val Lys Ile Ile Gly Arg Gln Ser Leu Gly Arg Lys Pro Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Gly Asn Gly Leu
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
      35           40
```

<210> 446

<211> 43

<212> PRT

<213> Microcoleus chthonoplastes

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 446

```
Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
      35           40
```

<210> 447

<211> 43

<212> PRT

<213> Oscillatoria limnetica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 447

```
Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
1          5          10          15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
          20          25          30
```

```
Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
          35          40
```

<210> 448

<211> 43

<212> PRT

<213> Synechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 448

```
Met Val Lys Ile Val Arg Arg Arg Ser Leu Gly Val Gln Pro Val Tyr
1          5          10          15
```

```
Asp Leu Gly Val Ala Thr Val His Asn Phe Val Leu Ala Asn Gly Leu
          20          25          30
```

```
Val Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
          35          40
```

<210> 449

<211> 43

<212> PRT

<213> Synechococcus PCC7002

$\langle 220 \rangle$

<221> MISC_FEATURE

$\langle 222 \rangle$ (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

 $\langle 220 \rangle$

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexanoic acid

<400> 449

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

Asp Ile Gly Leu Ser Gln Asp His Asn Phe Leu Leu Gly Gln Gly Leu
20 25 30

Ile Ala Ala Xaa Xaa Phe Asn Ser Gly Gly Cys
35 40

<210> 450

<211> 42

<212> PRT

<213> *Thermosynechococcus elongatus*

$\langle 220 \rangle$

<221> MISC_FEATURE

$\langle 222 \rangle$ (35)..(35)

<223> Xaa is any amino acid excluding Asn and/or Gln

$\langle 220 \rangle$

<221> MISC FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexanoic acid

<400> 450

Met Lys Ile Val Gly Arg Arg Leu Met Gly Trp Gln Ala Val Tyr Asp
1 5 10 15

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

Ala Ala Xaa Xaa Phe Asn Ser Gly Gly Cys

35

40

<210> 451

<211> 43

<212> PRT

<213> Trichodesmium erythraeum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 451

Met	Val	Lys	Ile	Val	Ser	Arg	Lys	Leu	Ala	Lys	Thr	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Thr	Lys	Asp	His	Asn	Phe	Val	Leu	Ala	Asn	Gly	Leu
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 452

<211> 42

<212> PRT

<213> Thermosynechococcus vulcanus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 452

Met	Lys	Ile	Val	Gly	Arg	Arg	Leu	Val	Gly	Trp	Gln	Ala	Val	Tyr	Asp
1				5					10					15	

Ile Gly Leu Ala Gly Asp His Asn Phe Leu Leu Ala Asn Gly Ala Ile
 20 25 30

Ala Ala Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 453

<211> 43

<212> PRT

<213> Nostoc punctiforme

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 453

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

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

Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 454

<211> 43

<212> PRT

<213> Synechocystis PCC6803

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 454

Met Val Lys Val Ile Gly Arg Arg Ser Leu Gly Val Gln Arg Ile Phe
 1 5 10 15

Asp Ile Gly Leu Pro Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ala
 20 25 30

Ile Ala Ala Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 455

<211> 43

<212> PRT

<213> Aphanothece halophytica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 455

Met Val Lys Ile Ile Lys Arg Gln Ser Leu Gly Arg Gln Asn Val Tyr
 1 5 10 15

Asp Val Cys Val Glu Thr Asp His Asn Phe Val Leu Ala Asn Gly Cys
 20 25 30

Val Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 456

<211> 43

<212> PRT

<213> Aphanizomenon ovalisporum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 456

Met Val Lys Ile Thr Ala Arg Lys Phe Val Gly Arg Glu Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Glu His His His Asn Phe Ala Ile Lys Asn Gly Leu
 20 25 30

Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 457

<211> 43

<212> PRT

<213> Anabaena PCC7120

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 457

Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Arg Arg Asp His Asn Phe Phe Ile Lys Asn Gly Leu
 20 25 30

Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 458

<211> 43

<212> PRT

<213> Anabaena variabilis

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 458

Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Gly Arg Asp His Asn Phe Phe Val Lys Asn Gly Leu
 20 25 30

-- -- - -- -- -- - - -- -- -

Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 459

<211> 43

<212> PRT

<213> Cylindrospermopsis raciborskii

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 459

Met Val Lys Ile Val Ser Arg Arg Tyr Leu Gly Lys Ala Asp Val Tyr
 1 5 10 15

Asp Ile Gly Val Ala Lys Asp His Asn Phe Ile Ile Lys Asn Gly Leu
 20 25 30

Val Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 460

<211> 43

<212> PRT

<213> Cyanothece CCY0110

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 460

Met Val Lys Ile Ile Glu Arg Arg Ser Leu Gly Lys Gln Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ser Asn Asn Leu
 20 25 30

Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

-- --

<210> 461
 <211> 43
 <212> PRT
 <213> Cyanothecce PCC8801

<220>
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 <223> Xaa is any amino acid excluding Asn and/or Gln

<220>
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 <222> (37)..(37)
 <223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 461
 Met Val Lys Ile Val Ser Tyr Arg Ser Leu Gly Lys Gln Phe Val Tyr
 1 5 10 15
 Asp Ile Gly Val Ala Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ser
 20 25 30
 Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 462
 <211> 43
 <212> PRT
 <213> Crocosphaera watsonii

<220>
 <221> MISC_FEATURE
 <222> (36)..(36)
 <223> Xaa is any amino acid excluding Asn and/or Gln

<220>
 <221> MISC_FEATURE
 <222> (37)..(37)
 <223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 462
 Met Val Lys Ile Ile Gly Cys Arg Ser Leu Gly Thr Gln Lys Val Tyr
 1 5 10 15
 Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Ser
 20 25 30
 Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 463

<211> 43

<212> PRT

<213> Microcystis aeruginosa

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 463

Met	Val	Lys	Ile	Ile	Gly	Arg	Gln	Ser	Leu	Gly	Arg	Lys	Pro	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Gly	Asn	Gly	Leu
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 464

<211> 43

<212> PRT

<213> Microcoleus chthonoplastes

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 464

Met	Val	Lys	Ile	Val	Arg	Arg	Gln	Ser	Leu	Gly	Val	Gln	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Cys	Leu	Ala	Ser	Gly	Glu
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 465

<211> 43
 <212> PRT
 <213> *Oscillatoria limnetica*

<220>
 <221> MISC_FEATURE
 <222> (36)..(36)
 <223> Xaa is any amino acid excluding Asn and/or Gln

<220>
 <221> MISC_FEATURE
 <222> (37)..(37)
 <223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 465
 Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
 1 5 10 15
 Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
 20 25 30
 Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 466
 <211> 43
 <212> PRT
 <213> *Synechococcus elongatus*

<220>
 <221> MISC_FEATURE
 <222> (36)..(36)
 <223> Xaa is any amino acid excluding Asn and/or Gln

<220>
 <221> MISC_FEATURE
 <222> (37)..(37)
 <223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 466
 Met Val Lys Ile Val Arg Arg Arg Ser Leu Gly Val Gln Pro Val Tyr
 1 5 10 15
 Asp Leu Gly Val Ala Thr Val His Asn Phe Val Leu Ala Asn Gly Leu
 20 25 30
 Val Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 467

<211> 43

<212> PRT

<213> Synechococcus PCC7002

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 467

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

Asp	Ile	Gly	Leu	Ser	Gln	Asp	His	Asn	Phe	Leu	Leu	Gly	Gln	Gly	Leu
			20					25					30		

Ile	Ala	Ala	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
			35				40			

<210> 468

<211> 42

<212> PRT

<213> Thermosynechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 468

Met	Lys	Ile	Val	Gly	Arg	Arg	Leu	Met	Gly	Trp	Gln	Ala	Val	Tyr	Asp
1				5					10					15	

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

Ala	Ala	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
			35				40		

<210> 469

<211> 43

<212> PRT

<213> Trichodesmium erythraeum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 469

Met	Val	Lys	Ile	Val	Ser	Arg	Lys	Leu	Ala	Lys	Thr	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Thr	Lys	Asp	His	Asn	Phe	Val	Leu	Ala	Asn	Gly	Leu
				20				25						30	

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 470

<211> 42

<212> PRT

<213> Thermosynechococcus vulcanus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 470

Met	Lys	Ile	Val	Gly	Arg	Arg	Leu	Val	Gly	Trp	Gln	Ala	Val	Tyr	Asp
1				5					10					15	

Ile	Gly	Leu	Ala	Gly	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Ala	Ile
			20					25					30		

Ala	Ala	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40		

<210> 471

<211> 43

<212> PRT

<213> Nostoc punctiforme

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 471

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

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

Ile	Ala	Ser	Xaa	Ala	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 472

<211> 43

<212> PRT

<213> Synechocystis PCC6803

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 472

Met	Val	Lys	Val	Ile	Gly	Arg	Arg	Ser	Leu	Gly	Val	Gln	Arg	Ile	Phe
1				5					10					15	

Asp	Ile	Gly	Leu	Pro	Gln	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Ala
			20					25					30		

Ile	Ala	Ala	Xaa	Ala	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 473

<211> 43

<212> PRT

<213> Aphanothece halophytica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 473

Met	Val	Lys	Ile	Ile	Lys	Arg	Gln	Ser	Leu	Gly	Arg	Gln	Asn	Val	Tyr
1				5					10					15	

Asp Val Cys Val Glu Thr Asp His Asn Phe Val Leu Ala Asn Gly Cys
 20 25 30

Val Ala Ser Xaa Ala Phe Asn Ser Gly Gly Cys
 35 40

<210> 474

<211> 43

<212> PRT

<213> Aphanizomenon ovalisporum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 474

Met Val Lys Ile Thr Ala Arg Lys Phe Val Gly Arg Glu Asn Val Tyr

1 5 10 15

Asp Ile Gly Val Glu His His His Asn Phe Ala Ile Lys Asn Gly Leu
 20 25 30

Ile Ala Ser Xaa Ala Phe Asn Ser Gly Gly Cys
 35 40

<210> 475

<211> 43

<212> PRT

<213> Anabaena PCC7120

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 475

Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Arg Arg Asp His Asn Phe Phe Ile Lys Asn Gly Leu
 20 25 30

Ile Ala Ser Xaa Ala Phe Asn Ser Gly Gly Cys
 35 40

<210> 476

<211> 43

<212> PRT

<213> *Anabaena variabilis*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 476

Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
1 5 10 15

Asp Ile Gly Val Gly Arg Asp His Asn Phe Phe Val Lys Asn Gly Leu
20 25 30

Ile Ala Ser Xaa Ala Phe Asn Ser Gly Gly Cys
35 40

<210> 477

<211> 43

<212> PRT

<213> *Cylindrospermopsis raciborskii*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 477

Met Val Lys Ile Val Ser Arg Arg Tyr Leu Gly Lys Ala Asp Val Tyr
1 5 10 15

Asp Ile Gly Val Ala Lys Asp His Asn Phe Ile Ile Lys Asn Gly Leu
20 25 30

Val Ala Ser Xaa Ala Phe Asn Ser Gly Gly Cys
35 40

<210> 478

<211> 43

<212> PRT

<213> *Cyanothece CCY0110*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 478

Met Val Lys Ile Ile Glu Arg Arg Ser Leu Gly Lys Gln Asn Val Tyr
1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ser Asn Asn Leu

Ile Ala Ser Xaa Ala Phe Asn Ser Gly Gly Cys
35 40

<210> 479

<211> 43

<212> PRT

<213> Cyanothece PCC8801

$\langle 220 \rangle$

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 479

Met Val Lys Ile Val Ser Tyr Arg Ser Leu Gly Lys Gln Phe Val Tyr
1 5 10 15

Asp Ile Gly Val Ala Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ser
20 25 30

Ile Ala Ser Xaa Ala Phe Asn Ser Gly Gly Cys
35 40

<210> 480

<211> 43

<212> PRT

<213> Crocosphaera watsonii

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 480

Met Val Lys Ile Ile Gly Cys Arg Ser Leu Gly Thr Gln Lys Val Tyr
1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Ser
20 25 30

Ile Ala Ser Xaa Ala Phe Asn Ser Gly Gly Cys
35 40

<210> 481

<211> 43

<212> PRT

<213> *Microcystis aeruginosa*

$\langle 220 \rangle$

<221> MISC FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 481

```
Met Val Lys Ile Ile Gly Arg Gln Ser Leu Gly Arg Lys Pro Val Tyr
 1           5           10          15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Gly Asn Gly Leu
      20           25           30
```

```
Ile Ala Ser Xaa Ala Phe Asn Ser Gly Gly Cys
      35           40
```

<210> 482

<211> 43

<212> PRT

<213> Microcoleus chthonoplastes

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 482

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Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
 1           5           10          15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
      20           25           30
```

```
Ile Ala Ser Xaa Ala Phe Asn Ser Gly Gly Cys
      35           40
```

<210> 483

<211> 43

<212> PRT

<213> Oscillatoria limnetica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 483

```
Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
 1           5           10          15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
      20           25           30
```

```
Ile Ala Ser Xaa Ala Phe Asn Ser Gly Gly Cys
      35           40
```

<210> 484

<211> 43

<212> PRT

<213> Synechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 484

```

Met Val Lys Ile Val Arg Arg Arg Ser Leu Gly Val Gln Pro Val Tyr
1          5          10          15

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

Val Ala Ser Xaa Ala Phe Asn Ser Gly Gly Cys
35          40

```

<210> 485

<211> 43

<212> PRT

<213> Synechococcus PCC7002

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 485

```

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

Asp Ile Gly Leu Ser Gln Asp His Asn Phe Leu Leu Gly Gln Gly Leu
20          25          30

Ile Ala Ala Xaa Ala Phe Asn Ser Gly Gly Cys
35          40

```

<210> 486

<211> 42

<212> PRT

<213> Thermosynechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 486

Met Lys Ile Val Gly Arg Arg Leu Met Gly Trp Gln Ala Val Tyr Asp
1 5 10 15

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

Ala Ala Xaa Ala Phe Asn Ser Gly Gly Cys
35 40

<210> 487

<211> 43

<212> PRT

<213> Trichodesmium erythraeum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 487

Met Val Lys Ile Val Ser Arg Lys Leu Ala Lys Thr Glu Asn Val Tyr
1 5 10 15

Asp Ile Gly Val Thr Lys Asp His Asn Phe Val Leu Ala Asn Gly Leu
20 25 30

Ile Ala Ser Xaa Ala Phe Asn Ser Gly Gly Cys
35 40

<210> 488

<211> 42

<212> PRT

<213> Thermosynechococcus vulcanus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 488

Met Lys Ile Val Gly Arg Arg Leu Val Gly Trp Gln Ala Val Tyr Asp
1 5 10 15

Ile Gly Leu Ala Gly Asp His Asn Phe Leu Leu Ala Asn Gly Ala Ile
20 25 30

Ala Ala Xaa Ala Phe Asn Ser Gly Gly Cys
35 40

<210> 489

<211> 43

<212> PRT

<213> Nostoc punctiforme

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 489

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

```
Asp Ile Gly Val Glu Arg Asp His Asn Phe Ala Leu Lys Asn Gly Phe
      20             25             30
```

```
Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
      35             40
```

<210> 490

<211> 43

<212> PRT

<213> Synechocystis PCC6803

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 490

```
Met Val Lys Val Ile Gly Arg Arg Ser Leu Gly Val Gln Arg Ile Phe
 1             5             10             15
```

```
Asp Ile Gly Leu Pro Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ala
      20             25             30
```

```
Ile Ala Ala Xaa Xaa Phe Asn Ser Gly Gly Cys
      35             40
```

<210> 491

<211> 43

<212> PRT

<213> Aphanothece halophytica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 491

Met	Val	Lys	Ile	Ile	Lys	Arg	Gln	Ser	Leu	Gly	Arg	Gln	Asn	Val	Tyr
1				5					10					15	

Asp	Val	Cys	Val	Glu	Thr	Asp	His	Asn	Phe	Val	Leu	Ala	Asn	Gly	Cys
			20					25					30		

Val	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 492

<211> 43

<212> PRT

<213> Aphanizomenon ovalisporum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 492

Met	Val	Lys	Ile	Thr	Ala	Arg	Lys	Phe	Val	Gly	Arg	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	His	His	His	Asn	Phe	Ala	Ile	Lys	Asn	Gly	Leu
			20					25					30		

Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 493

<211> 43

<212> PRT

<213> Anabaena PCC7120

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 493

Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Arg Arg Asp His Asn Phe Phe Ile Lys Asn Gly Leu
 20 25 30

Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 494

<211> 43

<212> PRT

<213> Anabaena variabilis

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 494

Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr

```

1         5         10        15
Asp Ile Gly Val Gly Arg Asp His Asn Phe Phe Val Lys Asn Gly Leu
      20              25              30

```

```

Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
      35              40

```

<210> 495

<211> 43

<212> PRT

<213> Cylindrospermopsis raciborskii

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 495

```

Met Val Lys Ile Val Ser Arg Arg Tyr Leu Gly Lys Ala Asp Val Tyr
1         5         10        15

```

```

Asp Ile Gly Val Ala Lys Asp His Asn Phe Ile Ile Lys Asn Gly Leu
      20              25              30

```

```

Val Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
      35              40

```

<210> 496

<211> 43

<212> PRT

<213> Cyanothece CCY0110

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 496

```
Met Val Lys Ile Ile Glu Arg Arg Ser Leu Gly Lys Gln Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ser Asn Asn Leu
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
          35           40
```

<210> 497

<211> 43

<212> PRT

<213> Cyanothecce PCC8801

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 497

```
Met Val Lys Ile Val Ser Tyr Arg Ser Leu Gly Lys Gln Phe Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Ala Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ser
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
          35           40
```

<210> 498

<211> 43

<212> PRT

<213> Crocosphaera watsonii

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 498

Met	Val	Lys	Ile	Ile	Gly	Cys	Arg	Ser	Leu	Gly	Thr	Gln	Lys	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Ser
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 499

<211> 43

<212> PRT

<213> Microcystis aeruginosa

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 499

Met	Val	Lys	Ile	Ile	Gly	Arg	Gln	Ser	Leu	Gly	Arg	Lys	Pro	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Gly	Asn	Gly	Leu
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 500

<211> 43

<212> PRT

<213> Microcoleus chthonoplastes

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 500

```
Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
          35           40
```

<210> 501

<211> 43

<212> PRT

<213> *Oscillatoria limnetica*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 501

```
Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
          35           40
```

<210> 502

<211> 43

<212> PRT

<213> *Synechococcus elongatus*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 502

Met	Val	Lys	Ile	Val	Arg	Arg	Arg	Ser	Leu	Gly	Val	Gln	Pro	Val	Tyr
1				5					10					15	

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

Val	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 503

<211> 43

<212> PRT

<213> Synechococcus PCC7002

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 503

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

Asp	Ile	Gly	Leu	Ser	Gln	Asp	His	Asn	Phe	Leu	Leu	Gly	Gln	Gly	Leu
			20					25					30		

Ile	Ala	Ala	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 504

<211> 42

<212> PRT

<213> Thermosynechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Cys

<400> 504

```
Met Lys Ile Val Gly Arg Arg Leu Met Gly Trp Gln Ala Val Tyr Asp
1           5           10          15
```

```
Ile Gly Leu Ala Ala Asp His Asn Phe Val Leu Ala Asn Gly Ala Ile
```

20

25

30

```
Ala Ala Xaa Xaa Phe Asn Ser Gly Gly Cys
      35          40
```

<210> 505

<211> 43

<212> PRT

<213> Trichodesmium erythraeum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Asn

<400> 505

```
Met Val Lys Ile Val Ser Arg Lys Leu Ala Lys Thr Glu Asn Val Tyr
1           5           10          15
```

```
Asp Ile Gly Val Thr Lys Asp His Asn Phe Val Leu Ala Asn Gly Leu
      20          25          30
```

Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
35 40

<210> 506

<211> 42

<212> PRT

<213> Thermosynechococcus vulcanus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopantoic acid, or 2-aminohexanoic acid

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Cys

<400> 506

Met Lys Ile Val Gly Arg Arg Leu Val Gly Trp Gln Ala Val Tyr Asp
1 5 10 15

Ile Gly Leu Ala Gly Asp His Asn Phe Leu Leu Ala Asn Gly Ala Ile
20 25 30

Ala Ala Xaa Xaa Phe Asn Ser Gly Gly Cys
35 40

<210> 507

<211> 43

<212> PRT

<213> Nostoc punctiforme

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopantoic acid, or 2-aminohexanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopantoic acid, or 2-aminohexanoic acid

<400> 507

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

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

Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 508

<211> 43

<212> PRT

<213> Synechocystis PCC6803

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 508

Met Val Lys Val Ile Gly Arg Arg Ser Leu Gly Val Gln Arg Ile Phe
 1 5 10 15

Asp Ile Gly Leu Pro Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ala
 20 25 30

Ile Ala Ala Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 509

<211> 43

<212> PRT

<213> Aphanothece halophytica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-

aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 509

Met	Val	Lys	Ile	Ile	Lys	Arg	Gln	Ser	Leu	Gly	Arg	Gln	Asn	Val	Tyr
1				5					10					15	

Asp	Val	Cys	Val	Glu	Thr	Asp	His	Asn	Phe	Val	Leu	Ala	Asn	Gly	Cys
			20					25					30		

Val	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35				40				

<210> 510

<211> 43

<212> PRT

<213> Aphanizomenon ovalisporum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 510

Met	Val	Lys	Ile	Thr	Ala	Arg	Lys	Phe	Val	Gly	Arg	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	His	His	His	Asn	Phe	Ala	Ile	Lys	Asn	Gly	Leu
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35				40				

<210> 511

<211> 43

<212> PRT

<213> Anabaena PCC7120

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 511

Met	Ile	Lys	Ile	Ala	Ser	Arg	Lys	Phe	Leu	Gly	Val	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Arg	Arg	Asp	His	Asn	Phe	Phe	Ile	Lys	Asn	Gly	Leu
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 512

<211> 43

<212> PRT

<213> Anabaena variabilis

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 512

Met	Ile	Lys	Ile	Ala	Ser	Arg	Lys	Phe	Leu	Gly	Val	Glu	Asn	Val	Tyr
1				5					10					15	

Asp Ile Gly Val Gly Arg Asp His Asn Phe Phe Val Lys Asn Gly Leu
 20 25 30

Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 513

<211> 43

<212> PRT

<213> *Cylindrospermopsis raciborskii*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 513

Met Val Lys Ile Val Ser Arg Arg Tyr Leu Gly Lys Ala Asp Val Tyr
 1 5 10 15

Asp Ile Gly Val Ala Lys Asp His Asn Phe Ile Ile Lys Asn Gly Leu
 20 25 30

Val Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 514

<211> 43

<212> PRT

<213> *Cyanothece CCY0110*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexaanoic acid

<400> 514

```
Met Val Lys Ile Ile Glu Arg Arg Ser Leu Gly Lys Gln Asn Val Tyr
 1             5             10             15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ser Asn Asn Leu
      20             25             30
```

```
Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
      35             40
```

<210> 515

<211> 43

<212> PRT

<213> Cyanotheca PCC8801

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexaanoic acid

<400> 515

```
Met Val Lys Ile Val Ser Tyr Arg Ser Leu Gly Lys Gln Phe Val Tyr
 1             5             10             15
```

```
Asp Ile Gly Val Ala Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ser
      20             25             30
```

```
Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
      35             40
```

<210> 516

<211> 43

<212> PRT

<213> Crocosphaera watsonii

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 516

Met	Val	Lys	Ile	Ile	Gly	Cys	Arg	Ser	Leu	Gly	Thr	Gln	Lys	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Ser
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 517

<211> 43

<212> PRT

<213> Microcystis aeruginosa

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 517

Met	Val	Lys	Ile	Ile	Gly	Arg	Gln	Ser	Leu	Gly	Arg	Lys	Pro	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Gly	Asn	Gly	Leu
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys

----- 35 ----- 40 -----

<210> 518

<211> 43

<212> PRT

<213> Microcoleus chthonoplastes

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 518

Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
20 25 30

Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
35 40

<210> 519

<211> 43

<212> PRT

<213> Oscillatoria limnetica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 519

```

Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
1           5           10           15

```

```

Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
          20           25           30

```

```

Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
          35           40

```

<210> 520

<211> 43

<212> PRT

<213> *Synechococcus elongatus*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexaanoic acid

<400> 520

```

Met Val Lys Ile Val Arg Arg Arg Ser Leu Gly Val Gln Pro Val Tyr
1           5           10           15

```

```

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

```

```

Val Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
          35           40

```

<210> 521

<211> 43

<212> PRT

<213> *Synechococcus PCC7002*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-

aminopentonic acid, or 2-aminohexanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 521

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

```
Asp Ile Gly Leu Ser Gln Asp His Asn Phe Leu Leu Gly Gln Gly Leu
          20           25           30
```

```
Ile Ala Ala Xaa Xaa Phe Asn Ser Gly Gly Cys
      35           40
```

