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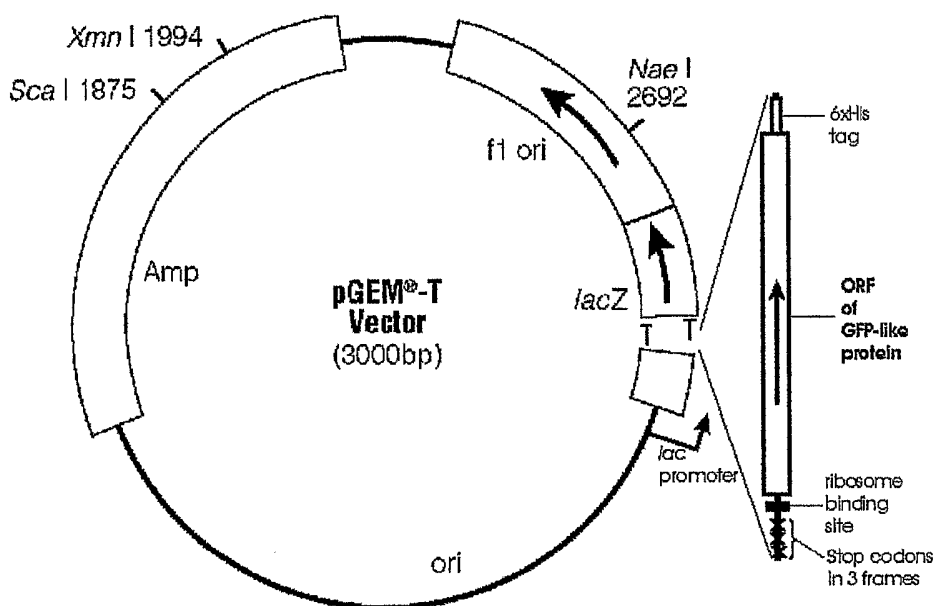
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[Continued on next page]

(54) Title: NOVEL FLUORESCENT AND COLORED PROTEINS, AND POLYNUCLEOTIDES THAT ENCODE THESE PROTEINS



(57) Abstract: The subject invention provides new fluorescent and/or colored proteins, and polynucleotide sequences that encode these proteins. The subject invention further provides materials and methods useful for expressing these detectable proteins in biological systems.

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DESCRIPTIONNOVEL FLUORESCENT AND COLORED PROTEINS, AND
POLYNUCLEOTIDES THAT ENCODE THESE PROTEINS

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Cross-Reference to a Related Application

This application claims the benefit of U.S. provisional patent application Serial No. 60/472,196, filed May 20, 2003.

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Field of the Invention

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The present invention relates to novel fluorescent and colored proteins, and their use. These materials and methods are particularly advantageous for labeling and detection technology. Specifically, exemplified are novel colored and/or fluorescent proteins, and mutants thereof, isolated from marine organisms. These new proteins offer a wider array of colors and biochemical features compared to existing wild-type green fluorescent protein (GFP) or its modified variants utilized in current labeling and detection technology.

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Background of the Invention

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Genetic markers are important for monitoring gene expression and tracking movement of proteins in cells. Markers have been extensively used for monitoring biological activity of genetic elements such as promoters, enhancers and terminators, and other aspects of gene regulation in numerous biological systems. Over the years numerous marker genes have been developed and utilized widely in molecular and genetic studies aimed at the identification, isolation and characterization of genetic regulatory elements and genes, and the development of gene transfer techniques.

In general, markers can be grouped into selectable markers and reporter markers. Selectable markers are typically enzymes with catalytic capability to

convert chemical substrates usually harmful to host cells into non-toxic products, thus providing transformed host cells a conditionally selectable growth advantage under selective environment and allowing the recovery of stable transformants after transformation. A number of commonly used selectable markers include those that confer resistance characteristics to antibiotics (Gritz and Davies 1983; Bevan *et al.*, 1983) and herbicides (De Block *et al.*, 1987), and those with enzymatic activity to detoxify metabolic compounds that can adversely affect cell growth (Joersbo and Okkels 1996).