<210> 522

<211> 42

<212> PRT

<213> Thermosynechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 522

```
Met Lys Ile Val Gly Arg Arg Leu Met Gly Trp Gln Ala Val Tyr Asp
1           5           10           15
```

```
Ile Gly Leu Ala Ala Asp His Asn Phe Val Leu Ala Asn Gly Ala Ile
          20           25           30
```

```
Ala Ala Xaa Xaa Phe Asn Ser Gly Gly Cys
      35           40
```

<210> 523

<211> 43

<212> PRT

<213> Trichodesmium erythraeum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 523

Met	Val	Lys	Ile	Val	Ser	Arg	Lys	Leu	Ala	Lys	Thr	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Thr	Lys	Asp	His	Asn	Phe	Val	Leu	Ala	Asn	Gly	Leu
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 524

<211> 42

<212> PRT

<213> Thermosynechococcus vulcanus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 524

Met	Lys	Ile	Val	Gly	Arg	Arg	Leu	Val	Gly	Trp	Gln	Ala	Val	Tyr	Asp
1				5					10					15	

Ile Gly Leu Ala Gly Asp His Asn Phe Leu Leu Ala Asn Gly Ala Ile
 20 25 30

Ala Ala Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 525

<211> 43

<212> PRT

<213> Nostoc punctiforme

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 525

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

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

Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 526

<211> 43

<212> PRT

<213> Synechocystis PCC6803

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 526

```

Met Val Lys Val Ile Gly Arg Arg Ser Leu Gly Val Gln Arg Ile Phe
1           5           10           15

```

```

Asp Ile Gly Leu Pro Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ala
          20           25           30

```

```

Ile Ala Ala Xaa Xaa Phe Asn Ser Gly Gly Cys
          35           40

```

<210> 527

<211> 43

<212> PRT

<213> Aphanothece halophytica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 527

```

Met Val Lys Ile Ile Lys Arg Gln Ser Leu Gly Arg Gln Asn Val Tyr
1           5           10           15

```

```

Asp Val Cys Val Glu Thr Asp His Asn Phe Val Leu Ala Asn Gly Cys
          20           25           30

```

```

Val Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
          35           40

```

<210> 528

<211> 43

<212> PRT

<213> Aphanizomenon ovalisporum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 528

```
Met Val Lys Ile Thr Ala Arg Lys Phe Val Gly Arg Glu Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu His His His Asn Phe Ala Ile Lys Asn Gly Leu
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
          35           40
```

<210> 529

<211> 43

<212> PRT

<213> Anabaena PCC7120

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 529

```
Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Arg Arg Asp His Asn Phe Phe Ile Lys Asn Gly Leu
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
          35           40
```

<210> 530

<211> 43

<212> PRT

<213> Anabaena variabilis

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural

aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 530

Met	Ile	Lys	Ile	Ala	Ser	Arg	Lys	Phe	Leu	Gly	Val	Glu	Asn	Val	Tyr
1			5						10				15		

Asp	Ile	Gly	Val	Gly	Arg	Asp	His	Asn	Phe	Phe	Val	Lys	Asn	Gly	Leu
		20						25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 531

<211> 43

<212> PRT

<213> *Cylindrospermopsis raciborskii*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 531

Met	Val	Lys	Ile	Val	Ser	Arg	Arg	Tyr	Leu	Gly	Lys	Ala	Asp	Val	Tyr
1			5						10				15		

Asp	Ile	Gly	Val	Ala	Lys	Asp	His	Asn	Phe	Ile	Ile	Lys	Asn	Gly	Leu
			20					25					30		

Val	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 532

<211> 43

<212> PRT

<213> *Cyanothece CCY0110*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 532

Met	Val	Lys	Ile	Ile	Glu	Arg	Arg	Ser	Leu	Gly	Lys	Gln	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ser	Asn	Asn	Leu
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35				40				

<210> 533

<211> 43

<212> PRT

<213> Cyanotheca PCC8801

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 533

Met	Val	Lys	Ile	Val	Ser	Tyr	Arg	Ser	Leu	Gly	Lys	Gln	Phe	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Ala	Gln	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Ser
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35				40				

<210> 534

<211> 43

<212> PRT

<213> *Crocospaera watsonii*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 534

Met	Val	Lys	Ile	Ile	Gly	Cys	Arg	Ser	Leu	Gly	Thr	Gln	Lys	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Ser
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 535

<211> 43

<212> PRT

<213> *Microcystis aeruginosa*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 535

Met	Val	Lys	Ile	Ile	Gly	Arg	Gln	Ser	Leu	Gly	Arg	Lys	Pro	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Gly	Asn	Gly	Leu
			20					25					30		

Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 536

<211> 43

<212> PRT

<213> Microcoleus chthonoplastes

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 536

Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
 20 25 30

Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 537

<211> 43

<212> PRT

<213> Oscillatoria limnetica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 537

Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
 20 25 30

Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 538

<211> 43

<212> PRT

<213> Synechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 538

Met Val Lys Ile Val Arg Arg Arg Ser Leu Gly Val Gln Pro Val Tyr
 1 5 10 15

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

Val Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 539

<211> 43

<212> PRT

<213> Synechococcus PCC7002

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 539

```

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

```

```

Asp Ile Gly Leu Ser Gln Asp His Asn Phe Leu Leu Gly Gln Gly Leu
          20           25           30

```

```

Ile Ala Ala Xaa Xaa Phe Asn Ser Gly Gly Cys
          35           40

```

<210> 540

<211> 42

<212> PRT

<213> Thermosynechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 540

```

Met Lys Ile Val Gly Arg Arg Leu Met Gly Trp Gln Ala Val Tyr Asp
1           5           10           15

```

```

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

```

```

Ala Ala Xaa Xaa Phe Asn Ser Gly Gly Cys
          35           40

```

<210> 541

<211> 43

<212> PRT

<213> Trichodesmium erythraeum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 541

```
Met Val Lys Ile Val Ser Arg Lys Leu Ala Lys Thr Glu Asn Val Tyr
 1             5             10             15
```

```
Asp Ile Gly Val Thr Lys Asp His Asn Phe Val Leu Ala Asn Gly Leu
      20             25             30
```

```
Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
      35             40
```

<210> 542

<211> 42

<212> PRT

<213> Thermosynechococcus vulcanus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 542

```
Met Lys Ile Val Gly Arg Arg Leu Val Gly Trp Gln Ala Val Tyr Asp
 1             5             10             15
```

```
Ile Gly Leu Ala Gly Asp His Asn Phe Leu Leu Ala Asn Gly Ala Ile
      20             25             30
```

```
Ala Ala Xaa Xaa Phe Asn Ser Gly Gly Cys
      35             40
```

<210> 543

<211> 43

<212> PRT

<213> Nostoc punctiforme

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural

aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexanoic acid

<400> 543

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

```
Asp Ile Gly Val Glu Arg Asp His Asn Phe Ala Leu Lys Asn Gly Phe
          20           25           30
```

```
Ile Ala Ser Xaa Ala Phe Asn Ser Gly Gly Cys
      35           40
```

<210> 544

<211> 43

<212> PRT

<213> Synechocystis PCC6803

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexanoic acid

<400> 544

```
Met Val Lys Val Ile Gly Arg Arg Ser Leu Gly Val Gln Arg Ile Phe
1           5           10           15
```

```
Asp Ile Gly Leu Pro Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ala
          20           25           30
```

```
Ile Ala Ala Xaa Ala Phe Asn Ser Gly Gly Cys
      35           40
```

<210> 545

<211> 43

<212> PRT

<213> Aphanothece halophytica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexanoic acid

<400> 545

```
Met Val Lys Ile Ile Lys Arg Gln Ser Leu Gly Arg Gln Asn Val Tyr
1           5           10           15
```

- - - - -

Asp Val Cys Val Glu Thr Asp His Asn Phe Val Leu Ala Asn Gly Cys
 20 25 30

Val Ala Ser Xaa Ala Phe Asn Ser Gly Gly Cys
 35 40

<210> 546

<211> 43

<212> PRT

<213> Aphanizomenon ovalisporum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexaanoic acid

<400> 546

Met Val Lys Ile Thr Ala Arg Lys Phe Val Gly Arg Glu Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Glu His His His Asn Phe Ala Ile Lys Asn Gly Leu
 20 25 30

Ile Ala Ser Xaa Ala Phe Asn Ser Gly Gly Cys
 35 40

<210> 547

<211> 43

<212> PRT

<213> Anabaena PCC7120

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexaanoic acid

<400> 547

Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Arg Arg Asp His Asn Phe Phe Ile Lys Asn Gly Leu
 20 25 30

Ile Ala Ser Xaa Ala Phe Asn Ser Gly Gly Cys
 35 40

<210> 548

<211> 43

<212> PRT

<213> *Anabaena variabilis*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 548

```

Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
1           5           10           15

Asp Ile Gly Val Gly Arg Asp His Asn Phe Phe Val Lys Asn Gly Leu
          20           25           30

Ile Ala Ser Xaa Ala Phe Asn Ser Gly Gly Cys
          35           40

```

<210> 549

<211> 43

<212> PRT

<213> *Cylindrospermopsis raciborskii*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 549

```

Met Val Lys Ile Val Ser Arg Arg Tyr Leu Gly Lys Ala Asp Val Tyr
1           5           10           15

Asp Ile Gly Val Ala Lys Asp His Asn Phe Ile Ile Lys Asn Gly Leu
          20           25           30

Val Ala Ser Xaa Ala Phe Asn Ser Gly Gly Cys
          35           40

```

<210> 550

<211> 43

<212> PRT

<213> *Cyanothece CCY0110*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 550

```
Met Val Lys Ile Ile Glu Arg Arg Ser Leu Gly Lys Gln Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ser Asn Asn Leu
          20           25           30
```

```
Ile Ala Ser Xaa Ala Phe Asn Ser Gly Gly Cys
          35           40
```

<210> 551

<211> 43

<212> PRT

<213> Cyanothecce PCC8801

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 551

```
Met Val Lys Ile Val Ser Tyr Arg Ser Leu Gly Lys Gln Phe Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Ala Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ser
          20           25           30
```

```
Ile Ala Ser Xaa Ala Phe Asn Ser Gly Gly Cys
          35           40
```

<210> 552

<211> 43

<212> PRT

<213> Crocosphaera watsonii

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 552

```
Met Val Lys Ile Ile Gly Cys Arg Ser Leu Gly Thr Gln Lys Val Tyr
1           5           10           15
```

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Ser
 20 25 30

Ile Ala Ser Xaa Ala Phe Asn Ser Gly Gly Cys
 35 40

<210> 553

<211> 43

<212> PRT

<213> Microcystis aeruginosa

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 553

Met Val Lys Ile Ile Gly Arg Gln Ser Leu Gly Arg Lys Pro Val Tyr
 1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Gly Asn Gly Leu
 20 25 30

Ile Ala Ser Xaa Ala Phe Asn Ser Gly Gly Cys
 35 40

<210> 554

<211> 43

<212> PRT

<213> Microcoleus chthonoplastes

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 554

Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
 20 25 30

Ile Ala Ser Xaa Ala Phe Asn Ser Gly Gly Cys
 35 40

<210> 555

<211> 43

<212> PRT

<213> *Oscillatoria limnetica*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 555

Met	Val	Lys	Ile	Val	Arg	Arg	Gln	Ser	Leu	Gly	Val	Gln	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Cys	Leu	Ala	Ser	Gly	Glu
			20					25						30	

Ile	Ala	Ser	Xaa	Ala	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 556

<211> 43

<212> PRT

<213> *Synechococcus elongatus*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 556

Met	Val	Lys	Ile	Val	Arg	Arg	Arg	Ser	Leu	Gly	Val	Gln	Pro	Val	Tyr
1				5					10					15	

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

Val	Ala	Ser	Xaa	Ala	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 557

<211> 43

<212> PRT

<213> *Synechococcus PCC7002*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 557

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

```
Asp Ile Gly Leu Ser Gln Asp His Asn Phe Leu Leu Gly Gln Gly Leu
      20             25             30
```

```
Ile Ala Ala Xaa Ala Phe Asn Ser Gly Gly Cys
      35             40
```

<210> 558

<211> 42

<212> PRT

<213> Thermosynechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 558

```
Met Lys Ile Val Gly Arg Arg Leu Met Gly Trp Gln Ala Val Tyr Asp
 1             5             10             15
```

```
Ile Gly Leu Ala Ala Asp His Asn Phe Val Leu Ala Asn Gly Ala Ile
      20             25             30
```

```
Ala Ala Xaa Ala Phe Asn Ser Gly Gly Cys
      35             40
```

<210> 559

<211> 43

<212> PRT

<213> Trichodesmium erythraeum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 559

```
Met Val Lys Ile Val Ser Arg Lys Leu Ala Lys Thr Glu Asn Val Tyr
 1             5             10             15
```

Asp Ile Gly Val Thr Lys Asp His Asn Phe Val Leu Ala Asn Gly Leu
 20 25 30

Ile Ala Ser Xaa Ala Phe Asn Ser Gly Gly Cys
 35 40

<210> 560

<211> 42

<212> PRT

<213> Thermosynechococcus vulcanus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 560

Met Lys Ile Val Gly Arg Arg Leu Val Gly Trp Gln Ala Val Tyr Asp
 1 5 10 15

Ile Gly Leu Ala Gly Asp His Asn Phe Leu Leu Ala Asn Gly Ala Ile
 20 25 30

Ala Ala Xaa Ala Phe Asn Ser Gly Gly Cys
 35 40

<210> 561

<211> 43

<212> PRT

<213> Nostoc punctiforme

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

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<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 561

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

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

Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 562

<211> 43

<212> PRT

<213> Synechocystis PCC6803

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 562

Met Val Lys Val Ile Gly Arg Arg Ser Leu Gly Val Gln Arg Ile Phe
 1 5 10 15

Asp Ile Gly Leu Pro Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ala
 20 25 30

Ile Ala Ala Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 563

<211> 43

<212> PRT

<213> Aphanothece halophytica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 563

Met Val Lys Ile Ile Lys Arg Gln Ser Leu Gly Arg Gln Asn Val Tyr
 1 5 10 15

Asp Val Cys Val Glu Thr Asp His Asn Phe Val Leu Ala Asn Gly Cys
 20 25 30

Val Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

33

40

<210> 564

<211> 43

<212> PRT

<213> Aphanizomenon ovalisporum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 564

Met	Val	Lys	Ile	Thr	Ala	Arg	Lys	Phe	Val	Gly	Arg	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	His	His	His	Asn	Phe	Ala	Ile	Lys	Asn	Gly	Leu
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 565

<211> 43

<212> PRT

<213> Anabaena PCC7120

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 565

Met	Ile	Lys	Ile	Ala	Ser	Arg	Lys	Phe	Leu	Gly	Val	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Arg	Arg	Asp	His	Asn	Phe	Phe	Ile	Lys	Asn	Gly	Leu
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 566

<211> 43

<212> PRT

<213> *Anabaena variabilis*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 566

Met	Ile	Lys	Ile	Ala	Ser	Arg	Lys	Phe	Leu	Gly	Val	Glu	Asn	Val	Tyr
1				5					10				15		

Asp	Ile	Gly	Val	Gly	Arg	Asp	His	Asn	Phe	Phe	Val	Lys	Asn	Gly	Leu
		20						25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 567

<211> 43

<212> PRT

<213> *Cylindrospermopsis raciborskii*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 567

Met	Val	Lys	Ile	Val	Ser	Arg	Arg	Tyr	Leu	Gly	Lys	Ala	Asp	Val	Tyr
1				5					10				15		

Asp	Ile	Gly	Val	Ala	Lys	Asp	His	Asn	Phe	Ile	Ile	Lys	Asn	Gly	Leu
		20						25					30		

Val	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 568

<211> 43

<212> PRT

<213> Cyanothece CCY0110

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 568

Met	Val	Lys	Ile	Ile	Glu	Arg	Arg	Ser	Leu	Gly	Lys	Gln	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ser	Asn	Asn	Leu
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 569

<211> 43

<212> PRT

<213> Cyanothece PCC8801

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 569

Met	Val	Lys	Ile	Val	Ser	Tyr	Arg	Ser	Leu	Gly	Lys	Gln	Phe	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Ala	Gln	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Ser
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 570

<211> 43

<212> PRT

<213> *Crocospaera watsonii*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 570

Met	Val	Lys	Ile	Ile	Gly	Cys	Arg	Ser	Leu	Gly	Thr	Gln	Lys	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Ser
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 571

<211> 43

<212> PRT

<213> *Microcystis aeruginosa*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 571

Met	Val	Lys	Ile	Ile	Gly	Arg	Gln	Ser	Leu	Gly	Arg	Lys	Pro	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Gly	Asn	Gly	Leu
				20					25					30	

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 572

<211> 43

<212> PRT

<213> Microcoleus chthonoplastes

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 572

Met	Val	Lys	Ile	Val	Arg	Arg	Gln	Ser	Leu	Gly	Val	Gln	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Cys	Leu	Ala	Ser	Gly	Glu
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 573

<211> 43

<212> PRT

<213> Oscillatoria limnetica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 573

Met	Val	Lys	Ile	Val	Arg	Arg	Gln	Ser	Leu	Gly	Val	Gln	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Cys	Leu	Ala	Ser	Gly	Glu
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 574

<211> 43

<212> PRT

<213> Synechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

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<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 574

Met	Val	Lys	Ile	Val	Arg	Arg	Arg	Ser	Leu	Gly	Val	Gln	Pro	Val	Tyr
1				5					10					15	

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

Val	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 575

<211> 43

<212> PRT

<213> Synechococcus PCC7002

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 575

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

Asp	Ile	Gly	Leu	Ser	Gln	Asp	His	Asn	Phe	Leu	Leu	Gly	Gln	Gly	Leu
			20					25					30		

Ile	Ala	Ala	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 576

<211> 42

<212> PRT

<213> Thermosynechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Cys

<400> 576

Met	Lys	Ile	Val	Gly	Arg	Arg	Leu	Met	Gly	Trp	Gln	Ala	Val	Tyr	Asp
1				5					10					15	

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

Ala	Ala	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40		

<210> 577

<211> 43

<212> PRT

<213> Trichodesmium erythraeum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 577

Met	Val	Lys	Ile	Val	Ser	Arg	Lys	Leu	Ala	Lys	Thr	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Thr	Lys	Asp	His	Asn	Phe	Val	Leu	Ala	Asn	Gly	Leu
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 578

<211> 42

<212> PRT

<213> Thermosynechococcus vulcanus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Cys

<400> 578

```
Met Lys Ile Val Gly Arg Arg Leu Val Gly Trp Gln Ala Val Tyr Asp
1           5           10           15
```

```
Ile Gly Leu Ala Gly Asp His Asn Phe Leu Leu Ala Asn Gly Ala Ile
          20           25           30
```

```
Ala Ala Xaa Xaa Phe Asn Ser Gly Gly Cys
          35           40
```

<210> 579

<211> 43

<212> PRT

<213> Nostoc punctiforme

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexanoic acid

<400> 579

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

```
Asp Ile Gly Val Glu Arg Asp His Asn Phe Ala Leu Lys Asn Gly Phe
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
          35           40
```

<210> 580

<211> 43

<212> PRT

<213> Synechocystis PCC6803

<220>

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<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

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<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 580

```
Met Val Lys Val Ile Gly Arg Arg Ser Leu Gly Val Gln Arg Ile Phe
1              5              10              15
```

```
Asp Ile Gly Leu Pro Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ala
          20              25              30
```

```
Ile Ala Ala Xaa Xaa Phe Asn Ser Gly Gly Cys
          35              40
```

<210> 581

<211> 43

<212> PRT

<213> Aphanothece halophytica

<220>

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<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

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<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 581

```
Met Val Lys Ile Ile Lys Arg Gln Ser Leu Gly Arg Gln Asn Val Tyr
1              5              10              15
```

```
Asp Val Cys Val Glu Thr Asp His Asn Phe Val Leu Ala Asn Gly Cys
          20              25              30
```


Val Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
35 40

<210> 582

<211> 43

<212> PRT

<213> Aphanizomenon ovalisporum

<220>

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<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

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<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 582

Met Val Lys Ile Thr Ala Arg Lys Phe Val Gly Arg Glu Asn Val Tyr
1 5 10 15

Asp Ile Gly Val Glu His His His Asn Phe Ala Ile Lys Asn Gly Leu
20 25 30

Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
35 40

<210> 583

<211> 43

<212> PRT

<213> Anabaena PCC7120

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

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<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 583

Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
1 5 10 15

Asp Ile Gly Val Arg Arg Asp His Asn Phe Phe Ile Lys Asn Gly Leu
 20 25 30

Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 584

<211> 43

<212> PRT

<213> Anabaena variabilis

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 584

Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Gly Arg Asp His Asn Phe Phe Val Lys Asn Gly Leu
 20 25 30

Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 585

<211> 43

<212> PRT

<213> Cylandropermopsis raciborskii

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

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<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 585

Met Val Lys Ile Val Ser Arg Arg Tyr Leu Gly Lys Ala Asp Val Tyr
 1 5 10 15

Asp Ile Gly Val Ala Lys Asp His Asn Phe Ile Ile Lys Asn Gly Leu

20

25

30

Val Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 586

<211> 43

<212> PRT

<213> Cyanotheca CCY0110

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

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<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural
 aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-
 aminopentonic acid, or 2-aminohexanoic acid

<400> 586

Met Val Lys Ile Ile Glu Arg Arg Ser Leu Gly Lys Gln Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ser Asn Asn Leu
 20 25 30

Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 587

<211> 43

<212> PRT

<213> Cyanotheca PCC8801

<220>

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<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

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<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 587

Met Val Lys Ile Val Ser Tyr Arg Ser Leu Gly Lys Gln Phe Val Tyr
1 5 10 15

Asp Ile Gly Val Ala Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ser
20 25 30

Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
35 40

<210> 588

<211> 43

<212> PRT

<213> Crocosphaera watsonii

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

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<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 588

Met Val Lys Ile Ile Gly Cys Arg Ser Leu Gly Thr Gln Lys Val Tyr
1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Ser
20 25 30

Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
35 40

<210> 589

<211> 43

<212> PRT

<213> Microcystis aeruginosa

<220>

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<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

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<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 589

```
Met Val Lys Ile Ile Gly Arg Gln Ser Leu Gly Arg Lys Pro Val Tyr
1           5           10          15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Gly Asn Gly Leu
          20          25          30
```

```
Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
          35          40
```

<210> 590

<211> 43

<212> PRT

<213> Microcoleus chthonoplastes

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

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<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 590

```
Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
1           5           10          15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
          20          25          30
```

```
Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
          35          40
```

<210> 591

<211> 43

<212> PRT

<213> Oscillatoria limnetica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

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<400> 591

```
Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
          20           25           30
```

```
Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
          35           40
```

<210> 592

<211> 43

<212> PRT

<213> Synechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

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<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 592

```
Met Val Lys Ile Val Arg Arg Arg Ser Leu Gly Val Gln Pro Val Tyr
1           5           10           15
```

```
Asp Leu Gly Val Ala Thr Val His Asn Phe Val Leu Ala Asn Gly Leu
          20           25           30
```

```
Val Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
          35           40
```

<210> 593

<211> 43

<212> PRT

<213> Synechococcus PCC7002

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

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<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 593

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

Asp	Ile	Gly	Leu	Ser	Gln	Asp	His	Asn	Phe	Leu	Leu	Gly	Gln	Gly	Leu
		20					25					30			

Ile	Ala	Ala	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
	35					40				

<210> 594

<211> 42

<212> PRT

<213> Thermosynechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

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<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 594

Met	Lys	Ile	Val	Gly	Arg	Arg	Leu	Met	Gly	Trp	Gln	Ala	Val	Tyr	Asp
1			5					10					15		

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

Ala Ala Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 595

<211> 43

<212> PRT

<213> Trichodesmium erythraeum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexaanoic acid

<400> 595

Met Val Lys Ile Val Ser Arg Lys Leu Ala Lys Thr Glu Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Thr Lys Asp His Asn Phe Val Leu Ala Asn Gly Leu
 20 25 30

Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 596

<211> 42

<212> PRT

<213> Thermosynechococcus vulcanus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

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<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexaanoic acid

<400> 596

Met Lys Ile Val Gly Arg Arg Leu Val Gly Trp Gln Ala Val Tyr Asp
 1 5 10 15

Ile Gly Leu Ala Gly Asp His Asn Phe Leu Leu Ala Asn Gly Ala Ile
 20 25 30

Ala Ala Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 597

<211> 43

<212> PRT

<213> Nostoc punctiforme

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 597

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

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

Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 598

<211> 43

<212> PRT

<213> Synechocystis PCC6803

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

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<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 598

Met Val Lys Val Ile Gly Arg Arg Ser Leu Gly Val Gln Arg Ile Phe
 1 5 10 15

Asp Ile Gly Leu Pro Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ala
 20 25 30

Ile Ala Ala Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 599

<211> 43

<212> PRT

<213> Aphanothece halophytica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 599

Met Val Lys Ile Ile Lys Arg Gln Ser Leu Gly Arg Gln Asn Val Tyr
 1 5 10 15

Asp Val Cys Val Glu Thr Asp His Asn Phe Val Leu Ala Asn Gly Cys
 20 25 30

Val Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 600

<211> 43

<212> PRT

<213> Aphanizomenon ovalisporum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 600

Met Val Lys Ile Thr Ala Arg Lys Phe Val Gly Arg Glu Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Glu His His His Asn Phe Ala Ile Lys Asn Gly Leu
 20 25 30

20

25

30

Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 601

<211> 43

<212> PRT

<213> Anabaena PCC7120

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 601

Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Arg Arg Asp His Asn Phe Phe Ile Lys Asn Gly Leu
 20 25 30

Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 602

<211> 43

<212> PRT

<213> Anabaena variabilis

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 602

Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Gly Arg Asp His Asn Phe Phe Val Lys Asn Gly Leu
 20 25 30

Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 603

<211> 43

<212> PRT

<213> *Cylindrospermopsis raciborskii*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 603

Met Val Lys Ile Val Ser Arg Arg Tyr Leu Gly Lys Ala Asp Val Tyr
 1 5 10 15

Asp Ile Gly Val Ala Lys Asp His Asn Phe Ile Ile Lys Asn Gly Leu
 20 25 30

Val Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 604

<211> 43

<212> PRT

<213> *Cyanothece CCY0110*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 604

Met Val Lys Ile Ile Glu Arg Arg Ser Leu Gly Lys Gln Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ser Asn Asn Leu
 20 25 30

Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 605

<211> 43

<212> PRT

<213> Cyanothece PCC8801

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 605

Met Val Lys Ile Val Ser Tyr Arg Ser Leu Gly Lys Gln Phe Val Tyr
 1 5 10 15

Asp Ile Gly Val Ala Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ser
 20 25 30

Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 606

<211> 43

<212> PRT

<213> Crocosphaera watsonii

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 606

Met Val Lys Ile Ile Gly Cys Arg Ser Leu Gly Thr Gln Lys Val Tyr
 1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Ser
 20 25 30

Ile Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 607

<211> 43

<212> PRT

<213> Microcystis aeruginosa

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 607

Met	Val	Lys	Ile	Ile	Gly	Arg	Gln	Ser	Leu	Gly	Arg	Lys	Pro	Val	Tyr
1			5						10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Gly	Asn	Gly	Leu

20

25

30

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 608

<211> 43

<212> PRT

<213> Microcoleus chthonoplastes

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 608

Met	Val	Lys	Ile	Val	Arg	Arg	Gln	Ser	Leu	Gly	Val	Gln	Asn	Val	Tyr
1			5						10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Cys	Leu	Ala	Ser	Gly	Glu
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

33

40

<210> 609

<211> 43

<212> PRT

<213> *Oscillatoria limnetica*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 609

Met	Val	Lys	Ile	Val	Arg	Arg	Gln	Ser	Leu	Gly	Val	Gln	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Cys	Leu	Ala	Ser	Gly	Glu
			20					25						30	

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 610

<211> 43

<212> PRT

<213> *Synechococcus elongatus*

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 610

Met	Val	Lys	Ile	Val	Arg	Arg	Arg	Ser	Leu	Gly	Val	Gln	Pro	Val	Tyr
1				5					10					15	

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

Val	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 611

<211> 43

<212> PRT

<213> Synechococcus PCC7002

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 611

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

Asp	Ile	Gly	Leu	Ser	Gln	Asp	His	Asn	Phe	Leu	Leu	Gly	Gln	Gly	Leu
			20					25					30		

Ile	Ala	Ala	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
			35				40			

<210> 612

<211> 42

<212> PRT

<213> Thermosynechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 612

Met	Lys	Ile	Val	Gly	Arg	Arg	Leu	Met	Gly	Trp	Gln	Ala	Val	Tyr	Asp
1				5					10					15	

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

Ala	Ala	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
			35				40		

<210> 613

<211> 43

<212> PRT

<213> Trichodesmium erythraeum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 613

Met	Val	Lys	Ile	Val	Ser	Arg	Lys	Leu	Ala	Lys	Thr	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Thr	Lys	Asp	His	Asn	Phe	Val	Leu	Ala	Asn	Gly	Leu
			20					25					30		

Ile	Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35				40				

<210> 614

<211> 42

<212> PRT

<213> Thermosynechococcus vulcanus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 614

Met	Lys	Ile	Val	Gly	Arg	Arg	Leu	Val	Gly	Trp	Gln	Ala	Val	Tyr	Asp
1				5					10					15	

Ile	Gly	Leu	Ala	Gly	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Ala	Ile
			20					25					30		

Ala	Ala	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35				40			

<210> 615

<211> 43
 <212> PRT
 <213> Nostoc punctiforme

<220>
 <221> MISC_FEATURE
 <222> (36)..(36)
 <223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 615
 Met Ile Lys Ile Ala Thr Arg Lys Tyr Leu Gly Lys Gln Asn Val Tyr
 1 5 10 15
 Asp Ile Gly Val Glu Arg Asp His Asn Phe Ala Leu Lys Asn Gly Phe
 20 25 30
 Ile Ala Ser Xaa Ala Phe Asn Ser Gly Gly Cys
 35 40

<210> 616
 <211> 43
 <212> PRT
 <213> Synechocystis PCC6803

<220>
 <221> MISC_FEATURE
 <222> (36)..(36)
 <223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 616
 Met Val Lys Val Ile Gly Arg Arg Ser Leu Gly Val Gln Arg Ile Phe
 1 5 10 15
 Asp Ile Gly Leu Pro Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ala
 20 25 30
 Ile Ala Ala Xaa Ala Phe Asn Ser Gly Gly Cys
 35 40

<210> 617
 <211> 43
 <212> PRT
 <213> Aphanothece halophytica

<220>
 <221> MISC_FEATURE
 <222> (36)..(36)
 <223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 617
 Met Val Lys Ile Ile Lys Arg Gln Ser Leu Gly Arg Gln Asn Val Tyr
 1 5 10 15

Asp Val Cys Val Glu Thr Asp His Asn Phe Val Leu Ala Asn Gly Cys
 20 25 30

Val Ala Ser Xaa Ala Phe Asn Ser Gly Gly Cys
 35 40

<210> 618

<211> 43

<212> PRT

<213> Aphanizomenon ovalisporum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 618

Met Val Lys Ile Thr Ala Arg Lys Phe Val Gly Arg Glu Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Glu His His His Asn Phe Ala Ile Lys Asn Gly Leu
 20 25 30

Ile Ala Ser Xaa Ala Phe Asn Ser Gly Gly Cys
 35 40

<210> 619

<211> 43

<212> PRT

<213> Anabaena PCC7120

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 619

Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Arg Arg Asp His Asn Phe Phe Ile Lys Asn Gly Leu
 20 25 30

Ile Ala Ser Xaa Ala Phe Asn Ser Gly Gly Cys
 35 40

<210> 620

<211> 43

<212> PRT

<213> Anabaena variabilis

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 620

Met	Ile	Lys	Ile	Ala	Ser	Arg	Lys	Phe	Leu	Gly	Val	Glu	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Gly	Arg	Asp	His	Asn	Phe	Phe	Val	Lys	Asn	Gly	Leu
			20					25					30		

Ile	Ala	Ser	Xaa	Ala	Phe	Asn	Ser	Gly	Gly	Cys
			35					40		

<210> 621

<211> 43

<212> PRT

<213> Cylindrospermopsis raciborskii

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 621

Met	Val	Lys	Ile	Val	Ser	Arg	Arg	Tyr	Leu	Gly	Lys	Ala	Asp	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Ala	Lys	Asp	His	Asn	Phe	Ile	Ile	Lys	Asn	Gly	Leu
			20					25					30		

Val	Ala	Ser	Xaa	Ala	Phe	Asn	Ser	Gly	Gly	Cys
			35					40		

<210> 622

<211> 43

<212> PRT

<213> Cyanothece CCY0110

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 622

Met	Val	Lys	Ile	Ile	Glu	Arg	Arg	Ser	Leu	Gly	Lys	Gln	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ser	Asn	Asn	Leu
			20					25					30		

Ile Ala Ser Xaa Ala Phe Asn Ser Gly Gly Cys
 35 40

<210> 623

<211> 43

<212> PRT

<213> Cyanotheca PCC8801

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 623

Met Val Lys Ile Val Ser Tyr Arg Ser Leu Gly Lys Gln Phe Val Tyr
 1 5 10 15

Asp Ile Gly Val Ala Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ser
 20 25 30

Ile Ala Ser Xaa Ala Phe Asn Ser Gly Gly Cys
 35 40

<210> 624

<211> 43

<212> PRT

<213> Crocosphaera watsonii

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 624

Met Val Lys Ile Ile Gly Cys Arg Ser Leu Gly Thr Gln Lys Val Tyr
 1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Ser
 20 25 30

Ile Ala Ser Xaa Ala Phe Asn Ser Gly Gly Cys
 35 40

<210> 625

<211> 43

<212> PRT

<213> Microcystis aeruginosa

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 625

```
Met Val Lys Ile Ile Gly Arg Gln Ser Leu Gly Arg Lys Pro Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Gly Asn Gly Leu
          20           25           30
```

```
Ile Ala Ser Xaa Ala Phe Asn Ser Gly Gly Cys
          35           40
```

<210> 626

<211> 43

<212> PRT

<213> Microcoleus chthonoplastes

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 626

```
Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
          20           25           30
```

```
Ile Ala Ser Xaa Ala Phe Asn Ser Gly Gly Cys
          35           40
```

<210> 627

<211> 43

<212> PRT

<213> Oscillatoria limnetica

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 627

```
Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
          20           25           30
```

```
Ile Ala Ser Xaa Ala Phe Asn Ser Gly Gly Cys
          35           40
```

<210> 628

<211> 43
 <212> PRT
 <213> Synechococcus elongatus

<220>
 <221> MISC_FEATURE
 <222> (36)..(36)
 <223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 628
 Met Val Lys Ile Val Arg Arg Arg Ser Leu Gly Val Gln Pro Val Tyr
 1 5 10 15
 Asp Leu Gly Val Ala Thr Val His Asn Phe Val Leu Ala Asn Gly Leu
 20 25 30
 Val Ala Ser Xaa Ala Phe Asn Ser Gly Gly Cys
 35 40

<210> 629
 <211> 43
 <212> PRT
 <213> Synechococcus PCC7002

<220>
 <221> MISC_FEATURE
 <222> (36)..(36)
 <223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 629
 Met Val Lys Ile Ile Arg Arg Lys Phe Ile Gly His Ala Pro Thr Tyr
 1 5 10 15
 Asp Ile Gly Leu Ser Gln Asp His Asn Phe Leu Leu Gly Gln Gly Leu
 20 25 30
 Ile Ala Ala Xaa Ala Phe Asn Ser Gly Gly Cys
 35 40

<210> 630
 <211> 42
 <212> PRT
 <213> Thermosynechococcus elongatus

<220>
 <221> MISC_FEATURE
 <222> (35)..(35)
 <223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 630
 Met Lys Ile Val Gly Arg Arg Leu Met Gly Trp Gln Ala Val Tyr Asp
 1 5 10 15 20 25 30 35 40 45 50

1 5 10 15

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

Ala Ala Xaa Ala Phe Asn Ser Gly Gly Cys
 35 40

<210> 631

<211> 43

<212> PRT

<213> Trichodesmium erythraeum

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 631

Met Val Lys Ile Val Ser Arg Lys Leu Ala Lys Thr Glu Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Thr Lys Asp His Asn Phe Val Leu Ala Asn Gly Leu
 20 25 30

Ile Ala Ser Xaa Ala Phe Asn Ser Gly Gly Cys
 35 40

<210> 632

<211> 42

<212> PRT

<213> Thermosynechococcus vulcanus

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Ile Val Leu, Tyr, Gly or Phe

<400> 632

Met Lys Ile Val Gly Arg Arg Leu Val Gly Trp Gln Ala Val Tyr Asp
 1 5 10 15

Ile Gly Leu Ala Gly Asp His Asn Phe Leu Leu Ala Asn Gly Ala Ile
 20 25 30

Ala Ala Xaa Ala Phe Asn Ser Gly Gly Cys
 35 40

<210> 633

<211> 43

<212> PRT

<213> Nostoc punctiforme

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 633

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

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

Ile	Ala	Ser	Ala	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 634

<211> 39

<212> PRT

<213> Synechocystis PCC6803

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 634

Met	Val	Lys	Val	Ile	Gly	Arg	Arg	Ser	Leu	Gly	Val	Gln	Arg	Ile	Phe
1				5					10					15	

Asp	Ile	Gly	Leu	Pro	Gln	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Ala
			20					25					30		

Ile	Ala	Ala	Ala	Xaa	Phe	Asn
			35			

<210> 635

<211> 39

<212> PRT

<213> Aphanothece halophytica

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 635

Met	Val	Lys	Ile	Ile	Lys	Arg	Gln	Ser	Leu	Gly	Arg	Gln	Asn	Val	Tyr
1				5					10					15	

Asp	Val	Cys	Val	Glu	Thr	Asp	His	Asn	Phe	Val	Leu	Ala	Asn	Gly	Cys
			20					25					30		

Val Ala Ser Ala Xaa Phe Asn
35

<210> 636

<211> 43

<212> PRT

<213> Aphanizomenon ovalisporum

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 636

Met Val Lys Ile Thr Ala Arg Lys Phe Val Gly Arg Glu Asn Val Tyr

1 5 10 15

Asp Ile Gly Val Glu His His His Asn Phe Ala Ile Lys Asn Gly Leu
20 25 30

Ile Ala Ser Ala Xaa Phe Asn Ser Gly Gly Cys
35 40

<210> 637

<211> 43

<212> PRT

<213> Anabaena PCC7120

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 637

Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
1 5 10 15

Asp Ile Gly Val Arg Arg Asp His Asn Phe Phe Ile Lys Asn Gly Leu
20 25 30

Ile Ala Ser Ala Xaa Phe Asn Ser Gly Gly Cys
35 40

<210> 638

<211> 43

<212> PRT

<213> Anabaena variabilis

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 638

```
Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Gly Arg Asp His Asn Phe Phe Val Lys Asn Gly Leu
          20           25           30
```

```
Ile Ala Ser Ala Xaa Phe Asn Ser Gly Gly Cys
          35           40
```

<210> 639

<211> 43

<212> PRT

<213> Cylindrospermopsis raciborskii

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 639

```
Met Val Lys Ile Val Ser Arg Arg Tyr Leu Gly Lys Ala Asp Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Ala Lys Asp His Asn Phe Ile Ile Lys Asn Gly Leu
          20           25           30
```

```
Val Ala Ser Ala Xaa Phe Asn Ser Gly Gly Cys
          35           40
```

<210> 640

<211> 43

<212> PRT

<213> Cyanothece CCY0110

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 640

```
Met Val Lys Ile Ile Glu Arg Arg Ser Leu Gly Lys Gln Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ser Asn Asn Leu
          20           25           30
```

```
Ile Ala Ser Ala Xaa Phe Asn Ser Gly Gly Cys
          35           40
```

<210> 641

<211> 43

<212> PRT

<213> Cyanothece PCC8801

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 641

Met	Val	Lys	Ile	Val	Ser	Tyr	Arg	Ser	Leu	Gly	Lys	Gln	Phe	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Ala	Gln	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Ser
			20					25					30		

Ile	Ala	Ser	Ala	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 642

<211> 43

<212> PRT

<213> Crocosphaera watsonii

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 642

Met	Val	Lys	Ile	Ile	Gly	Cys	Arg	Ser	Leu	Gly	Thr	Gln	Lys	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Ser
			20					25					30		

Ile	Ala	Ser	Ala	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 643

<211> 43

<212> PRT

<213> Microcystis aeruginosa

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 643

```

Met Val Lys Ile Ile Gly Arg Gln Ser Leu Gly Arg Lys Pro Val Tyr
1           5           10           15

```

```

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Gly Asn Gly Leu
          20           25           30

```

```

Ile Ala Ser Ala Xaa Phe Asn Ser Gly Gly Cys
      35           40

```

<210> 644

<211> 43

<212> PRT

<213> Microcoleus chthonoplastes

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 644

```

Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
1           5           10           15

```

```

Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
          20           25           30

```

```

Ile Ala Ser Ala Xaa Phe Asn Ser Gly Gly Cys
      35           40

```

<210> 645

<211> 43

<212> PRT

<213> Oscillatoria limnetica

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 645

```

Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
1           5           10           15

```

```

Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
          20           25           30

```

```

Ile Ala Ser Ala Xaa Phe Asn Ser Gly Gly Cys
      35           40

```

<210> 646

<211> 43

<212> PRT

<213> Synechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 646

Met	Val	Lys	Ile	Val	Arg	Arg	Arg	Ser	Leu	Gly	Val	Gln	Pro	Val	Tyr
1				5					10					15	

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

Val	Ala	Ser	Ala	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 647

<211> 43

<212> PRT

<213> Synechococcus PCC7002

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 647

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

Asp	Ile	Gly	Leu	Ser	Gln	Asp	His	Asn	Phe	Leu	Leu	Gly	Gln	Gly	Leu
			20					25					30		

Ile	Ala	Ala	Ala	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
			35				40			

<210> 648

<211> 42

<212> PRT

<213> Thermosynechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Cys

<400> 648

Met	Lys	Ile	Val	Gly	Arg	Arg	Leu	Met	Gly	Trp	Gln	Ala	Val	Tyr	Asp
1				5					10					15	

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

Ala Ala Ala Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 649

<211> 43

<212> PRT

<213> Trichodesmium erythraeum

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is any amino acid excluding Cys

<400> 649

Met Val Lys Ile Val Ser Arg Lys Leu Ala Lys Thr Glu Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Thr Lys Asp His Asn Phe Val Leu Ala Asn Gly Leu
 20 25 30

Ile Ala Ser Ala Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 650

<211> 42

<212> PRT

<213> Thermosynechococcus vulcanus

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Cys

<400> 650

Met Lys Ile Val Gly Arg Arg Leu Val Gly Trp Gln Ala Val Tyr Asp
 1 5 10 15

Ile Gly Leu Ala Gly Asp His Asn Phe Leu Leu Ala Asn Gly Ala Ile
 20 25 30

Ala Ala Ala Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 651

<211> 43

<212> PRT

<213> Nostoc punctiforme

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 651

Met Ile Lys Ile Ala Thr Arg Lys Tyr Leu Gly Lys Gln Asn Val Tyr

1

5

10

15

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

Ile Ala Ser Ala Xaa Phe Asn Ser Gly Gly Cys
35 40

<210> 652

<211> 43

<212> PRT

<213> Synechocystis PCC6803

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 652

Met Val Lys Val Ile Gly Arg Arg Ser Leu Gly Val Gln Arg Ile Phe
1 5 10 15

Asp Ile Gly Leu Pro Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ala
20 25 30

Ile Ala Ala Ala Xaa Phe Asn Ser Gly Gly Cys
35 40

<210> 653

<211> 43

<212> PRT

<213> Aphanothece halophytica

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 653

```

Met Val Lys Ile Ile Lys Arg Gln Ser Leu Gly Arg Gln Asn Val Tyr
1           5           10           15

```

```

Asp Val Cys Val Glu Thr Asp His Asn Phe Val Leu Ala Asn Gly Cys
          20           25           30

```

```

Val Ala Ser Ala Xaa Phe Asn Ser Gly Gly Cys
          35           40

```

<210> 654

<211> 43

<212> PRT

<213> Aphanizomenon ovalisporum

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 654

```

Met Val Lys Ile Thr Ala Arg Lys Phe Val Gly Arg Glu Asn Val Tyr
1           5           10           15

```

```

Asp Ile Gly Val Glu His His His Asn Phe Ala Ile Lys Asn Gly Leu
          20           25           30

```

```

Ile Ala Ser Ala Xaa Phe Asn Ser Gly Gly Cys
          35           40

```

<210> 655

<211> 43

<212> PRT

<213> Anabaena PCC7120

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 655

```

Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
1           5           10           15

```

```

Asp Ile Gly Val Arg Arg Asp His Asn Phe Phe Ile Lys Asn Gly Leu
          20           25           30

```

Ile Ala Ser Ala Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 656

<211> 43

<212> PRT

<213> Anabaena variabilis

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 656

Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Gly Arg Asp His Asn Phe Phe Val Lys Asn Gly Leu
 20 25 30

Ile Ala Ser Ala Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 657

<211> 43

<212> PRT

<213> Cylandrospermopsis raciborskii

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 657

Met Val Lys Ile Val Ser Arg Arg Tyr Leu Gly Lys Ala Asp Val Tyr
 1 5 10 15

Asp Ile Gly Val Ala Lys Asp His Asn Phe Ile Ile Lys Asn Gly Leu
 20 25 30

Val Ala Ser Ala Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 658

<211> 43

<212> PRT

<213> Cyanothece CCY0110

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 658

```
Met Val Lys Ile Ile Glu Arg Arg Ser Leu Gly Lys Gln Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ser Asn Asn Leu
          20           25           30
```

```
Ile Ala Ser Ala Xaa Phe Asn Ser Gly Gly Cys
          35           40
```

<210> 659

<211> 43

<212> PRT

<213> Cyanotheca PCC8801

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 659

```
Met Val Lys Ile Val Ser Tyr Arg Ser Leu Gly Lys Gln Phe Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Ala Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ser
          20           25           30
```

```
Ile Ala Ser Ala Xaa Phe Asn Ser Gly Gly Cys
          35           40
```

<210> 660

<211> 43

<212> PRT

<213> Crocosphaera watsonii

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 660

Met Val Lys Ile Ile Gly Cys Arg Ser Leu Gly Thr Gln Lys Val Tyr

1

5

10

15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Ser
20 25 30Ile Ala Ser Ala Xaa Phe Asn Ser Gly Gly Cys
35 40

<210> 661

<211> 43

<212> PRT

<213> Microcystis aeruginosa

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 661

Met Val Lys Ile Ile Gly Arg Gln Ser Leu Gly Arg Lys Pro Val Tyr
1 5 10 15Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Gly Asn Gly Leu
20 25 30Ile Ala Ser Ala Xaa Phe Asn Ser Gly Gly Cys
35 40

<210> 662

<211> 43

<212> PRT

<213> Microcoleus chthonoplastes

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 662

Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
1 5 10 15Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
20 25 30

-- -- --

Ile Ala Ser Ala Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 663

<211> 43

<212> PRT

<213> *Oscillatoria limnetica*

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexaanoic acid

<400> 663

Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
 20 25 30

Ile Ala Ser Ala Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 664

<211> 43

<212> PRT

<213> *Synechococcus elongatus*

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexaanoic acid

<400> 664

Met Val Lys Ile Val Arg Arg Arg Ser Leu Gly Val Gln Pro Val Tyr
 1 5 10 15

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

Val Ala Ser Ala Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 665

<211> 43

<212> PRT

<213> Synechococcus PCC7002

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 665

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

```
Asp Ile Gly Leu Ser Gln Asp His Asn Phe Leu Leu Gly Gln Gly Leu
          20          25          30
```

```
Ile Ala Ala Ala Xaa Phe Asn Ser Gly Gly Cys
          35          40
```

<210> 666

<211> 42

<212> PRT

<213> Thermosynechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 666

```
Met Lys Ile Val Gly Arg Arg Leu Met Gly Trp Gln Ala Val Tyr Asp
1           5           10          15
```

```
Ile Gly Leu Ala Ala Asp His Asn Phe Val Leu Ala Asn Gly Ala Ile
          20          25          30
```

```
Ala Ala Ala Xaa Phe Asn Ser Gly Gly Cys
          35          40
```

<210> 667

<211> 43

<212> PRT

<213> Trichodesmium erythraeum

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural

aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexanoic acid

<400> 667

```
Met Val Lys Ile Val Ser Arg Lys Leu Ala Lys Thr Glu Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Thr Lys Asp His Asn Phe Val Leu Ala Asn Gly Leu
          20           25           30
```

```
Ile Ala Ser Ala Xaa Phe Asn Ser Gly Gly Cys
          35           40
```

<210> 668

<211> 42

<212> PRT

<213> Thermosynechococcus vulcanus

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexanoic acid

<400> 668

```
Met Lys Ile Val Gly Arg Arg Leu Val Gly Trp Gln Ala Val Tyr Asp
1           5           10           15
```

```
Ile Gly Leu Ala Gly Asp His Asn Phe Leu Leu Ala Asn Gly Ala Ile
          20           25           30
```

```
Ala Ala Ala Xaa Phe Asn Ser Gly Gly Cys
          35           40
```

<210> 669

<211> 43

<212> PRT

<213> Nostoc punctiforme

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 669

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

```
Asp Ile Gly Val Glu Arg Asp His Asn Phe Ala Leu Lys Asn Gly Phe
          20           25           30
```