Reporter markers are compounds that provide biochemically assayable or identifiable activities. Reporter markers have been widely used in studies to reveal biological functions and modes of action of genetic elements such as promoters, enhancers, terminators, and regulatory proteins including signal peptides, transcription factors and related gene products. Over the years, several reporter markers have been developed for use in both prokaryotic and eukaryotic systems, including β -galactosidase (LacZ) (Stanley and Luzio 1984), β -glucuronidase (GUS) (Jefferson *et al.*, 1987; U.S. Patent No. 5,268,463), chloramphenicol acetyltransferase (CAT) (Gorman *et al.*, 1982), green fluorescent protein (GFP) (Prasher *et al.*, 1992; U.S. Patent No. 5,491,084) and luciferase (Luc) (Ow *et al.*, 1986).

Among reporter markers, GUS offers a sensitive and versatile reporting capability for gene expression in plants. β -glucuronidase or GUS, encoded by the *uidA* gene from *Escherichia coli*, catalyzes the conversion of several colorigenic and fluorogenic glucorogenic substrates such as p-nitrophenyl β -D-glucuronide and 4-methylumbelliferyl β -D-glucuronide into easily detectable products. GUS activity can be measured by highly sensitive colorimetric and fluorimetric methods (Jefferson *et al.*, 1987). However, the GUS assay often requires total destruction of the sample tissues or exposure of sample tissues to phytotoxic chemical substrates. This prevents repeated use of the same sample tissue for continuous expression analysis and precludes the recovery of transformants from analyzed materials.

Recently, GFP isolated from the Pacific Northwest jellyfish (*Aequorea victoria*) has become an important reporter marker for non-destructive analysis of gene expression. GFP fluoresces *in vivo* by receiving light energy without the involvement of any chemical substrates. Thus, GFP is especially suitable for real

time and continuous monitoring of temporal and spatial control of gene expression and protein activities without any physical damage to assay samples.

The gene for GFP has been cloned and used as a reporter gene, which can be expressed as a functional transgene in living organisms, marking the organisms with fluorescent color and thus allowing detection of those organisms. Accordingly, GFP has become a versatile fluorescent marker for monitoring a variety of physiological processes, visualizing protein localization and detecting the expression of transferred genes in various living systems, including bacteria, fungi, and mammalian tissues.

This *in vivo* labeling and detection technology was originally based on a single fluorescent protein: the green fluorescent protein from *Aequorea victoria*. Numerous modifications have been made to alter the spectral properties of GFP to provide for significant enhancement in fluorescence intensity (Prasher *et al.*, 1992; Cubitt *et al.*, 1995, Heim *et al.*, 1994, 1995; Cormack *et al.*, 1996; U.S. Patent No. 5,804,387). In addition, GFP genes have been modified to contain more silent base mutations that correspond to codon-usage preferences in order to improve its expression efficacy, making it a reporter gene in both animal and plant systems (U.S. Patent Nos. 5,874,304; 5,968,750; and 6,020,192).

In addition to GFP, there are now a number of other fluorescent proteins, substantially different from GFP, which are being developed into biotechnology tools. Most prominent of these proteins is the red fluorescent protein DsRed. See, for example, Labas, Y. A., N. G. Gurskaya, Y. G. Yanushevich, A. F. Fradkov, K. A. Lukyanov, S. A. Lukyanov and M. V. Matz. (2002) "Diversity and evolution of the green fluorescent protein family" *Proc Natl Acad Sci USA* 99:4256-4261 and Matz, M. V., K. A. Lukyanov and S. A. Lukyanov (2002) "Family of the green fluorescent protein: journey to the end of the rainbow" *Bioessays* 24: 953-959.

Labeling technologies based on GFP and related proteins have become indispensable in such areas as basic biomedical research, cell and molecular biology, transgenic research and drug discovery. The number of PubMed records containing the phrase "green fluorescent protein" exceeds 5500 only within the last three years. Demand for labeling and detection based on the fluorescent protein technology is large and steady.

Currently, there are very few known natural pigments essentially encoded by a single gene, wherein both the substrate for pigment biosynthesis and the necessary

catalytic moieties are provided within a single polypeptide chain. The limited availability of fluorescent marker proteins makes the current technology based on fluorescent proteins very expensive, rendering it unaffordable and inaccessible to many mid-size (or smaller) companies that are interested in using the technology. Therefore, there is a need for less expensive, readily available fluorescent and/or colored materials.

Brief Summary of the Invention

The subject invention provides new fluorescent and/or colored proteins, and polynucleotide sequences that encode these proteins. The subject invention further provides materials and methods useful for expressing these detectable proteins in biological systems.