Ile Ala Ser Ala Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 670

<211> 43

<212> PRT

<213> Synechocystis PCC6803

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 670

Met Val Lys Val Ile Gly Arg Arg Ser Leu Gly Val Gln Arg Ile Phe
 1 5 10 15

Asp Ile Gly Leu Pro Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ala
 20 25 30

Ile Ala Ala Ala Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 671

<211> 43

<212> PRT

<213> Aphanothece halophytica

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 671

Met Val Lys Ile Ile Lys Arg Gln Ser Leu Gly Arg Gln Asn Val Tyr
 1 5 10 15

Asp Val Cys Val Glu Thr Asp His Asn Phe Val Leu Ala Asn Gly Cys
 20 25 30

Val Ala Ser Ala Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 672

<211> 43

<212> PRT

<213> Aphanizomenon ovalisporum

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 672

```
Met Val Lys Ile Thr Ala Arg Lys Phe Val Gly Arg Glu Asn Val Tyr
1           5           10          15
```

```
Asp Ile Gly Val Glu His His His Asn Phe Ala Ile Lys Asn Gly Leu
          20           25          30
```

```
Ile Ala Ser Ala Xaa Phe Asn Ser Gly Gly Cys
          35           40
```

<210> 673

<211> 43

<212> PRT

<213> Anabaena PCC7120

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 673

```
Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
1           5           10          15
```

```
Asp Ile Gly Val Arg Arg Asp His Asn Phe Phe Ile Lys Asn Gly Leu
          20           25          30
```

```
Ile Ala Ser Ala Xaa Phe Asn Ser Gly Gly Cys
          35           40
```

<210> 674

<211> 43

<212> PRT

<213> Anabaena variabilis

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 674

```
Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
1           5           10          15
```

```
Asp Ile Gly Val Gly Arg Asp His Asn Phe Phe Val Lys Asn Gly Leu
          20           25          30
```

```
Ile Ala Ser Ala Xaa Phe Asn Ser Gly Gly Cys
          35           40
```

<210> 675

<211> 43

<212> PRT

<213> *Cylindrospermopsis raciborskii*

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 675

Met	Val	Lys	Ile	Val	Ser	Arg	Arg	Tyr	Leu	Gly	Lys	Ala	Asp	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Ala	Lys	Asp	His	Asn	Phe	Ile	Ile	Lys	Asn	Gly	Leu
			20					25					30		

Val	Ala	Ser	Ala	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 676

<211> 43

<212> PRT

<213> *Cyanothece CCY0110*

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 676

Met	Val	Lys	Ile	Ile	Glu	Arg	Arg	Ser	Leu	Gly	Lys	Gln	Asn	Val	Tyr
1				5					10					15	

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ser	Asn	Asn	Leu
			20					25					30		

Ile	Ala	Ser	Ala	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 677

<211> 43

<212> PRT

<213> *Cyanothece PCC8801*

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 677

```

Met Val Lys Ile Val Ser Tyr Arg Ser Leu Gly Lys Gln Phe Val Tyr
1           5           10           15

```

```

Asp Ile Gly Val Ala Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ser
          20           25           30

```

```

Ile Ala Ser Ala Xaa Phe Asn Ser Gly Gly Cys
          35           40

```

<210> 678

<211> 43

<212> PRT

<213> *Crocospaera watsonii*

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 678

```

Met Val Lys Ile Ile Gly Cys Arg Ser Leu Gly Thr Gln Lys Val Tyr
1           5           10           15

```

```

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Ser
          20           25           30

```

```

Ile Ala Ser Ala Xaa Phe Asn Ser Gly Gly Cys
          35           40

```

<210> 679

<211> 43

<212> PRT

<213> *Microcystis aeruginosa*

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 679

```

Met Val Lys Ile Ile Gly Arg Gln Ser Leu Gly Arg Lys Pro Val Tyr
1           5           10           15

```

```

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Gly Asn Gly Leu
          20           25           30

```

```

Ile Ala Ser Ala Xaa Phe Asn Ser Gly Gly Cys
          35           40

```

<210> 680

<211> 43

<212> PRT

<213> Microcoleus chthonoplastes

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 680

Met	Val	Lys	Ile	Val	Arg	Arg	Gln	Ser	Leu	Gly	Val	Gln	Asn	Val	Tyr
1				5					10				15		

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Cys	Leu	Ala	Ser	Gly	Glu
			20					25					30		

Ile	Ala	Ser	Ala	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 681

<211> 43

<212> PRT

<213> Oscillatoria limnetica

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 681

Met	Val	Lys	Ile	Val	Arg	Arg	Gln	Ser	Leu	Gly	Val	Gln	Asn	Val	Tyr
1				5					10				15		

Asp	Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Cys	Leu	Ala	Ser	Gly	Glu
			20					25					30		

Ile	Ala	Ser	Ala	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40			

<210> 682

<211> 43

<212> PRT

<213> Synechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 682

Met	Val	Lys	Ile	Val	Arg	Arg	Arg	Ser	Leu	Gly	Val	Gln	Pro	Val	Tyr
1				5					10				15		

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

Val Ala Ser Ala Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 683

<211> 43

<212> PRT

<213> Synechococcus PCC7002

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 683

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

Asp Ile Gly Leu Ser Gln Asp His Asn Phe Leu Leu Gly Gln Gly Leu
 20 25 30

Ile Ala Ala Ala Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 684

<211> 42

<212> PRT

<213> Thermosynechococcus elongatus

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 684

Met Lys Ile Val Gly Arg Arg Leu Met Gly Trp Gln Ala Val Tyr Asp
 1 5 10 15

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

Ala Ala Ala Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 685

<211> 43

<212> PRT

<213> Trichodesmium erythraeum

<220>

<221> MISC_FEATURE

<222> (37)..(37)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 685

```
Met Val Lys Ile Val Ser Arg Lys Leu Ala Lys Thr Glu Asn Val Tyr
1           5           10           15
```

```
Asp Ile Gly Val Thr Lys Asp His Asn Phe Val Leu Ala Asn Gly Leu
          20           25           30
```

```
Ile Ala Ser Ala Xaa Phe Asn Ser Gly Gly Cys
          35           40
```

<210> 686

<211> 42

<212> PRT

<213> Thermosynechococcus vulcanus

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 686

```
Met Lys Ile Val Gly Arg Arg Leu Val Gly Trp Gln Ala Val Tyr Asp
1           5           10           15
```

```
Ile Gly Leu Ala Gly Asp His Asn Phe Leu Leu Ala Asn Gly Ala Ile
          20           25           30
```

```
Ala Ala Ala Xaa Phe Asn Ser Gly Gly Cys
          35           40
```

<210> 687

<211> 43

<212> PRT

<213> Nostoc punctiforme

<400> 687

```
Met Ile Lys Ile Ala Thr Arg Lys Tyr Leu Gly Lys Gln Asn Val Tyr
```

```
1           5           10           15
```

```
Asp Ile Gly Val Glu Arg Asp His Asn Phe Ala Leu Lys Asn Gly Phe
          20           25           30
```

```
Ile Ala Ser Ala Ala Phe Asn Ser Gly Gly Cys
          35           40
```

<210> 688

<211> 43

<212> PRT

<213> Synechocystis PCC6803

<400> 688

Met Val Lys Val Ile Gly Arg Arg Ser Leu Gly Val Gln Arg Ile Phe
 1 5 10 15

Asp Ile Gly Leu Pro Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ala
 20 25 30

Ile Ala Ala Ala Ala Phe Asn Ser Gly Gly Cys
 35 40

<210> 689

<211> 43

<212> PRT

<213> Aphanothece halophytica

<400> 689

Met Val Lys Ile Ile Lys Arg Gln Ser Leu Gly Arg Gln Asn Val Tyr
 1 5 10 15

Asp Val Cys Val Glu Thr Asp His Asn Phe Val Leu Ala Asn Gly Cys
 20 25 30

Val Ala Ser Ala Ala Phe Asn Ser Gly Gly Cys
 35 40

<210> 690

<211> 43

<212> PRT

<213> Aphanizomenon ovalisporum

<400> 690

Met Val Lys Ile Thr Ala Arg Lys Phe Val Gly Arg Glu Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Glu His His His Asn Phe Ala Ile Lys Asn Gly Leu
 20 25 30

Ile Ala Ser Ala Ala Phe Asn Ser Gly Gly Cys
 35 40

<210> 691

<211> 39

<212> PRT

<213> Anabaena PCC7120

<400> 691

Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Arg Arg Asp His Asn Phe Phe Ile Lys Asn Gly Leu
 20 25 30

Ile Ala Ser Ala Ala Phe Asn
35

<210> 692

<211> 43

<212> PRT

<213> *Anabaena variabilis*

<400> 692

Met Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr
1 5 10 15

Asp Ile Gly Val Gly Arg Asp His Asn Phe Phe Val Lys Asn Gly Leu
20 25 30

Ile Ala Ser Ala Ala Phe Asn Ser Gly Gly Cys
35 40

<210> 693

<211> 43

<212> PRT

<213> *Cylindrospermopsis raciborskii*

<400> 693

Met Val Lys Ile Val Ser Arg Arg Tyr Leu Gly Lys Ala Asp Val Tyr
1 5 10 15

Asp Ile Gly Val Ala Lys Asp His Asn Phe Ile Ile Lys Asn Gly Leu
20 25 30

Val Ala Ser Ala Ala Phe Asn Ser Gly Gly Cys
35 40

<210> 694

<211> 43

<212> PRT

<213> *Cyanothece CCY0110*

<400> 694

Met Val Lys Ile Ile Glu Arg Arg Ser Leu Gly Lys Gln Asn Val Tyr
1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ser Asn Asn Leu
20 25 30

Ile Ala Ser Ala Ala Phe Asn Ser Gly Gly Cys
35 40

<210> 695

<211> 43

<212> PRT

<213> *Cyanothece PCC8801*

<400> 695

Met Val Lys Ile Val Ser Tyr Arg Ser Leu Gly Lys Gln Phe Val Tyr
 1 5 10 15

Asp Ile Gly Val Ala Gln Asp His Asn Phe Leu Leu Ala Asn Gly Ser
 20 25 30

Ile Ala Ser Ala Ala Phe Asn Ser Gly Gly Cys
 35 40

<210> 696

<211> 43

<212> PRT

<213> *Crocospaera watsonii*

<400> 696

Met Val Lys Ile Ile Gly Cys Arg Ser Leu Gly Thr Gln Lys Val Tyr
 1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Ser
 20 25 30

Ile Ala Ser Ala Ala Phe Asn Ser Gly Gly Cys
 35 40

<210> 697

<211> 43

<212> PRT

<213> *Microcystis aeruginosa*

<400> 697

Met Val Lys Ile Ile Gly Arg Gln Ser Leu Gly Arg Lys Pro Val Tyr
 1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Gly Asn Gly Leu
 20 25 30

Ile Ala Ser Ala Ala Phe Asn Ser Gly Gly Cys
 35 40

<210> 698

<211> 43

<212> PRT

<213> *Microcoleus chthonoplastes*

<400> 698

Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
 20 25 30

Ile Ala Ser Ala Ala Phe Asn Ser Gly Gly Cys
 35 40

35 40
 <210> 699
 <211> 43
 <212> PRT
 <213> *Oscillatoria limnetica*

 <400> 699
 Met Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr
 1 5 10 15
 Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu
 20 25 30
 Ile Ala Ser Ala Ala Phe Asn Ser Gly Gly Cys
 35 40
 <210> 700
 <211> 43
 <212> PRT
 <213> *Synechococcus elongatus*

 <400> 700
 Met Val Lys Ile Val Arg Arg Arg Ser Leu Gly Val Gln Pro Val Tyr
 1 5 10 15
 Asp Leu Gly Val Ala Thr Val His Asn Phe Val Leu Ala Asn Gly Leu
 20 25 30
 Val Ala Ser Ala Ala Phe Asn Ser Gly Gly Cys
 35 40
 <210> 701
 <211> 43
 <212> PRT
 <213> *Synechococcus PCC7002*

 <400> 701
 Met Val Lys Ile Ile Arg Arg Lys Phe Ile Gly His Ala Pro Thr Tyr
 1 5 10 15
 Asp Ile Gly Leu Ser Gln Asp His Asn Phe Leu Leu Gly Gln Gly Leu
 20 25 30
 Ile Ala Ala Ala Ala Phe Asn Ser Gly Gly Cys
 35 40
 <210> 702
 <211> 42
 <212> PRT
 <213> *Thermosynechococcus elongatus*

 <400> 702
 Met Lys Ile Val Gly Arg Arg Leu Met Gly Trp Gln Ala Val Tyr Asp

1 5 10 15

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

Ala Ala Ala Ala Phe Asn Ser Gly Gly Cys
 35 40

<210> 703

<211> 43

<212> PRT

<213> Trichodesmium erythraeum

<400> 703

Met Val Lys Ile Val Ser Arg Lys Leu Ala Lys Thr Glu Asn Val Tyr
 1 5 10 15

Asp Ile Gly Val Thr Lys Asp His Asn Phe Val Leu Ala Asn Gly Leu
 20 25 30

Ile Ala Ser Ala Ala Phe Asn Ser Gly Gly Cys
 35 40

<210> 704

<211> 42

<212> PRT

<213> Thermosynechococcus vulcanus

<400> 704

Met Lys Ile Val Gly Arg Arg Leu Val Gly Trp Gln Ala Val Tyr Asp
 1 5 10 15

Ile Gly Leu Ala Gly Asp His Asn Phe Leu Leu Ala Asn Gly Ala Ile
 20 25 30

Ala Ala Ala Ala Phe Asn Ser Gly Gly Cys
 35 40

<210> 705

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<400> 705

Ser Gly Gly Cys
 1

<210> 706

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<400> 706

Ala Ala Phe Asn Ser Gly Gly Cys
1 5

<210> 707

<211> 35

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<400> 707

Val Lys Ile Ile Ser Arg Gln Ser Leu Gly Lys Gln Asn Val Tyr Asp
1 5 10 15

Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Leu Ile
20 25 30

Ala Ser Asn
35

<210> 708

<211> 35

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 708

Val Lys Ile Ile Ser Arg Gln Ser Leu Gly Lys Gln Asn Val Tyr Asp
1 5 10 15

Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Leu Ile
20 25 30

Ala Ser Xaa
35

<210> 709

<211> 35

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 709

Val	Lys	Ile	Ile	Ser	Arg	Gln	Ser	Leu	Gly	Lys	Gln	Asn	Val	Tyr	Asp
1				5					10					15	

Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Leu	Ile
			20					25					30		

Ala	Ser	Xaa
		35

<210> 710

<211> 35

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 710

Val	Lys	Ile	Ile	Ser	Arg	Gln	Ser	Leu	Gly	Lys	Gln	Asn	Val	Tyr	Asp
1				5					10					15	

Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Leu	Ile
			20					25					30		

Ala	Ser	Xaa
		35

<210> 711

<211> 35

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<400> 711

Val	Lys	Ile	Ile	Ser	Arg	Gln	Ser	Leu	Gly	Lys	Gln	Asn	Val	Tyr	Asp
1				5					10					15	

Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Leu	Ile
			20					25					30		

Ala	Ser	Ala
		35

<210> 712

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Cys

<400> 712

Val	Lys	Ile	Ile	Ser	Arg	Gln	Ser	Leu	Gly	Lys	Gln	Asn	Val	Tyr	Asp
1				5					10					15	

Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Leu	Ile
			20					25					30		

Ala	Ser	Xaa	Xaa
			35

<210> 713

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 713

Val	Lys	Ile	Ile	Ser	Arg	Gln	Ser	Leu	Gly	Lys	Gln	Asn	Val	Tyr	Asp
1				5					10					15	
Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Leu	Ile
			20					25					30		
Ala	Ser	Xaa	Xaa												
			35												

<210> 714

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 714

Val	Lys	Ile	Ile	Ser	Arg	Gln	Ser	Leu	Gly	Lys	Gln	Asn	Val	Tyr	Asp
1				5					10					15	
Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Leu	Ile
			20					25					30		
Ala	Ser	Xaa	Xaa												
			35												

<210> 715

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 715

Val	Lys	Ile	Ile	Ser	Arg	Gln	Ser	Leu	Gly	Lys	Gln	Asn	Val	Tyr	Asp
1				5					10					15	

Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Leu	Ile
			20					25					30		

Ala	Ser	Xaa	Ala
		35	

<210> 716

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Cys

<400> 716

Val	Lys	Ile	Ile	Ser	Arg	Gln	Ser	Leu	Gly	Lys	Gln	Asn	Val	Tyr	Asp
1				5					10					15	

Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Leu	Ile
			20					25					30		

Ala	Ser	Xaa	Xaa
		35	

<210> 717

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 717

Val	Lys	Ile	Ile	Ser	Arg	Gln	Ser	Leu	Gly	Lys	Gln	Asn	Val	Tyr	Asp
1				5					10					15	

Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Leu	Ile
			20					25					30		

Ala	Ser	Xaa	Xaa
			35

<210> 718

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 718

```
Val Lys Ile Ile Ser Arg Gln Ser Leu Gly Lys Gln Asn Val Tyr Asp
1           5           10           15
```

```
Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Leu Ile
      20           25           30
```

```
Ala Ser Xaa Xaa
      35
```

<210> 719

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 719

```
Val Lys Ile Ile Ser Arg Gln Ser Leu Gly Lys Gln Asn Val Tyr Asp
1           5           10           15
```

```
Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Leu Ile
      20           25           30
```

```
Ala Ser Xaa Ala
      35
```

<210> 720

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Cys

<400> 720

```
Val Lys Ile Ile Ser Arg Gln Ser Leu Gly Lys Gln Asn Val Tyr Asp
1           5           10           15
```

```
Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Leu Ile
          20           25           30
```

```
Ala Ser Xaa Xaa
          35
```

<210> 721

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 721

```
Val Lys Ile Ile Ser Arg Gln Ser Leu Gly Lys Gln Asn Val Tyr Asp
1           5           10           15
```

```
Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Leu Ile
          20           25           30
```

```
Ala Ser Xaa Xaa
          35
```

<210> 722

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 722

Val	Lys	Ile	Ile	Ser	Arg	Gln	Ser	Leu	Gly	Lys	Gln	Asn	Val	Tyr	Asp
1				5					10					15	

Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Leu	Ile
			20					25					30		

Ala	Ser	Xaa	Xaa
		35	

<210> 723

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 723

Val	Lys	Ile	Ile	Ser	Arg	Gln	Ser	Leu	Gly	Lys	Gln	Asn	Val	Tyr	Asp
1				5					10					15	

Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Leu	Ile
			20					25					30		

Ala	Ser	Xaa	Ala
		35	

<210> 724

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Cys

<400> 724

Val	Lys	Ile	Ile	Ser	Arg	Gln	Ser	Leu	Gly	Lys	Gln	Asn	Val	Tyr	Asp
1				5					10					15	

Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Leu	Ile
			20					25					30		

Ala	Ser	Ala	Xaa
			35

<210> 725

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 725

Val	Lys	Ile	Ile	Ser	Arg	Gln	Ser	Leu	Gly	Lys	Gln	Asn	Val	Tyr	Asp
1				5					10					15	

Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Leu	Ile
			20					25					30		

Ala	Ser	Ala	Xaa
			35

<210> 726

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 726

```
Val Lys Ile Ile Ser Arg Gln Ser Leu Gly Lys Gln Asn Val Tyr Asp
1           5           10           15
```

```
Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Leu Ile
          20           25           30
```

```
Ala Ser Ala Xaa
          35
```

<210> 727

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<400> 727

```
Val Lys Ile Ile Ser Arg Gln Ser Leu Gly Lys Gln Asn Val Tyr Asp
1           5           10           15
```

```
Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Leu Ile
          20           25           30
```

```
Ala Ser Ala Ala
          35
```

<210> 728

<211> 38

<212> **PRT**

<213> **Artificial Sequence**

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Cys

<400> 728

```
Val Lys Ile Ile Ser Arg Gln Ser Leu Gly Lys Gln Asn Val Tyr Asp
1           5           10           15
```

Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Leu Ile
 20 25 30

Ala Ser Xaa Xaa Phe Asn
 35

<210> 729

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 729

Val Lys Ile Ile Ser Arg Gln Ser Leu Gly Lys Gln Asn Val Tyr Asp
 1 5 10 15

Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Leu Ile
 20 25 30

Ala Ser Xaa Xaa Phe Asn
 35

<210> 730

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 730

Val	Lys	Ile	Ile	Ser	Arg	Gln	Ser	Leu	Gly	Lys	Gln	Asn	Val	Tyr	Asp
1				5					10					15	

Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Leu	Ile
			20					25					30		

Ala	Ser	Xaa	Xaa	Phe	Asn
					35

<210> 731

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 731

Val	Lys	Ile	Ile	Ser	Arg	Gln	Ser	Leu	Gly	Lys	Gln	Asn	Val	Tyr	Asp
1				5					10					15	

Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Leu	Ile
			20					25					30		

Ala	Ser	Xaa	Ala	Phe	Asn
					35

<210> 732

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-

aminopentonic acid, or 2-aminohexanoic acid

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Cys

<400> 732

Val	Lys	Ile	Ile	Ser	Arg	Gln	Ser	Leu	Gly	Lys	Gln	Asn	Val	Tyr	Asp
1				5					10					15	

Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Leu	Ile
			20					25					30		

Ala	Ser	Xaa	Xaa	Phe	Asn
					35

<210> 733

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 733

Val	Lys	Ile	Ile	Ser	Arg	Gln	Ser	Leu	Gly	Lys	Gln	Asn	Val	Tyr	Asp
1				5					10					15	

Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Leu	Ile
			20					25					30		

Ala	Ser	Xaa	Xaa	Phe	Asn
					35

<210> 734

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 734

Val	Lys	Ile	Ile	Ser	Arg	Gln	Ser	Leu	Gly	Lys	Gln	Asn	Val	Tyr	Asp
1				5					10					15	

Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Leu	Ile
			20					25					30		

Ala	Ser	Xaa	Xaa	Phe	Asn
					35

<210> 735

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 735

Val	Lys	Ile	Ile	Ser	Arg	Gln	Ser	Leu	Gly	Lys	Gln	Asn	Val	Tyr	Asp
1				5					10					15	

Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Leu	Ile
			20					25					30		

Ala Ser Xaa Ala Phe Asn
35

<210> 736

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Cys

<400> 736

Val Lys Ile Ile Ser Arg Gln Ser Leu Gly Lys Gln Asn Val Tyr Asp
1 5 10 15

Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Leu Ile
20 25 30

Ala Ser Xaa Xaa Phe Asn
35

<210> 737

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-

aminopentonic acid, or 2-aminohexanoic acid

<400> 737

```
Val Lys Ile Ile Ser Arg Gln Ser Leu Gly Lys Gln Asn Val Tyr Asp
1           5           10           15
```

```
Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Leu Ile
      20           25           30
```

```
Ala Ser Xaa Xaa Phe Asn
      35
```

<210> 738

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 738

```
Val Lys Ile Ile Ser Arg Gln Ser Leu Gly Lys Gln Asn Val Tyr Asp
1           5           10           15
```

```
Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Leu Ile
      20           25           30
```

```
Ala Ser Xaa Xaa Phe Asn
      35
```

<210> 739

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 739

```
Val Lys Ile Ile Ser Arg Gln Ser Leu Gly Lys Gln Asn Val Tyr Asp
1           5           10           15
```

```
Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Leu Ile
      20           25           30
```

```
Ala Ser Xaa Ala Phe Asn
      35
```

<210> 740

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Cys

<400> 740

```
Val Lys Ile Ile Ser Arg Gln Ser Leu Gly Lys Gln Asn Val Tyr Asp
1           5           10           15
```

```
Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Leu Ile
      20           25           30
```

```
Ala Ser Ala Xaa Phe Asn
      35
```

<210> 741

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 741

```
Val Lys Ile Ile Ser Arg Gln Ser Leu Gly Lys Gln Asn Val Tyr Asp
```

Val Lys Ile Ile Ser Arg Gln Ser Leu Gly Lys Gln Asn Val Tyr Asp
 1 5 10 15

Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Leu Ile
 20 25 30

Ala Ser Ala Xaa Phe Asn
 35

<210> 742

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 742

Val Lys Ile Ile Ser Arg Gln Ser Leu Gly Lys Gln Asn Val Tyr Asp
 1 5 10 15

Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Leu Ile
 20 25 30

Ala Ser Ala Xaa Phe Asn
 35

<210> 743

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<400> 743

Val Lys Ile Ile Ser Arg Gln Ser Leu Gly Lys Gln Asn Val Tyr Asp
 1 5 10 15

Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Leu Ile
 20 25 30

Ala Ser Ala Ala Phe Asn

35

<210> 744

<211> 42

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Cys

<400> 744

Val	Lys	Ile	Ile	Ser	Arg	Gln	Ser	Leu	Gly	Lys	Gln	Asn	Val	Tyr	Asp
1				5					10					15	

Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Leu	Ile
			20					25					30		

Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40		

<210> 745

<211> 42

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 745

Val	Lys	Ile	Ile	Ser	Arg	Gln	Ser	Leu	Gly	Lys	Gln	Asn	Val	Tyr	Asp
1				5					10					15	

Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Leu Ile
 20 25 30

Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 746

<211> 42

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is any amino acid excluding Asn and/or Gln

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 746

Val Lys Ile Ile Ser Arg Gln Ser Leu Gly Lys Gln Asn Val Tyr Asp
 1 5 10 15

Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Leu Ile
 20 25 30

Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 747

<211> 42

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is any amino acid excluding Asn and/or Gln

<400> 747

Val Lys Ile Ile Ser Arg Gln Ser Leu Gly Lys Gln Asn Val Tyr Asp
 1 5 10 15

Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Leu Ile

20

25

30

Ala Ser Xaa Ala Phe Asn Ser Gly Gly Cys
35 40

<210> 748

<211> 42

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Cys

<400> 748

Val Lys Ile Ile Ser Arg Gln Ser Leu Gly Lys Gln Asn Val Tyr Asp
1 5 10 15

Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Leu Ile
20 25 30

Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
35 40

<210> 749

<211> 42

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural

aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 749

```
Val Lys Ile Ile Ser Arg Gln Ser Leu Gly Lys Gln Asn Val Tyr Asp
1          5          10          15

Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Leu Ile
      20          25          30

Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
      35          40
```

<210> 750

<211> 42

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 750

```
Val Lys Ile Ile Ser Arg Gln Ser Leu Gly Lys Gln Asn Val Tyr Asp
1          5          10          15

Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Leu Ile
      20          25          30

Ala Ser Xaa Xaa Phe Asn Ser Gly Gly Cys
      35          40
```

<210> 751

<211> 42

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 751

Val	Lys	Ile	Ile	Ser	Arg	Gln	Ser	Leu	Gly	Lys	Gln	Asn	Val	Tyr	Asp
1				5					10					15	

Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Leu	Ile
			20					25					30		

Ala	Ser	Xaa	Ala	Phe	Asn	Ser	Gly	Gly	Cys
		35					40		

<210> 752

<211> 42

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Cys

<400> 752

Val	Lys	Ile	Ile	Ser	Arg	Gln	Ser	Leu	Gly	Lys	Gln	Asn	Val	Tyr	Asp
1				5					10					15	

Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Leu	Ile
			20					25					30		

Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40		

<210> 753

<211> 42

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentoic acid, or 2-aminohexaanoic acid

<400> 753

Val	Lys	Ile	Ile	Ser	Arg	Gln	Ser	Leu	Gly	Lys	Gln	Asn	Val	Tyr	Asp
1				5					10					15	

Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Leu	Ile
			20					25					30		

Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40		

<210> 754

<211> 42

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 754

Val	Lys	Ile	Ile	Ser	Arg	Gln	Ser	Leu	Gly	Lys	Gln	Asn	Val	Tyr	Asp
1				5					10					15	

Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Leu	Ile
			20					25					30		

Ala	Ser	Xaa	Xaa	Phe	Asn	Ser	Gly	Gly	Cys
		35					40		

<210> 755

<211> 42

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (35)..(35)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 755

Val	Lys	Ile	Ile	Ser	Arg	Gln	Ser	Leu	Gly	Lys	Gln	Asn	Val	Tyr	Asp
1				5					10					15	

Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Leu	Ile
			20					25					30		

Ala	Ser	Xaa	Ala	Phe	Asn	Ser	Gly	Gly	Cys
		35					40		

<210> 756

<211> 42

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is any amino acid excluding Cys

<400> 756

Val	Lys	Ile	Ile	Ser	Arg	Gln	Ser	Leu	Gly	Lys	Gln	Asn	Val	Tyr	Asp
1				5					10					15	

Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Leu	Ile
			20					25					30		

Ala Ser Ala Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 757

<211> 42

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Val, Ile, Ser, Met, His, Leu, Phe, Tyr, Gly or Trp or can be a unnatural aliphatic amino acid residue such as norleucine, 2-aminobutyric acid, nor-valine, 2-aminopentonic acid, or 2-aminohexanoic acid

<400> 757

Val Lys Ile Ile Ser Arg Gln Ser Leu Gly Lys Gln Asn Val Tyr Asp
 1 5 10 15

Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Leu Ile
 20 25 30

Ala Ser Ala Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 758

<211> 42

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> Xaa is Ala, Ile, Val, Leu, Tyr, Gly or Phe

<400> 758

Val Lys Ile Ile Ser Arg Gln Ser Leu Gly Lys Gln Asn Val Tyr Asp
 1 5 10 15

Ile Gly Val Glu Lys Asp His Asn Phe Leu Leu Ala Asn Gly Leu Ile
 20 25 30

Ala Ser Ala Xaa Phe Asn Ser Gly Gly Cys
 35 40

<210> 759

<211> 42

<212> PRT

<213> Artificial Sequence

<220>

<223> C-fragment consensus sequence

<400> 759

Val	Lys	Ile	Ile	Ser	Arg	Gln	Ser	Leu	Gly	Lys	Gln	Asn	Val	Tyr	Asp
1				5				10					15		

Ile	Gly	Val	Glu	Lys	Asp	His	Asn	Phe	Leu	Leu	Ala	Asn	Gly	Leu	Ile
			20					25					30		

Ala	Ser	Ala	Ala	Phe	Asn	Ser	Gly	Gly	Cys
		35					40		

<210> 760

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> c-myc epitope tag

<400> 760

Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu
1				5				10	

<210> 761

<211> 102

<212> PRT

<213> Artificial Sequence

<220>

<223> N-fragment modified consensus sequence

<220>

<221> MISC_FEATURE

<222> (28)..(28)

<223> Xaa is Ala or Ser

<220>

<221> MISC_FEATURE

<222> (59)..(59)

<223> Xaa is Ala or Ser

<400> 761

Cys	Leu	Ser	Tyr	Asp	Thr	Glu	Ile	Leu	Thr	Val	Glu	Tyr	Gly	Ala	Val
1				5				10					15		

Pro Ile Gly Lys Ile Val Glu Glu Asn Ile Glu Xaa Thr Val Tyr Ser
20 25 30

Val Asp Glu Asn Gly Phe Val Tyr Thr Gln Pro Ile Ala Gln Trp His
35 40 45

Asp Arg Gly Glu Gln Glu Val Phe Glu Tyr Xaa Leu Glu Asp Gly Ser
50 55 60

Thr Ile Arg Ala Thr Lys Asp His Lys Phe Met Thr Glu Asp Gly Glu
65 70 75 80

Met Leu Pro Ile Asp Glu Ile Phe Glu Gln Gly Leu Asp Leu Lys Gln
85 90 95

Val Lys Gly Leu Pro Asp
100

<210> 762

<211> 196

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 762

Met His His His His His Gly Gly Met Gln Ile Phe Val Lys Thr
1 5 10 15

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

Asp Asn Val Lys Ser Lys Ile Gln Asp Lys Glu Gly Ile Pro Pro Asp
35 40 45

Gln Gln Glu Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp Gly Arg Thr
50 55 60

Leu Ser Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His Leu Val Leu
65 70 75 80

Arg Leu Arg Gly Gly Gly Gly Gly Lys Phe Ala Glu Tyr Cys Leu
85 90 95

Ser Tyr Glu Thr Glu Ile Leu Thr Val Glu Tyr Gly Leu Leu Pro Ile
100 105 110

Gly Lys Ile Val Glu Lys Arg Ile Glu Cys Thr Val Tyr Ser Val Asp
115 120 125

Asn Asn Gly Asn Ile Tyr Thr Gln Pro Val Ala Gln Trp His Asp Arg
130 135 140

Gly Glu Gln Glu Val Phe Glu Tyr Cys Leu Glu Asp Gly Ser Leu Ile
 145 150 155 160

Arg Ala Thr Lys Asp His Lys Phe Met Thr Val Asp Gly Gln Met Leu
 165 170 175

Pro Ile Asp Glu Ile Phe Glu Arg Glu Leu Asp Leu Met Arg Val Asp
 180 185 190

Asn Leu Pro Asn
 195

<210> 763

<211> 192

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 763

Met His His His His His His Gly Gly Met Gln Ile Phe Val Lys Thr
 1 5 10 15

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

Asp Asn Val Lys Ser Lys Ile Gln Asp Lys Glu Gly Ile Pro Pro Asp
 35 40 45

Gln Gln Glu Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp Gly Arg Thr
 50 55 60

Leu Ser Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His Leu Val Leu
 65 70 75 80

Arg Leu Arg Gly Gly Lys Phe Ala Glu Tyr Cys Leu Ser Tyr Glu Thr
 85 90 95

Glu Ile Leu Thr Val Glu Tyr Gly Leu Leu Pro Ile Gly Lys Ile Val
 100 105 110

Glu Lys Arg Ile Glu Cys Thr Val Tyr Ser Val Asp Asn Asn Gly Asn
 115 120 125

Ile Tyr Thr Gln Pro Val Ala Gln Trp His Asp Arg Gly Glu Gln Glu
 130 135 140

Val Phe Glu Tyr Cys Leu Glu Asp Gly Ser Leu Ile Arg Ala Thr Lys
 145 150 155 160

Asp His Lys Phe Met Thr Val Asp Gly Gln Met Leu Pro Ile Asp Glu
 165 170 175

Ile Phe Glu Arg Glu Leu Asp Leu Met Arg Val Asp Asn Leu Pro Asn

180

185

190

<210> 764

<211> 156

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 764

Gly Ile Lys Ile Ala Thr Arg Lys Tyr Leu Gly Lys Gln Asn Val Tyr
 1 5 10 15

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

Ile Ala Ser Asn Cys Phe Asn Ser Gly Leu Val Pro Arg Gly Ser Ala
 35 40 45

Ser Met Ser Asp Ser Glu Val Asn Gln Glu Ala Lys Pro Glu Val Lys
 50 55 60

Pro Glu Val Lys Pro Glu Thr His Ile Asn Leu Lys Val Ser Asp Gly
 65 70 75 80

Ser Ser Glu Ile Phe Phe Lys Ile Lys Lys Thr Thr Pro Leu Arg Arg
 85 90 95

Leu Met Glu Ala Phe Ala Lys Arg Gln Gly Lys Glu Met Asp Ser Leu
 100 105 110

Arg Phe Leu Tyr Asp Gly Ile Arg Ile Gln Ala Asp Gln Thr Pro Glu
 115 120 125

Asp Leu Asp Met Glu Asp Asn Asp Ile Ile Glu Ala His Arg Glu Gln
 130 135 140

Ile Gly Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
 145 150 155

<210> 765

<211> 283

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 765

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

Val Glu Pro Ser Asp Thr Ile Glu Asn Val Lys Ala Lys Ile Gln Asp
 20 25 30 35 40 45 50 55 60

20	25	30
Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys		
35	40	45
Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu		
50	55	60
Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Cys Ile Thr Gly		
65	70	75
Asp Ala Leu Val Ala Leu Pro Glu Gly Glu Ser Val Arg Ile Ala Asp		
85	90	95
Ile Val Pro Gly Ala Arg Pro Asn Ser Asp Asn Ala Ile Asp Leu Lys		
100	105	110
Val Leu Asp Arg His Gly Asn Pro Val Leu Ala Asp Arg Leu Phe His		
115	120	125
Ser Gly Glu His Pro Val Tyr Thr Val Arg Thr Val Glu Gly Leu Arg		
130	135	140
Val Thr Gly Thr Ala Asn His Pro Leu Leu Cys Leu Val Asp Val Ala		
145	150	155
Gly Val Pro Thr Leu Leu Trp Lys Leu Ile Asp Glu Ile Lys Pro Gly		
165	170	175
Asp Tyr Ala Val Ile Gln Arg Ser Ala Phe Ser Val Asp Cys Ala Gly		
180	185	190
Phe Ala Arg Gly Lys Pro Glu Phe Ala Pro Thr Thr Tyr Thr Val Gly		
195	200	205
Val Pro Gly Leu Val Arg Phe Leu Glu Ala His His Arg Asp Pro Asp		
210	215	220
Ala Gln Ala Ile Ala Asp Glu Leu Thr Asp Gly Arg Phe Tyr Tyr Ala		
225	230	235
Lys Val Ala Ser Val Thr Asp Ala Gly Val Gln Pro Val Tyr Ser Leu		
245	250	255
Arg Val Asp Thr Ala Asp His Ala Phe Ile Thr Asn Gly Phe Val Ser		
260	265	270
His Ala Thr Glu Ala His His His His His His		
275	280	

<210> 766

<211> 222

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 766

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

Val Glu Pro Ser Asp Thr Ile Glu Asn Val Lys Ala Lys Ile Gln Asp
 20 25 30

Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys
 35 40 45

Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu
 50 55 60

Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Cys Leu Ser Tyr
 65 70 75 80

Glu Thr Glu Ile Leu Thr Val Glu Tyr Gly Leu Leu Pro Ile Gly Lys
 85 90 95

Ile Val Glu Lys Arg Ile Glu Cys Thr Val Tyr Ser Val Asp Asn Asn
 100 105 110

Gly Asn Ile Tyr Thr Gln Pro Val Ala Gln Trp His Asp Arg Gly Glu
 115 120 125

Gln Glu Val Phe Glu Tyr Cys Leu Glu Asp Gly Ser Leu Ile Arg Ala
 130 135 140

Thr Lys Asp His Lys Phe Met Thr Val Asp Gly Gln Met Leu Pro Ile
 145 150 155 160

Asp Glu Ile Phe Glu Arg Glu Leu Asp Leu Met Arg Val Asp Asn Leu
 165 170 175

Pro Asn Ile Lys Ile Ala Thr Arg Lys Tyr Leu Gly Lys Gln Asn Val
 180 185 190

Tyr Asp Ile Gly Val Glu Arg Asp His Asn Phe Ala Leu Lys Asn Gly
 195 200 205

Phe Ile Ala Ser Ala Ala Phe Asn His His His His His His
 210 215 220

<210> 767

<211> 222

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 767

Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu

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1             5             10             15
Val Glu Pro Ser Asp Thr Ile Glu Asn Val Lys Ala Lys Ile Gln Asp
      20             25             30
Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys
      35             40             45
Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu
      50             55             60
Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Cys Leu Ser Tyr
      65             70             75             80
Asp Thr Glu Val Leu Thr Val Glu Tyr Gly Phe Val Pro Ile Gly Glu
      85             90             95
Ile Val Asp Lys Gly Ile Glu Cys Ser Val Phe Ser Ile Asp Ser Asn
      100            105            110
Gly Ile Val Tyr Thr Gln Pro Ile Ala Gln Trp His His Arg Gly Lys
      115            120            125
Gln Glu Val Phe Glu Tyr Cys Leu Glu Asp Gly Ser Ile Ile Lys Ala
      130            135            140
Thr Lys Asp His Lys Phe Met Thr Gln Asp Gly Lys Met Leu Pro Ile
      145            150            155            160
Asp Glu Ile Phe Glu Gln Glu Leu Asp Leu Leu Gln Val Lys Gly Leu
      165            170            175
Pro Glu Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val
      180            185            190
Tyr Asp Ile Gly Val Gly Arg Asp His Asn Phe Phe Val Lys Asn Gly
      195            200            205
Leu Ile Ala Ser Ala Ala Phe Asn His His His His His His
      210            215            220

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<210> 768

<211> 224

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 768

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Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu
1             5             10             15
Val Glu Pro Ser Asp Thr Ile Glu Asn Val Lys Ala Lys Ile Gln Asp
      20             25             30

```

Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys
35 40 45

Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu
50 55 60

Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Cys Leu Ser Tyr
65 70 75 80

Asp Thr Gln Ile Leu Thr Val Glu Tyr Gly Ala Val Ala Ile Gly Glu
85 90 95

Ile Val Glu Lys Gln Ile Glu Cys Thr Val Tyr Ser Val Asp Glu Asn
100 105 110

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

Gln Glu Val Phe Glu Tyr Leu Leu Glu Asp Gly Ala Thr Ile Arg Ala
130 135 140

Thr Lys Asp His Lys Phe Met Thr Asp Glu Asp Gln Met Leu Pro Ile

145 150 155 160

Asp Gln Ile Phe Glu Gln Gly Leu Glu Leu Lys Gln Val Glu Val Leu
165 170 175

Gln Pro Val Phe Val Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln
180 185 190

Asn Val Tyr Asp Ile Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala
195 200 205

Ser Gly Glu Ile Ala Ser Ala Ala Phe Asn His His His His His His
210 215 220

<210> 769

<211> 283

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 769

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

Val Glu Pro Ser Asp Thr Ile Glu Asn Val Lys Ala Lys Ile Gln Asp
20 25 30

Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys

```

      35      40      45
Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu
 50      55      60
Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Cys Ile Thr Gly
 65      70      75      80
Asp Ala Leu Val Ala Leu Pro Glu Gly Glu Ser Val Arg Ile Ala Asp
      85      90      95
Ile Val Pro Gly Ala Arg Pro Asn Ser Asp Asn Ala Ile Asp Leu Lys
      100      105      110
Val Leu Asp Arg His Gly Asn Pro Val Leu Ala Asp Arg Leu Phe His
      115      120      125
Ser Gly Glu His Pro Val Tyr Thr Val Arg Thr Val Glu Gly Leu Arg
      130      135      140
Val Thr Gly Thr Ala Asn His Pro Leu Leu Cys Leu Val Asp Val Ala
      145      150      155      160
Gly Val Pro Thr Leu Leu Trp Lys Leu Ile Asp Glu Ile Lys Pro Gly
      165      170      175
Asp Tyr Ala Val Ile Gln Arg Ser Ala Phe Ser Val Asp Cys Ala Gly
      180      185      190
Phe Ala Arg Gly Lys Pro Glu Phe Ala Pro Thr Thr Tyr Thr Val Gly
      195      200      205
Val Pro Gly Leu Val Arg Phe Leu Glu Ala His His Arg Asp Pro Asp
      210      215      220
Ala Gln Ala Ile Ala Asp Glu Leu Thr Asp Gly Arg Phe Tyr Tyr Ala
      225      230      235      240
Lys Val Ala Ser Val Thr Asp Ala Gly Val Gln Pro Val Tyr Ser Leu
      245      250      255
Arg Val Asp Thr Ala Asp His Ala Phe Ile Thr Asn Gly Phe Val Ser
      260      265      270
His Ala Ala Glu Ala His His His His His His
      275      280

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<210> 770

<211> 201

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 770

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

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

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

Pro Lys Asn Tyr Ile Glu Met Cys Leu Ser Tyr Asp Thr Glu Val Leu
 50 55 60

Thr Val Glu Tyr Gly Phe Val Pro Ile Gly Glu Ile Val Asp Lys Gly
 65 70 75 80

Ile Glu Cys Ser Val Phe Ser Ile Asp Ser Asn Gly Ile Val Tyr Thr
 85 90 95

Gln Pro Ile Ala Gln Trp His His Arg Gly Lys Gln Glu Val Phe Glu
 100 105 110

Tyr Cys Leu Glu Asp Gly Ser Ile Ile Lys Ala Thr Lys Asp His Lys
 115 120 125

Phe Met Thr Gln Asp Gly Lys Met Leu Pro Ile Asp Glu Ile Phe Glu
 130 135 140

Gln Glu Leu Asp Leu Leu Gln Val Lys Gly Leu Pro Glu Ile Lys Ile
 145 150 155 160

Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr Asp Ile Gly Val
 165 170 175

Gly Arg Asp His Asn Phe Phe Val Lys Asn Gly Leu Ile Ala Ser Ala
 180 185 190

Ala Phe Asn His His His His His His
 195 200

<210> 771

<211> 202

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 771

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

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

Asp	Gln	Asn	Trp	Tyr	Lys	Ala	Glu	Leu	Asn	Gly	Lys	Asp	Gly	Phe	Ile	35	40	45
Pro	Lys	Asn	Tyr	Ile	Glu	Met	Gly	Cys	Leu	Ser	Tyr	Asp	Thr	Glu	Val	50	55	60
Leu	Thr	Val	Glu	Tyr	Gly	Phe	Val	Pro	Ile	Gly	Glu	Ile	Val	Asp	Lys	65	70	75
Gly	Ile	Glu	Cys	Ser	Val	Phe	Ser	Ile	Asp	Ser	Asn	Gly	Ile	Val	Tyr	85	90	95
Thr	Gln	Pro	Ile	Ala	Gln	Trp	His	His	Arg	Gly	Lys	Gln	Glu	Val	Phe	100	105	110
Glu	Tyr	Cys	Leu	Glu	Asp	Gly	Ser	Ile	Ile	Lys	Ala	Thr	Lys	Asp	His	115	120	125
Lys	Phe	Met	Thr	Gln	Asp	Gly	Lys	Met	Leu	Pro	Ile	Asp	Glu	Ile	Phe	130	135	140
Glu	Gln	Glu	Leu	Asp	Leu	Leu	Gln	Val	Lys	Gly	Leu	Pro	Glu	Ile	Lys	145	150	155
Ile	Ala	Ser	Arg	Lys	Phe	Leu	Gly	Val	Glu	Asn	Val	Tyr	Asp	Ile	Gly	165	170	175
Val	Gly	Arg	Asp	His	Asn	Phe	Phe	Val	Lys	Asn	Gly	Leu	Ile	Ala	Ser	180	185	190
Ala	Ala	Phe	Asn	His	His	His	His	His	His							195	200	

<210> 772

<211> 203

<212> PRT

<213> Artificial Sequence

$\langle 220 \rangle$

<223> Synthetic peptide

<400> 772

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

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

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

Pro Lys Asn Tyr Ile Glu Met Cys Leu Ser Tyr Asp Thr Gln Ile Leu
          50          55          60

```

Thr Val Glu Tyr Gly Ala Val Ala Ile Gly Glu Ile Val Glu Lys Gln

65 70 75 80

Ile Glu Cys Thr Val Tyr Ser Val Asp Glu Asn Gly Tyr Val Tyr Thr
85 90 95

Gln Pro Ile Ala Gln Trp His Asn Arg Gly Glu Gln Glu Val Phe Glu
100 105 110

Tyr Leu Leu Glu Asp Gly Ala Thr Ile Arg Ala Thr Lys Asp His Lys
115 120 125

Phe Met Thr Asp Glu Asp Gln Met Leu Pro Ile Asp Gln Ile Phe Glu
130 135 140

Gln Gly Leu Glu Leu Lys Gln Val Glu Val Leu Gln Pro Val Phe Val
145 150 155 160

Lys Ile Val Arg Arg Gln Ser Leu Gly Val Gln Asn Val Tyr Asp Ile
165 170 175

Gly Val Glu Lys Asp His Asn Phe Cys Leu Ala Ser Gly Glu Ile Ala
180 185 190

Ser Ala Ala Phe Asn His His His His His His
195 200

<210> 773

 $\langle 211 \rangle$ 243

<212> PRT

<213> Artificial Sequence

$\langle 220 \rangle$

<223> Synthetic peptide

<400> 773

Met Leu Glu Lys His Ser Trp Tyr His Gly Pro Val Ser Arg Asn Ala
1 5 10 15

Ala Glu Tyr Leu Leu Ser Ser Gly Ile Asn Gly Ser Phe Leu Val Arg
20 25 30

Glu Ser Glu Ser Ser Pro Gly Gln Arg Ser Ile Ser Leu Arg Tyr Glu
35 40 45

Gly Arg Val Tyr His Tyr Arg Ile Asn Thr Ala Ser Asp Gly Lys Leu
50 55 60

Tyr Val Ser Ser Glu Ser Arg Phe Asn Thr Leu Ala Glu Leu Val His
65 70 75 80

His His Ser Thr Val Ala Asp Gly Leu Ile Thr Thr Leu His Tyr Pro
85 90 95

Ala Cys Leu Ser Tyr Asp Thr Glu Val Leu Thr Val Glu Tyr Gly Phe
100 105 110

Val	Pro	Ile	Gly	Glu	Ile	Val	Asp	Lys	Gly	Ile	Glu	Cys	Ser	Val	Phe
		115					120					125			

Ser Ile Asp Ser Asn Gly Ile Val Tyr Thr Gln Pro Ile Ala Gln Trp
130 135 140

His His Arg Gly Lys Gln Glu Val Phe Glu Tyr Cys Leu Glu Asp Gly
145 150 155 160

Ser Ile Ile Lys Ala Thr Lys Asp His Lys Phe Met Thr Gln Asp Gly
165 170 175

Lys Met Leu Pro Ile Asp Glu Ile Phe Glu Gln Glu Leu Asp Leu Leu
180 185 190

Gln Val Lys Gly Leu Pro Glu Ile Lys Ile Ala Ser Arg Lys Phe Leu
195 200 205

Gly Val Glu Asn Val Tyr Asp Ile Gly Val Gly Arg Asp His Asn Phe
210 215 220

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

His His His

<210> 774

<211> 385

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 774

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

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

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Cys
 225 230 235 240

Leu Ser Tyr Asp Thr Glu Val Leu Thr Val Glu Tyr Gly Phe Val Pro
 245 250 255

Ile Gly Glu Ile Val Asp Lys Gly Ile Glu Cys Ser Val Phe Ser Ile
 260 265 270

Asp Ser Asn Gly Ile Val Tyr Thr Gln Pro Ile Ala Gln Trp His His
 275 280 285

Arg Gly Lys Gln Glu Val Phe Glu Tyr Cys Leu Glu Asp Gly Ser Ile
 290 295 300

Ile Lys Ala Thr Lys Asp His Lys Phe Met Thr Gln Asp Gly Lys Met
 305 310 315 320

Leu Pro Ile Asp Glu Ile Phe Glu Gln Glu Leu Asp Leu Leu Gln Val
 325 330 335

Lys Gly Leu Pro Glu Ile Lys Ile Ala Ser Arg Lys Phe Leu Gly Val
 340 345 350

Glu Asn Val Tyr Asp Ile Gly Val Gly Arg Asp His Asn Phe Phe Val
 355 360 365

Lys Asn Gly Leu Ile Ala Ser Ala Ala Phe Asn His His His His His
 370 375 380

His
 385

J03

<210> 775

<211> 505

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<400> 775

Met Val Asn Pro Gly Thr Lys Ser Lys Leu Pro Lys Pro Val Gln Asp
 1 5 10 15

Leu Ile Lys Met Ile Phe Asp Val Glu Ser Met Lys Lys Ala Met Val
 20 25 30

Glu Tyr Glu Ile Asp Leu Gln Lys Met Pro Leu Gly Lys Leu Ser Lys
 35 40 45

Arg Gln Ile Gln Ala Ala Tyr Ser Ile Leu Ser Glu Val Gln Gln Ala
 50 55 60

Val Ser Gln Gly Ser Ser Asp Ser Gln Ile Leu Asp Leu Ser Asn Arg
 65 70 75 80

Phe Tyr Thr Leu Ile Pro His Asp Phe Gly Met Lys Lys Pro Pro Leu
 85 90 95

Leu Asn Asn Ala Asp Ser Val Gln Ala Lys Ala Glu Met Leu Asp Asn
 100 105 110

Leu Leu Asp Ile Glu Val Ala Tyr Ser Leu Leu Arg Gly Gly Ser Asp
 115 120 125

Asp Ser Ser Lys Asp Pro Ile Asp Val Asn Tyr Glu Lys Leu Lys Thr
 130 135 140

Asp Ile Lys Val Val Asp Arg Asp Ser Glu Glu Ala Glu Ile Ile Arg
 145 150 155 160

Lys Tyr Val Lys Asn Thr His Ala Thr Thr His Asn Ala Tyr Asp Leu
 165 170 175

Glu Val Ile Asp Ile Phe Lys Ile Glu Arg Glu Gly Glu Cys Gln Arg
 180 185 190

Tyr Lys Pro Phe Lys Gln Leu His Asn Arg Arg Leu Leu Trp His Gly
 195 200 205

Ser Arg Thr Thr Asn Phe Ala Gly Ile Leu Ser Gln Gly Leu Arg Ile
 210 215 220

Ala Pro Pro Glu Ala Pro Val Thr Gly Tyr Met Phe Gly Lys Gly Ile
 225 230 235 240

Tyr Phe Ala Asp Met Val Ser Lys Ser Ala Asn Tyr Cys His Thr Ser
 245 250 255
 Gln Gly Asp Pro Ile Gly Leu Ile Leu Leu Gly Glu Val Ala Leu Gly
 260 265 270
 Asn Met Tyr Glu Leu Lys His Ala Ser His Ile Ser Lys Leu Pro Lys
 275 280 285
 Gly Lys His Ser Val Lys Gly Leu Gly Lys Thr Thr Pro Asp Pro Ser
 290 295 300
 Ala Asn Ile Ser Leu Asp Gly Val Asp Val Pro Leu Gly Thr Gly Ile
 305 310 315 320
 Ser Ser Gly Val Asn Asp Thr Ser Leu Leu Tyr Asn Glu Tyr Ile Val
 325 330 335
 Tyr Asp Ile Ala Gln Val Asn Leu Lys Tyr Leu Leu Lys Leu Lys Phe
 340 345 350
 Asn Phe Lys Thr Ser Leu Trp Cys Leu Ser Tyr Asp Thr Glu Val Leu
 355 360 365
 Thr Val Glu Tyr Gly Phe Val Pro Ile Gly Glu Ile Val Asp Lys Gly
 370 375 380
 Ile Glu Cys Ser Val Phe Ser Ile Asp Ser Asn Gly Ile Val Tyr Thr
 385 390 395 400
 Gln Pro Ile Ala Gln Trp His His Arg Gly Lys Gln Glu Val Phe Glu
 405 410 415
 Tyr Cys Leu Glu Asp Gly Ser Ile Ile Lys Ala Thr Lys Asp His Lys
 420 425 430
 Phe Met Thr Gln Asp Gly Lys Met Leu Pro Ile Asp Glu Ile Phe Glu
 435 440 445
 Gln Glu Leu Asp Leu Leu Gln Val Lys Gly Leu Pro Glu Ile Lys Ile
 450 455 460
 Ala Ser Arg Lys Phe Leu Gly Val Glu Asn Val Tyr Asp Ile Gly Val
 465 470 475 480
 Gly Arg Asp His Asn Phe Phe Val Lys Asn Gly Leu Ile Ala Ser Ala
 485 490 495
 Ala Phe Asn His His His His His His
 500 505

<210> 776

<211> 39

<212> PRT

<213> Nostoc punctiforme

<400> 776

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

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

```

```

Ile Ala Ser Asn Cys Phe Asn
          35

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<210> 777

<211> 43

<212> PRT

<213> Nostoc punctiforme

<400> 777

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