In specific embodiments, the subject invention provides a red fluorescent protein from *Scolymia cubensis* scubRFP, featuring rapid conversion from immature green to mature red form under UV-A light; and three fluorescent proteins from *Montastraea cavernosa*, namely g5.2 (cyan), mc6 (green) and R7 (green) proteins. The invention also includes proteins substantially similar to, or mutants or variants of, the exemplified proteins.

Another aspect of the subject invention pertains to polynucleotide sequences that encode the detectable proteins of the present invention. In one embodiment, the present invention provides polynucleotide constructs comprising cDNA encoding novel colored and/or fluorescent proteins and mutants thereof.

The subject invention also provides proteins from *Acropora* ("staghorn corals") and *Agarica fragilis* ("fragile saucer coral"), as well as polynucleotides encoding these proteins.

In one embodiment, the invention provides nucleotide sequences of the inserts in pGEM-T vector (Promega), the conceptual translations of these inserts, and special properties of purified protein products.

The proteins and polynucleotides of the present invention can be used as described herein as colored and/or fluorescent (detectable) labels in a variety of ways, including but not limited to, as reporter genes for monitoring gene expression in living organisms, as protein tags for tracing the location of proteins within living cells and organisms, as reporter molecules for engineering various protein-based biosensors,

and as genetically encoded pigments for modifying color and/or fluorescence of living organisms or their parts.

In a specific embodiment, the proteins of the subject invention can be used in molecular fluorescent tagging whereby the coding region of a protein of interest is fused with the coding region for a fluorescent protein of the subject invention. The product of such a gene shows the functional characteristics of the protein of interest, but bears the fluorescent label allowing tracing its movements.

Advantageously, the present invention provides proteins and polynucleotides to improve on the current technology of labeling and detection by offering a wider choice of colors and biochemical features never before provided by GFP and its modified variants.

Brief Description of the Figures

Figure 1 shows design of bacterial expression constructs for the proteins of interests of the present invention.

Figure 2 shows the bacterial colonies expressing genes described in the present invention (cyan, green and red) under UV-A light. The bacterial colonies affected by the expression show red and greenish color and fluorescent appearance. These bacterial colonies are normally non-fluorescent under UV-A light.

Figure 3A-3B shows maturation of scubRFP under low-intensity UV-A light, resulting in conversion from a green-emitting form (emission maximum 520 nm) into red-emitting form (emission maximum 575 nm). Figure 3A is a graph showing the change in ratio or emission amplitudes of 520 and 575 nm. Figure 3B graph shows changes in the emission spectra.

Figure 4 shows the excitation and emission spectra of *A. aculeus* 1-1 (green).

Figure 5 shows the excitation and emission spectra of *A. aculeus* 1-2 (green).

Figure 6 shows the excitation and emission spectra of *A. aculeus* 2-1 (green).

Figure 7 shows the excitation and emission spectra of *A. aculeus* 2-2 (green).

Figure 8 shows the excitation and emission spectra of *A. aculeus* 3-1 (green).

Figure 9 shows the excitation and emission spectra of *A. millepora* 8-2 (cyan).

Figure 10 shows the excitation and emission spectra of *A. millepora* 9-1 (green).

Figure 11 shows the excitation and emission spectra of *A. millepora* 9-2 (green).

Figure 12 shows the excitation and emission spectra of *A. millepora* 10-1 (green).

5 **Figure 13** shows the excitation and emission spectra of *A. millepora* 10-2 (cyan).

Figure 14 shows the excitation and emission spectra of *A. millepora* 11-1 (green).

10 **Figure 15** shows the excitation and emission spectra of *A. millepora* 12-1 (red).

Figure 16 shows the excitation and emission spectra of *A. nobilis* 15-1 (cyan).

Figure 17 shows the excitation and emission spectra of *A. nobilis* 16-1 (cyan).

Figure 18 shows the excitation and emission spectra of *A. nobilis* 17-1 (green).

15 **Figure 19** shows the excitation and emission spectra of *Agaricia fragilis* 1 (green).

Figure 20 shows the excitation and emission spectra of *Agaricia fragilis* 2 (green).

20 **Figure 21** shows the excitation and emission spectra of *Agaricia fragilis* 3 (green).

Figure 22 shows the excitation and emission spectra of *Agaricia fragilis* 4 (cyan).

Figure 23 shows the excitation and emission spectra of *Agaricia fragilis* 5 (green).

25 **Figure 24** shows the excitation and emission spectra of *Agaricia fragilis* 6 (green).

Figure 25 shows the excitation and emission spectra of *Agaricia fragilis* 8 (cyan).