```

```

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

```

```

Ile Ala Ser Ala Ala Phe Asn Ser Gly Gly Cys
          35           40

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This list of references cited by the applicant is for the reader's convenience only. It does not form part of the European patent document. Even though great care has been taken in compiling the references, errors or omissions cannot be excluded and the EPO disclaims all liability in this regard.

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PATENTKRAV

1. Fremgangsmåde, der omfatter

(a) etablering af kontakt (1) mellem et fusionsprotein, der omfatter et polypeptid, og et spaltet intein-N-fragment, der omfatter en sekvens valgt fra gruppen bestående af SEQ ID NO: 1-19, eller en variant deraf, hvor varianten består af en sekvens valgt fra gruppen bestående af SEQ ID NO: 21-38 og 761, og (2) et spaltet intein-C-fragment, der omfatter en sekvens valgt fra gruppen bestående af SEQ ID NO: 57-74 og 708 eller en variant deraf, hvor varianten består af en sekvens valgt fra gruppen bestående af SEQ ID NO: 75-128, 707 og 709-711,

hvor etablering af kontakt sker under forhold, der muliggør binding af det spaltede intein-N-fragment til det spaltede intein-C-fragment for at danne et intein-mellemprodukt; og

(b) etablering af kontakt mellem inteinmellemproduktet og en nukleofil for at danne et konjugat af proteinet og nukleofilen.

2. Fremgangsmåde ifølge krav 1, hvor det spaltede intein-C-fragment bindes til en bærer.

3. Fremgangsmåde ifølge et hvilket som helst af kravene 1 eller 2, hvor fusionsproteinet er i et helcellelysat eller er fra en cellesupernatant.

4. Fremgangsmåde ifølge krav 3, der endvidere omfatter vask af inteinmellemproduktet for at separere inteinmellemproduktet fra komponenter af helcellelysatet eller fra cellesupernatanten.

5. Fremgangsmåde ifølge et hvilket som helst af kravene 1 til 4, hvor polypeptidet har en molekylvægt på 40 kDa eller større, hvor polypeptidet er et antistof, eller fragment deraf, eller hvor polypeptidet sekreteres fra en celle.

6. Fremgangsmåde ifølge et hvilket som helst af kravene 1 til 5, der endvidere omfatter isolering af konjugatet.

7. Fremgangsmåde ifølge et hvilket som helst af kravene 1 til 6, hvor nukleofilen omfatter et andet polypeptid, et oligonukleotid, en nanopartikel, et lægemiddel eller en polymer.

8. Fremgangsmåde ifølge et hvilket som helst af kravene 1 til 7, hvor nukleofilen omfatter en thiol og konjugatet omfatter en thioester, hvor eventuelt thiolen er 2-mercaptoethansulfonat,

en alkylthiol eller en arylthiol.

9. Fremgangsmåde ifølge krav 8, der endvidere omfatter omsætning af thioesteren med en anden nukleofil for at danne et andet konjugat.

5

10. Fremgangsmåde ifølge krav 9, hvor den anden nukleofil omfatter et amin, et hydrazin eller en amino-oxy-del.

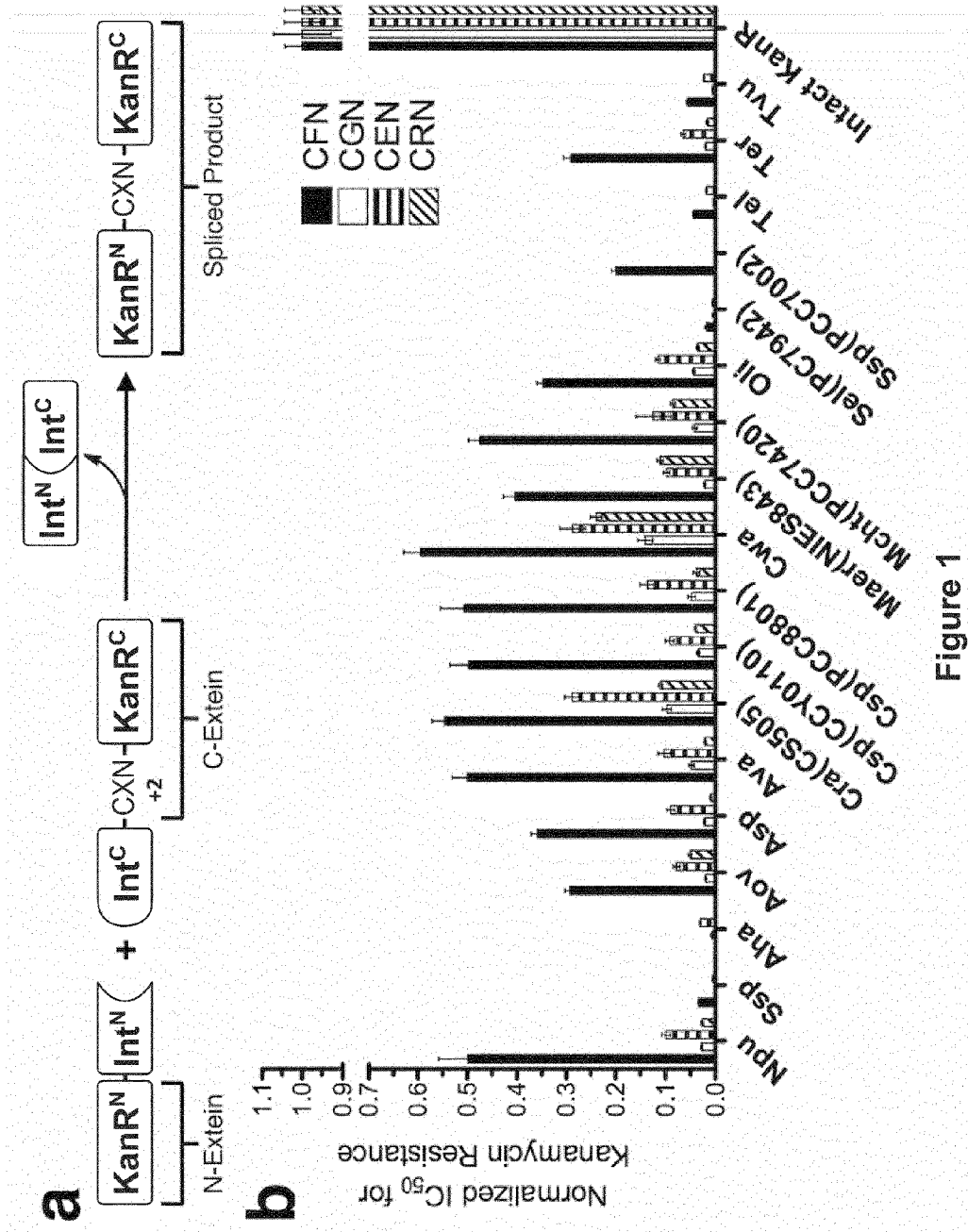
11. Komplex, der omfatter (i) et fusionsprotein omfattende et spaltet intein-N-fragment og et polypeptid, hvor det spaltede intein-N-fragment omfatter en sekvens valgt fra gruppen bestående af SEQ ID NO: 6, 1-5, 7-38 og 761, og (ii) et spaltet intein-C-fragment omfattende en sekvens valgt fra gruppen bestående af SEQ ID NO: 57-128, 417-704, 707-711 eller 745-759.

12. Komplex ifølge krav 11, hvor polypeptidet har en molekylvægt på 40 kDa eller større, hvor polypeptidet er et antistof eller fragment deraf, eller hvor polypeptidet er sekreteret fra en celle.

13. Komplex ifølge et hvilket som helst af kravene 11 eller 12, hvor det spaltede intein-C-fragment er bundet til en bærer.

20

DRAWINGS



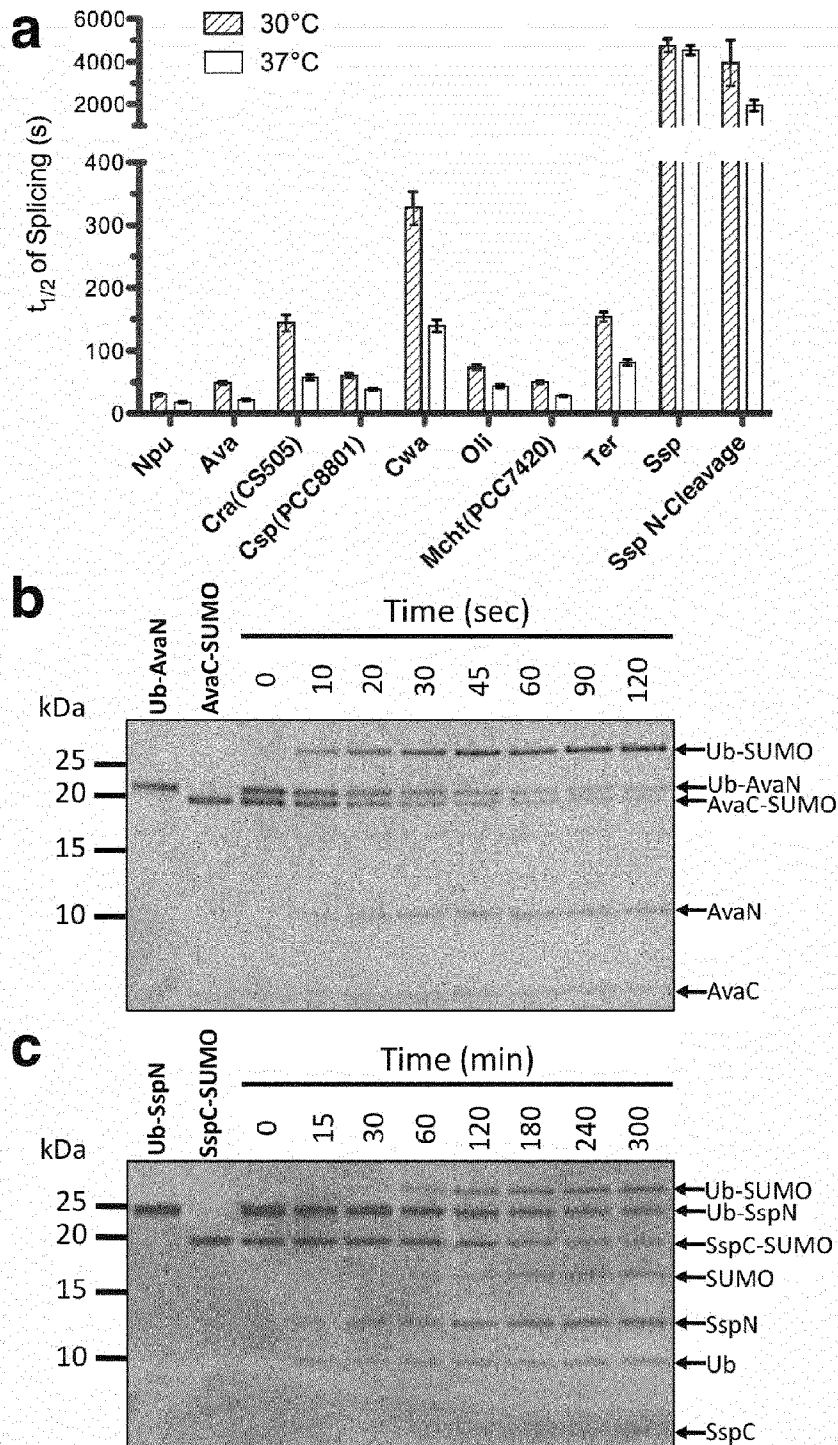


Figure 2

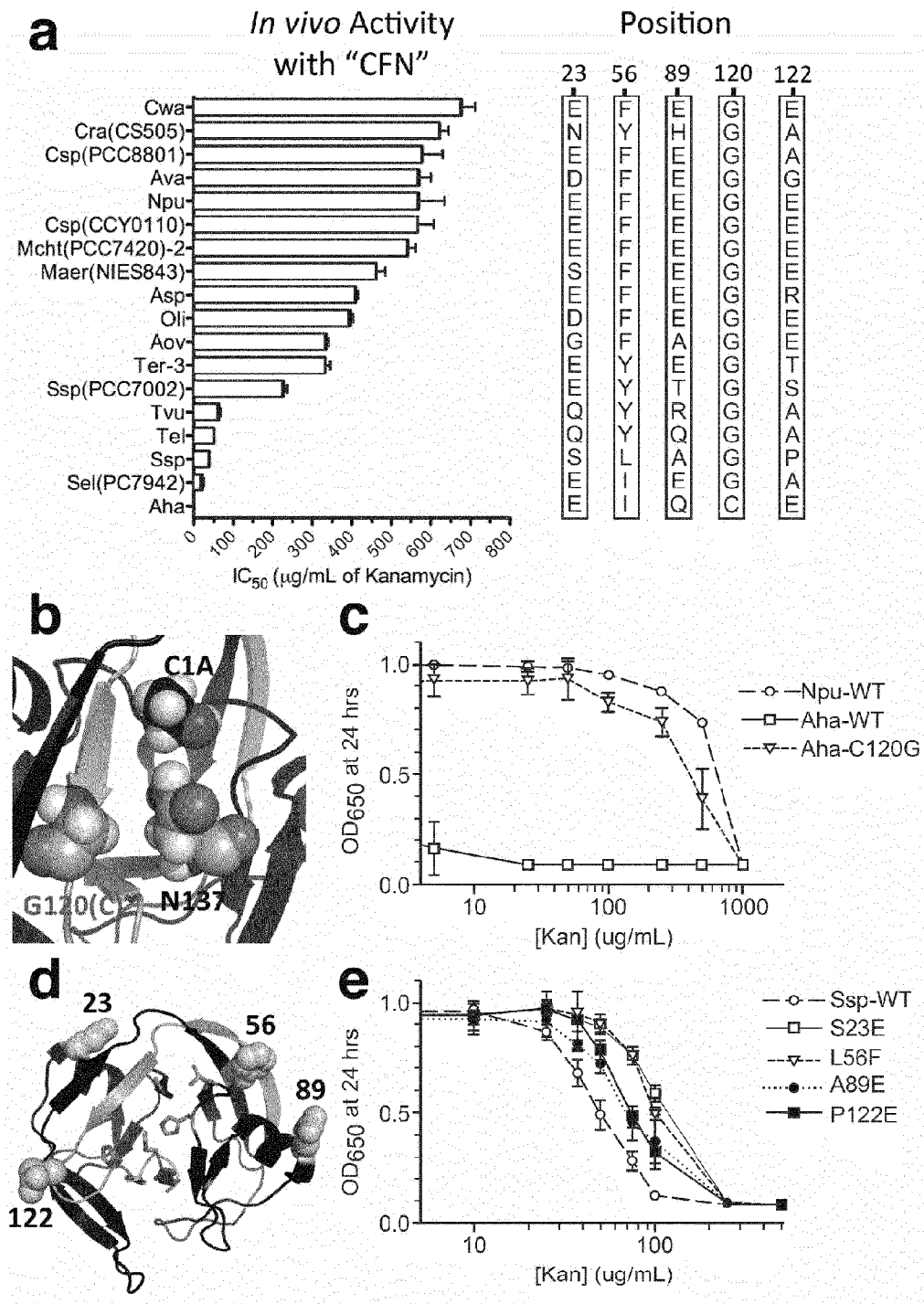


Figure 3

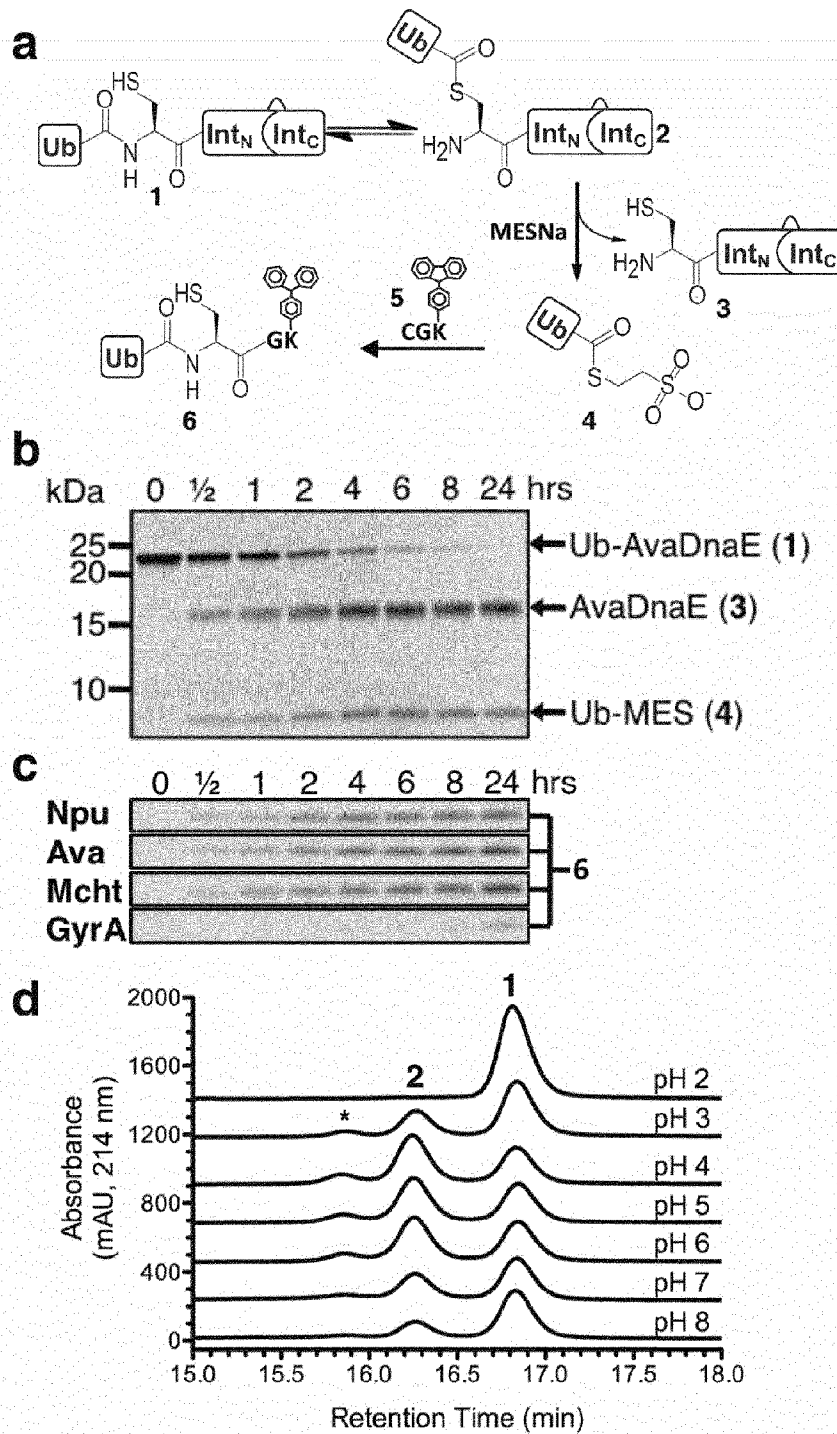


Figure 4

NAME N-INTEIN SEQUENCE

Npu	CLSYETELITVEYGLPIGKIVERN	ECTVYSVDNNGNITYTQPV	AQWHDREGQEVFEYCL	EDGS	IRATKDHKEMTV
Ssp	CLSFGTETLTVEYGPLPIGKIVSEK	INCSVYSDPDEGRVYTQA	IAQWHDREGQEVFEYCL	EDGS	IRATSDHRFLTT
Aha	CLSYDTEILTVEYGAMPPIGKIVSEK	IECSVYTVDENGCVYTQPI	IAQWHPGQOEI	IEYTL	EDGRKIRATKDHKMMTE
Aov	CLSADTEILTVEYGFPIGKIVGKA	IECBVYSDGNGNITYTQS	IAQWHDREGQEVFEYTL	EDGS	IRATKDHKEMTT
Asp	CLSYDTEILTVEYGFVPICEIVKSG	IECSVFSINNGIVYTQPI	IAQWHDREGQEVFEYCL	EDGS	IRATKDHKEMTQ
Ava	CLSYDTEILTVEYGFVPICEIVDRG	IECSVFSIDNSGIVYTQPI	IAQWHDREGQEVFEYCL	EDGS	IRATKDHKEMTQ
Cra(CS505)	CLSYETEVLITVEYGFVPICEIVNQ	IMQVCTVFSLNDGIVYTQPI	IAQWHDREGQEVFEYCL	EDGS	IRATKDHKEMTT
Csp(CCY0110)	CLSYDTEILTVEYGPMPPIGKIVERN	INCSVYTVNKGCVYTQS	IAQWHDREGQEVFEYCL	EDGS	IRATKDHKEMTT
Csp(PCC8801)	CLSYDTEILTVEYGAIPIGKIVERN	INDCTVYTVDRNGCVYTQN	IAQWHLRGQOEI	IEYCL	BDGSILRATKDHQFMTL
Cwa	CLSYDTEILTVEYGAMYIGKIVERN	INDCTVYTVDRNGCVYTQT	IAQWHDREGQEVFEYCL	EDGS	IRATKDHKEMTT
Maer(NIES843)	CLCGETLITVEYGLPIGKIVSEK	IEACTVYTVDRNGCVYTQPI	IAQWHDREGQEVFEYCL	EDGS	IRATKDHKEMTT
Mcht(PCC7420)	CLSYDTEILTVEYGAIPICEIVDRG	IECSVFSIDNSGIVYTQPI	IAQWHDREGQEVFEYCL	EDGS	IRATKDHKEMTT
Oli	CLSYNTEVLITVEYGPLPIGKIVDRQ	IEHCBVYSDENGCVYTQA	IAQWHDREGQEVFEYCL	EDGS	IRATKDHKEMTT
Sel(PC7942)	CLAADTEVLITVEYGPPIGKIVSEK	IEHCBVYSDENGCVYTQA	IAQWHDREGQEVFEYCL	EDGS	IRATKDHKEMTT
Ssp(PCC7002)	CLAGGTPTVTVEYGPLPIQITIVSEK	IEHCBVYSDAQGLIYAQL	IEQWHDREGQEVFEYCL	EDGS	IRATADHRFMTT
Tel	CLSGETAVMTVEYGAIPIRRLVOER	IESCHVYSLDGGHLYTQPI	IAQWHDREGQEVFEYCL	EDGS	IRATPDHRFMTT
Ter	CLTYETEIMTVEYGPLPIGKIVSEK	IEACTVYTVDRNGIVYTQPI	IAQWHDREGQEVFEYCL	EDGS	IRATPDHRFMTT
Tvu	CLSGETAVMTVEYGAIPIRRLVOER	IESCHVYSLDGGHLYTQPI	IAQWHDREGQEVFEYCL	EDGS	IRATPDHRFMTT
Npu	DGQMLPIDEIFEREIDIMRVDNLPN	-----	-----	-----	-----
Ssp	DYQLLAIEEIFARQLDLTLLENIKQ	TEEALDNHLPFPPLDAGT	IK	-----	-----
Aha	SGEMLPIDEIFQRELDLKVETTFH	MSLLRGAN	-----	-----	-----
Aov	DGEMLPIDEIFARQLDLMQVQGLH	-----	-----	-----	-----
Asp	VDGKMLPIDEIFEQELDLQVKGLP	-----	-----	-----	-----
Ava	VDGKMLPIDEIFEQELDLQVKGLP	-----	-----	-----	-----
Cra(CS505)	DGEMVPIDEIFHOGWELVQVSGIS	KLVQDNLPTIVDRSL	-----	-----	-----
Csp(CCY0110)	EGKMLPIDEIFENNLDKRLTY	-----	-----	-----	-----
Csp(PCC8801)	EGEMLPIDEIFERGLERKRT	-----	-----	-----	-----
Cwa	DGEMLPIDEIFERNLDLKQVSH	PDQYLV	-----	-----	-----
Maer(NIES843)	DGEMLAIDTIFERGLDLKSSDFS	-----	-----	-----	-----
Mcht(PCC7420)	EDQMLPIDQIFEQGLELKVQEVLP	VPF	-----	-----	-----
Oli	DGQMFPIDEIEWEGLDLKLPVQDL	PPAAVGYTVS	-----	-----	-----
Sel(PC7942)	EGEMLSLDEIFEESLELKIPTPLLA	IAQPSPLATA	-----	-----	-----
Ssp(PCC7002)	TGELLPIDEIFTQNLQLAAWAV	PDSPETA	-----	-----	-----
Tel	RGQMLPIEQIFQEGLELWQVAI	APPAALQGLP	PAVQMSG	-----	-----
Ter	DGQMLPIDEIFERNLDLKLGL	LE	-----	-----	-----
Tvu	SGQMLPIEQIFEGLELWQVAI	APPCALQGLP	PAVQMSG	-----	-----

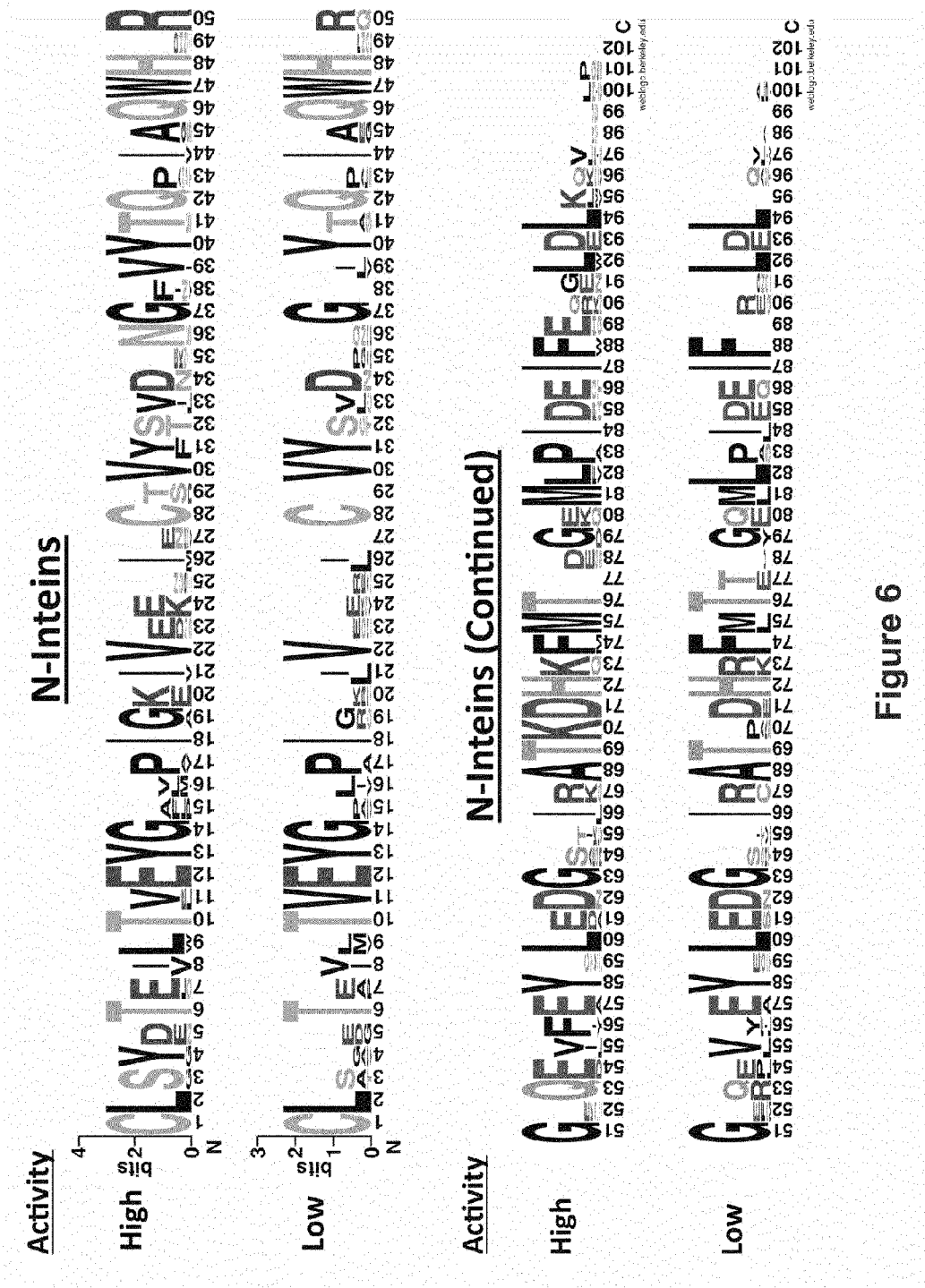
Figure 5

Name	C-Intron Sequence																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												
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Figure 5 (CONT)



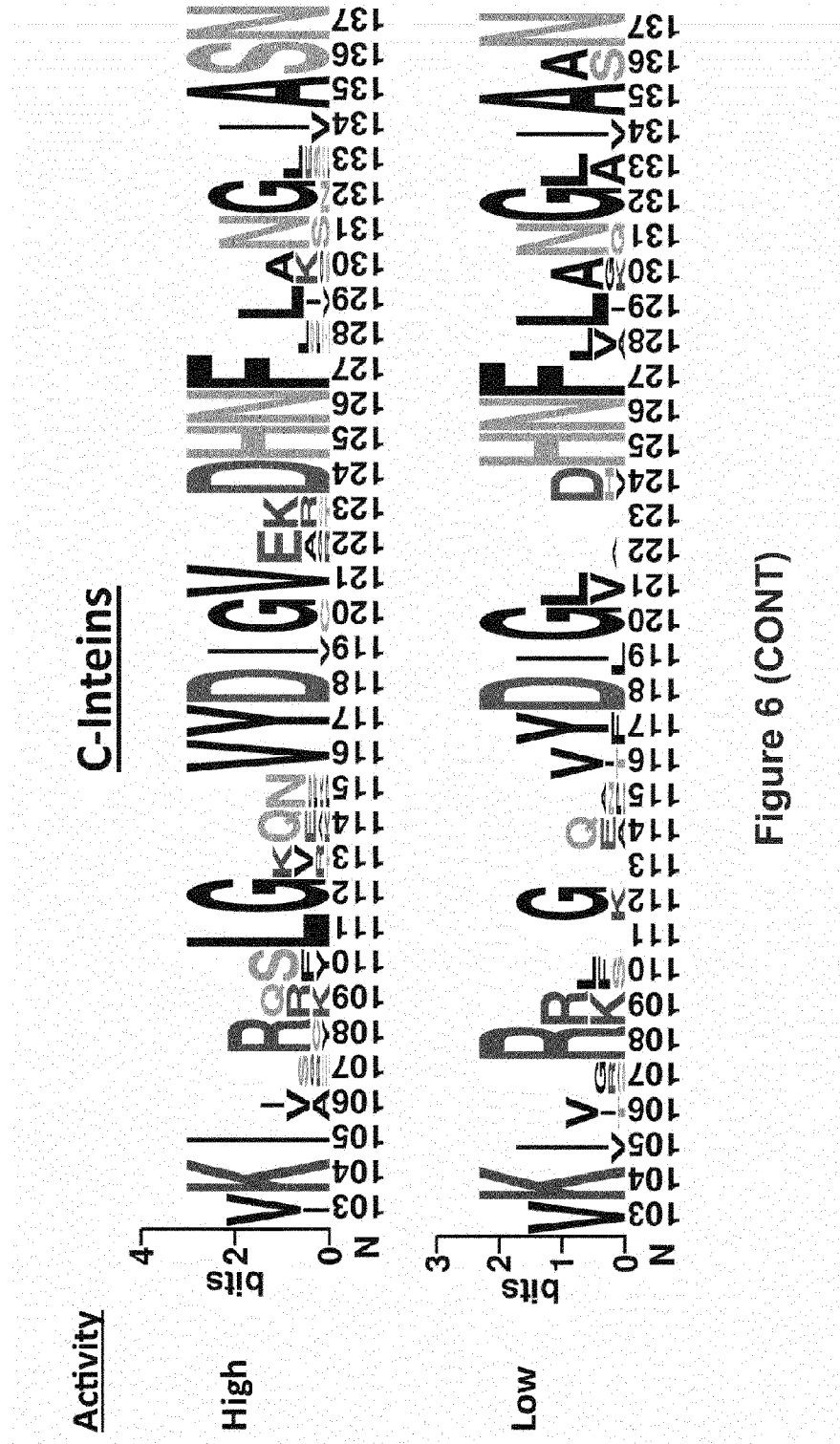


Figure 6 (CONT)

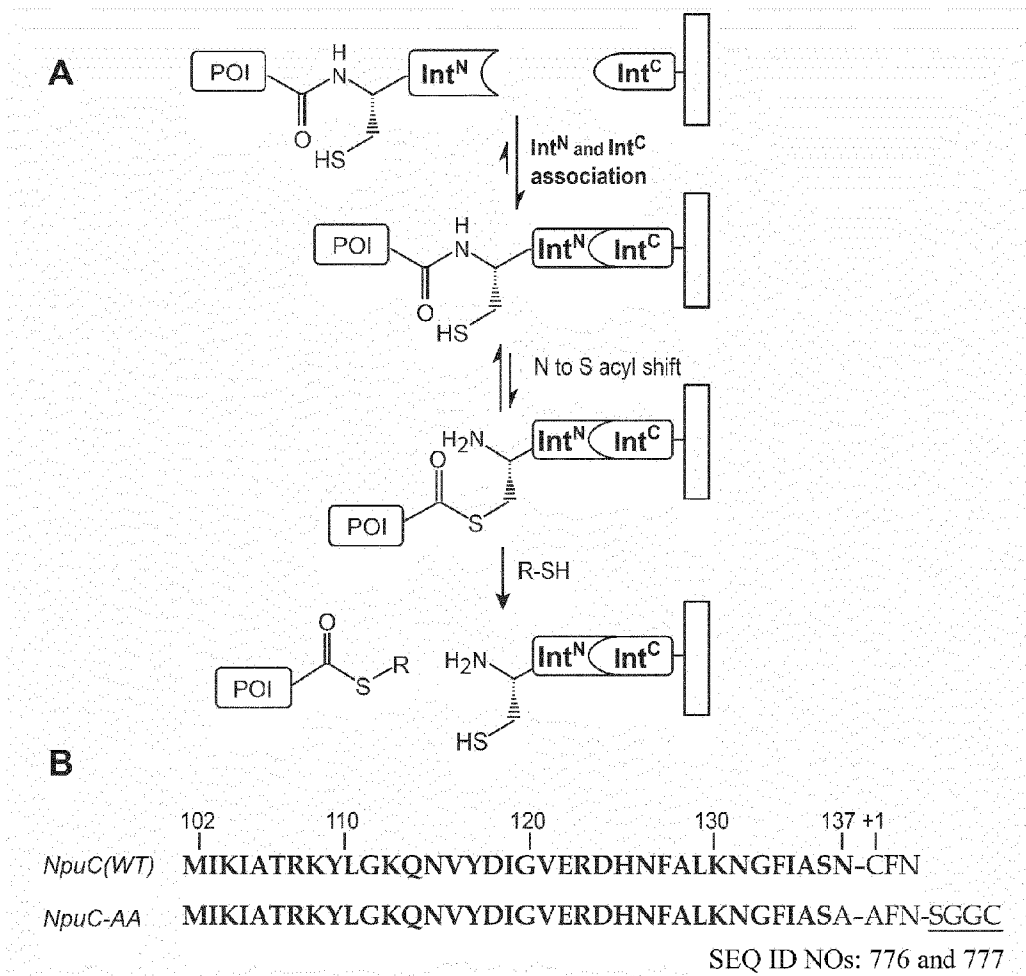
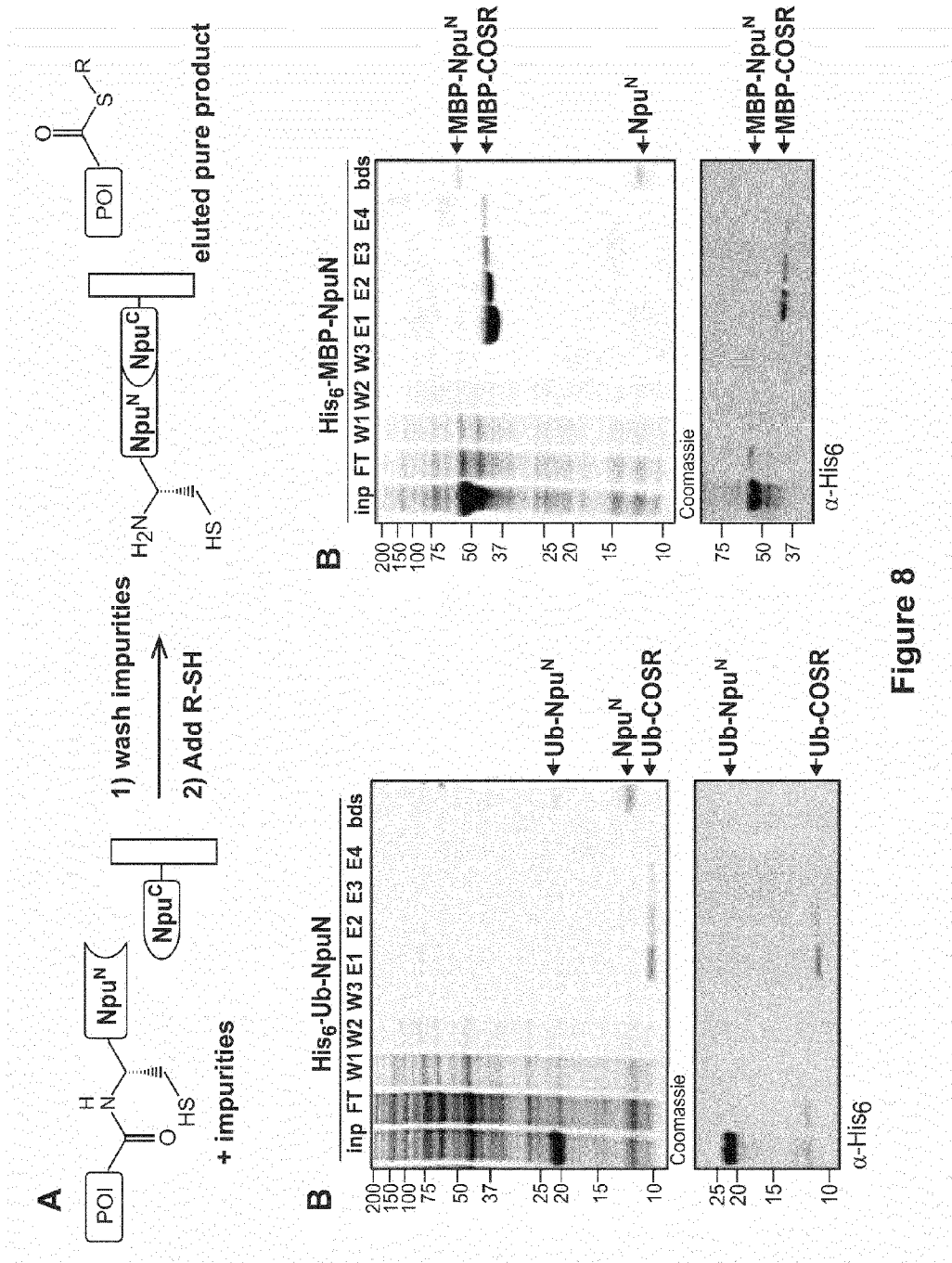
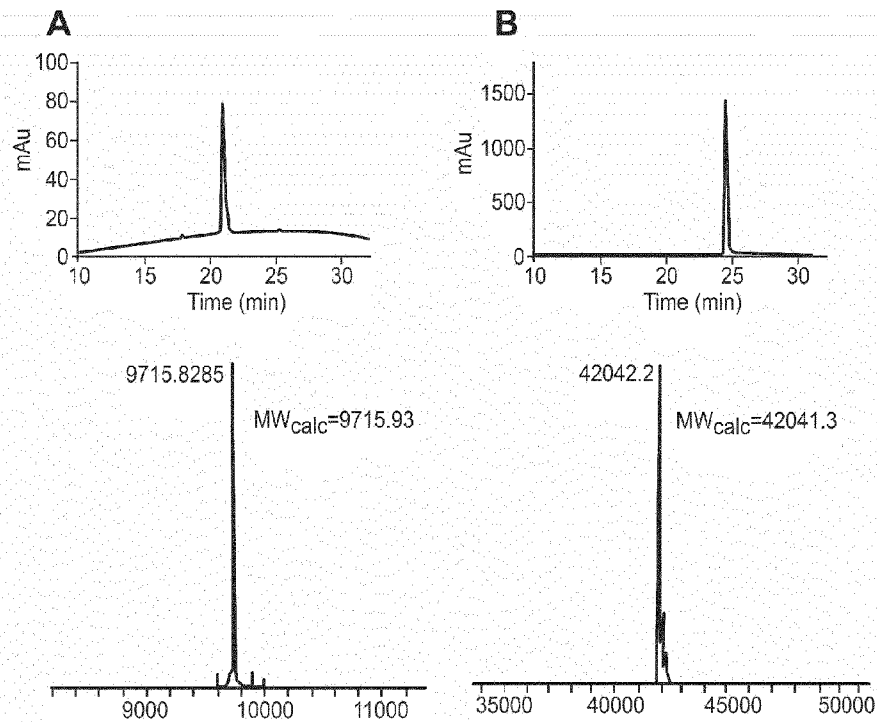
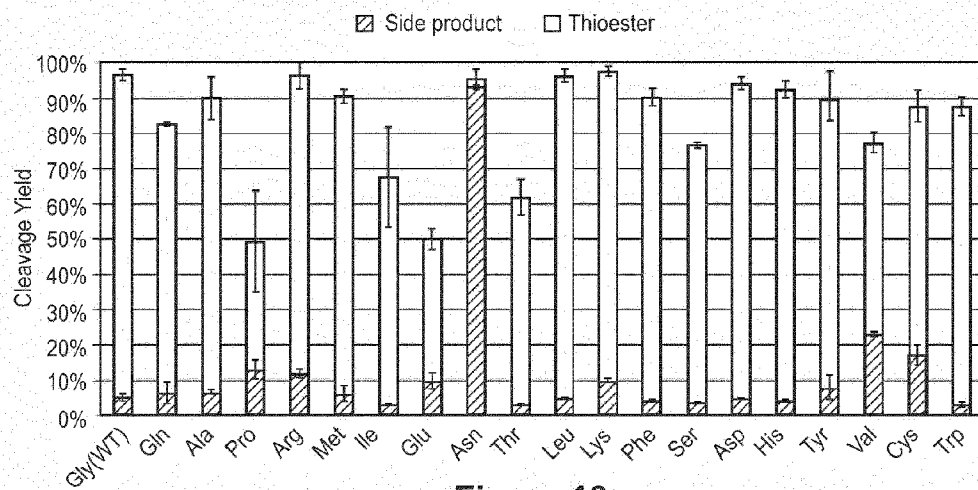


Figure 7



**Figure 9****Figure 10**

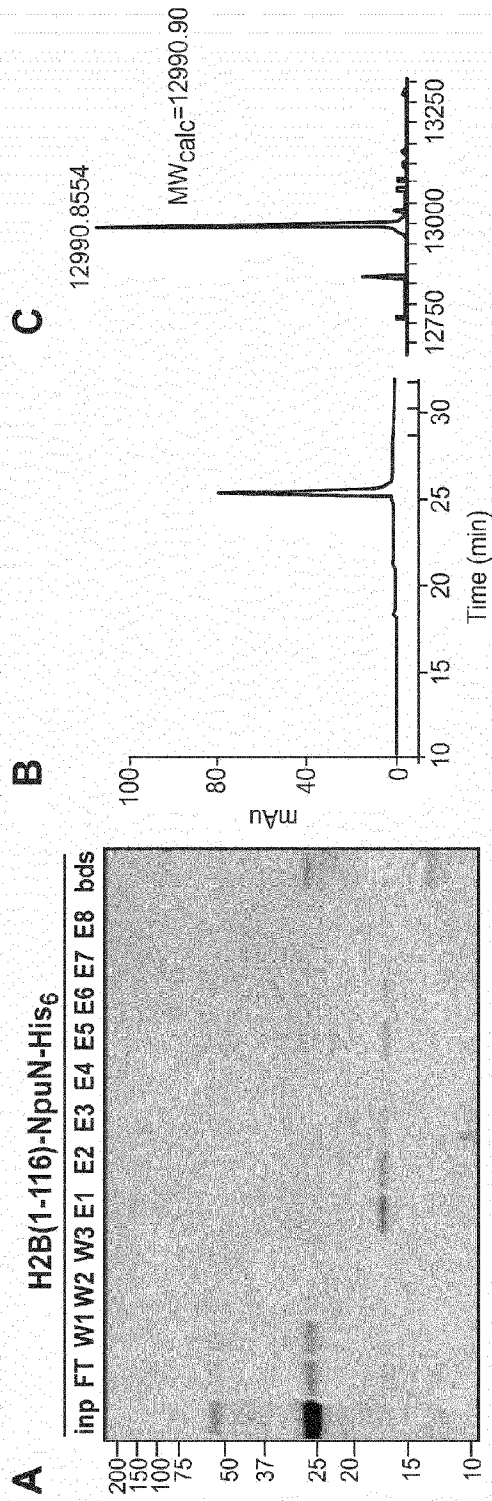


Figure 11

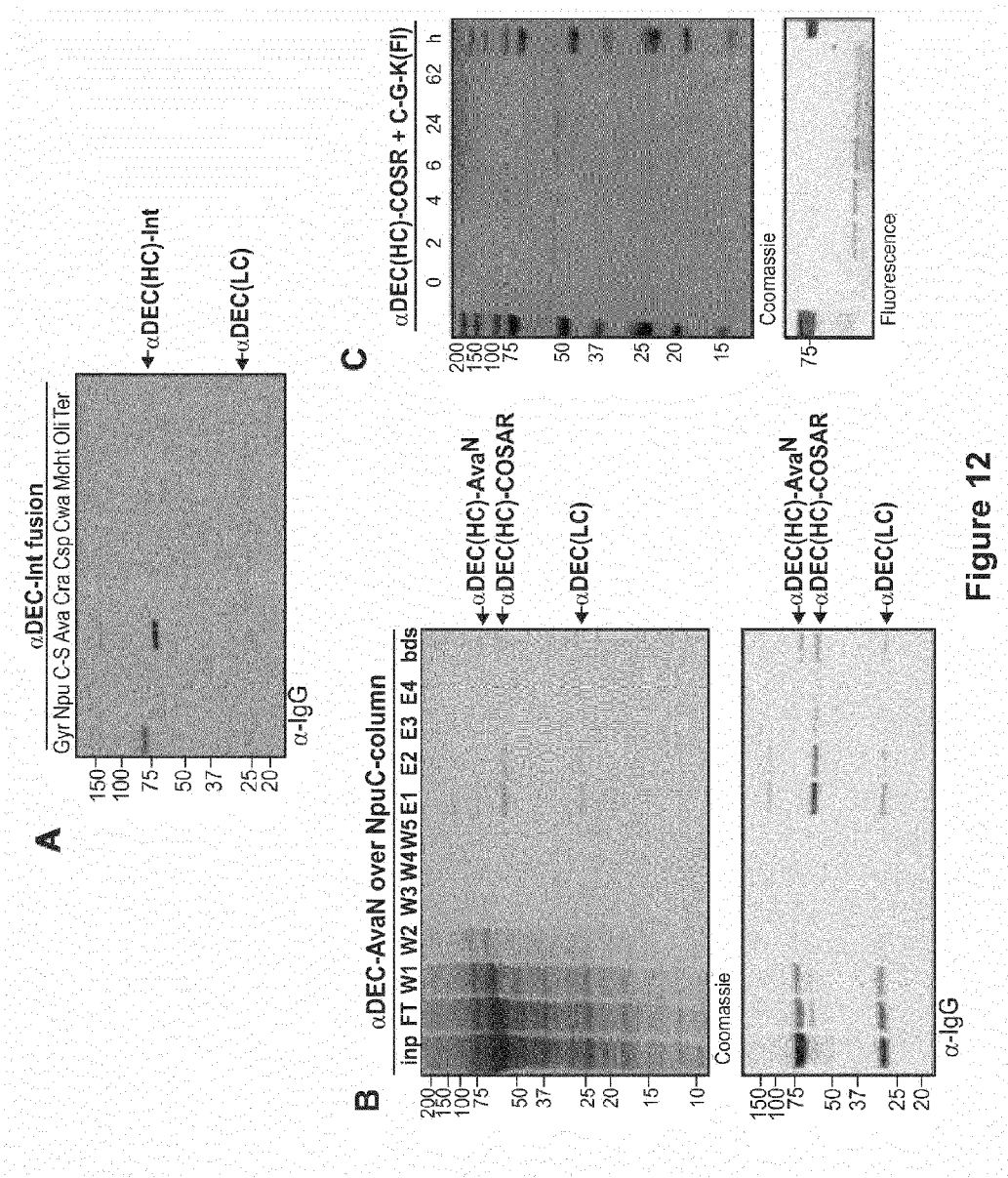
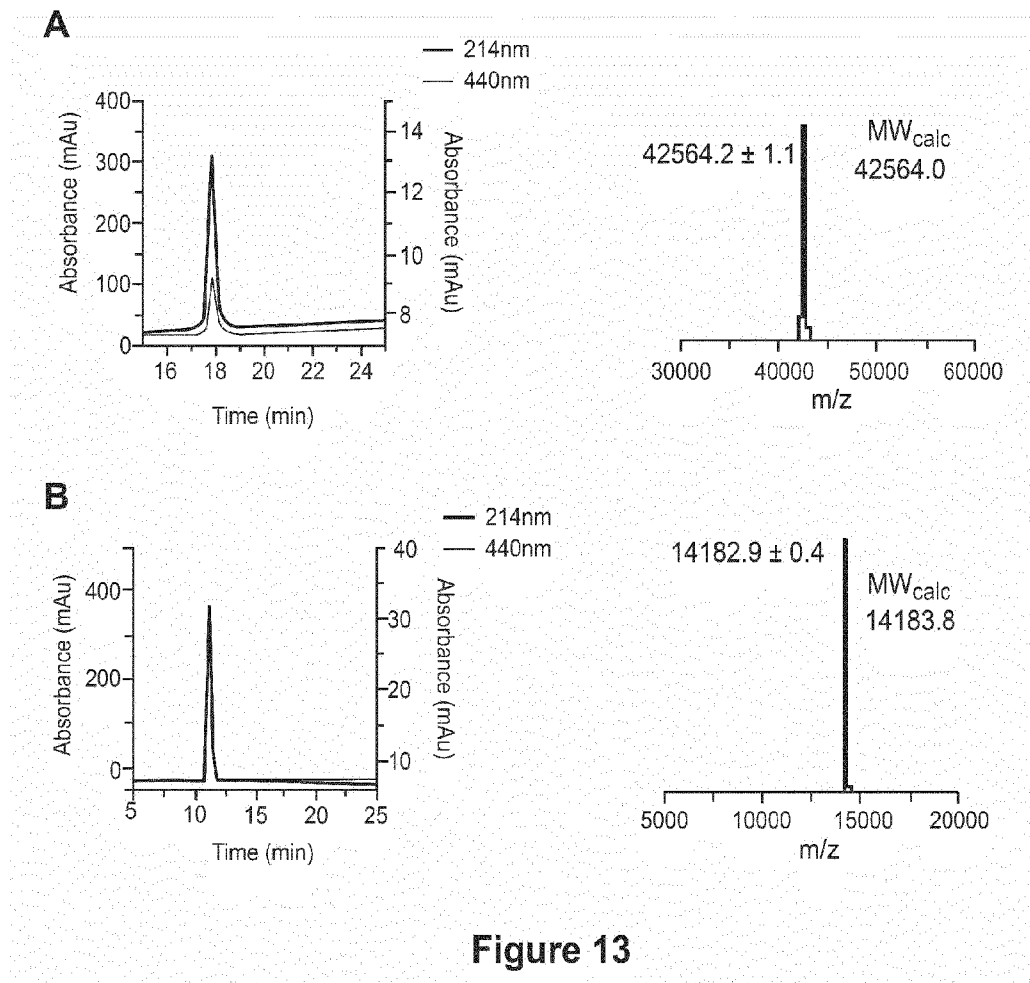
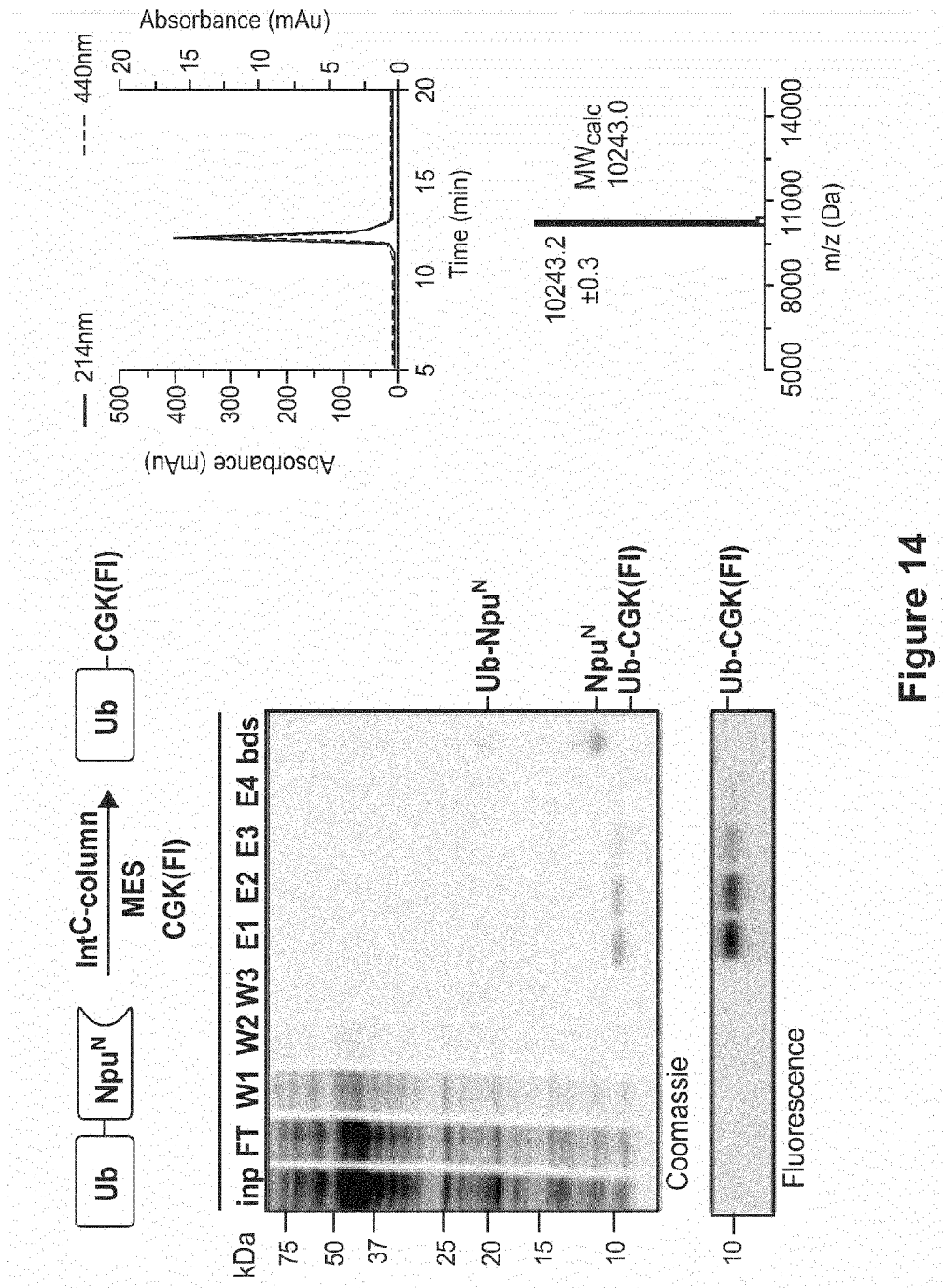


Figure 12





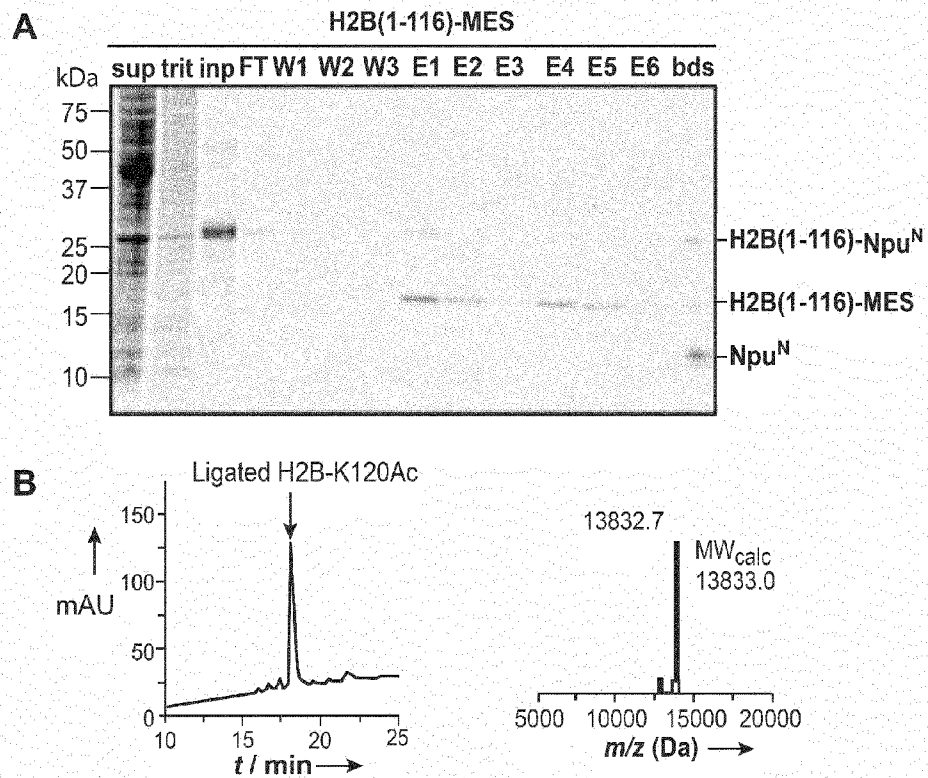
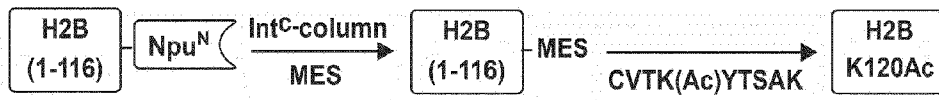


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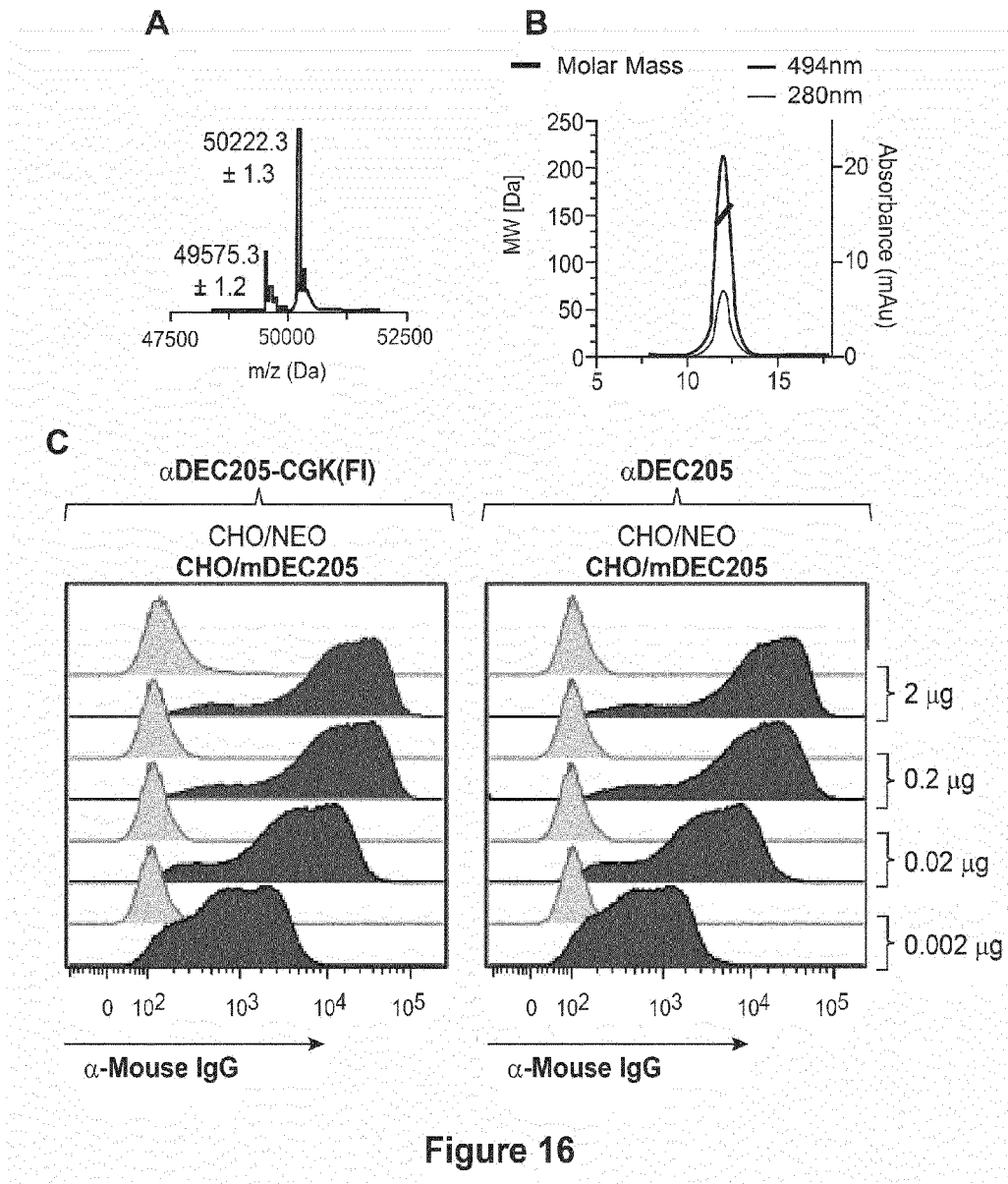


Figure 16

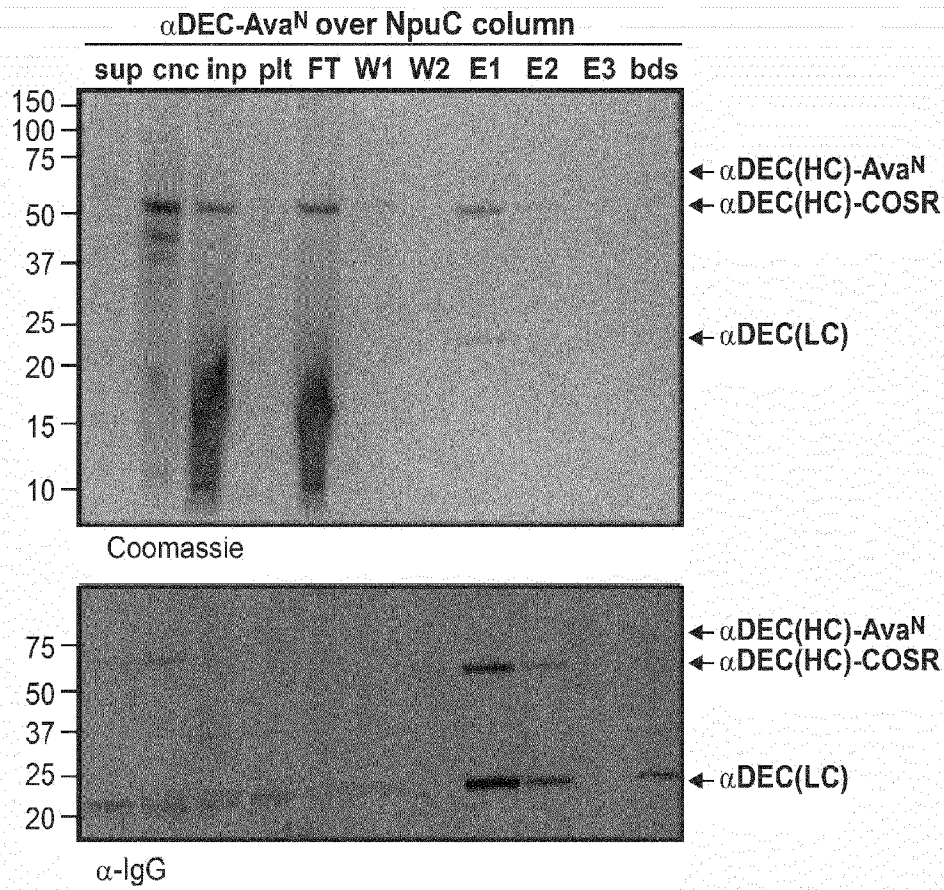


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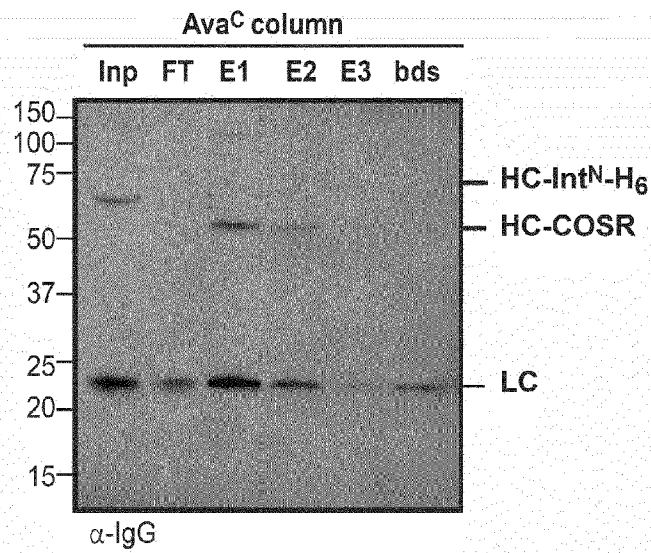


Figure 18

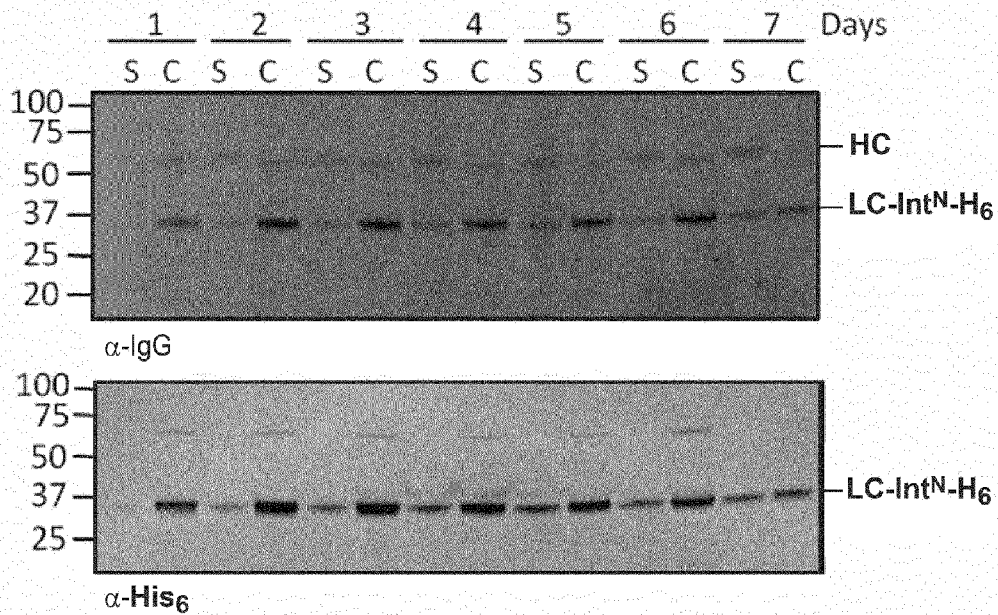


Figure 19