30 **Figure 26** shows the excitation and emission spectra of *A. aculeus* 5-2 (chromoprotein).

Figure 27 shows the excitation and emission spectra of *A. aculeus* 6-1 (chromoprotein).

Figure 28 shows the excitation and emission spectra of *A. hyacinthus* 7-1 (chromoprotein).

Figure 29 shows the excitation and emission spectra of *A. millepora* 14-1 (chromoprotein).

5

Brief Description of the Sequences

SEQ ID NO:1 is the 5' heel of an upstream primer used according to the subject invention.

10

SEQ ID NO:2 is the 5' heel of a downstream primer used according to the subject invention.

SEQ ID NO:3 is the open reading frame of the cDNA encoding the g5.2 (cyan) protein of interest from *Montastraea cavernosa*.

SEQ ID NO:4 is the open reading frame of the cDNA encoding the mc6 (green) protein of interest from *Montastraea cavernosa*.

15

SEQ ID NO:5 is the open reading frame of the cDNA encoding the R7 (green) protein of interest from *Montastraea cavernosa*.

SEQ ID NO:6 is the open reading frame of the cDNA encoding the scubRFP protein of interest from *Scolymia cubensis*.

SEQ ID NO:7 is the amino acid sequence encoded by SEQ ID NO:3.

20

SEQ ID NO:8 is the amino acid sequence encoded by SEQ ID NO:4.

SEQ ID NO:9 is the amino acid sequence encoded by SEQ ID NO:5.

SEQ ID NO:10 is the amino acid sequence encoded by SEQ ID NO:6.

SEQ ID NO:11 is the bacterial expression construct for the g5.2 (cyan) protein of interest from *Montastraea cavernosa*.

25

SEQ ID NO:12 is the bacterial expression construct for the mc6 (green) protein of interest from *Montastraea cavernosa*.

SEQ ID NO:13 is the bacterial expression construct for the R7 (green) protein of interest from *Montastraea cavernosa*.

30

SEQ ID NO:14 is the bacterial expression construct for the scubRFP protein of interest from *Scolymia cubensis*.

SEQ ID NO:15 is the amino acid sequence encoded by SEQ ID NO:11.

SEQ ID NO:16 is the amino acid sequence encoded by SEQ ID NO:12.

SEQ ID NO:17 is the amino acid sequence encoded by SEQ ID NO:13.

SEQ ID NO:18 is the amino acid sequence encoded by **SEQ ID NO:14**.

SEQ ID NO:19 is the nucleotide sequence of an insert in the pGEM-T vector, according to subject invention (Acropora aculeus 1-1 in pGEM-T).

5 **SEQ ID NO:20** is the nucleotide sequence of an insert in the pGEM-T vector, according to subject invention (Acropora aculeus 1-2 in pGEM-T).

SEQ ID NO:21 is the nucleotide sequence of an insert in the pGEM-T vector, according to subject invention (Acropora aculeus 2-1 in pGEM-T).

SEQ ID NO:22 is the nucleotide sequence of an insert in the pGEM-T vector, according to subject invention (Acropora aculeus 2-2 in pGEM-T).

10 **SEQ ID NO:23** is the nucleotide sequence of an insert in the pGEM-T vector, according to subject invention (Acropora aculeus 3-1 in pGEM-T).

SEQ ID NO:24 is the nucleotide sequence insert of the subject invention (Acropora aculeus 5-2 in pGEM-T).

15 **SEQ ID NO:25** is the nucleotide sequence of an insert in the pGEM-T vector, according to subject invention (Acropora aculeus 6-1 in pGEM-T).

SEQ ID NO:26 is the nucleotide sequence insert of the subject invention (Acropora hyacinthus 7-1 in pGEM-T).

SEQ ID NO:27 is the nucleotide sequence of an insert in the pGEM-T vector, according to subject invention Acropora millepora 8-2 in pGEM-T).

20 **SEQ ID NO:28** is the nucleotide sequence of an insert in the pGEM-T vector, according to subject invention (Acropora millepora 9-1 in pGEM-T).

SEQ ID NO:29 is the nucleotide sequence of an insert in the pGEM-T vector, according to subject invention (Acropora millepora 9-2 in pGEM-T).

25 **SEQ ID NO:30** is the nucleotide sequence of an insert in the pGEM-T vector, according to subject invention (Acropora millepora 10-1 in pGEM-T).

SEQ ID NO:31 is the nucleotide sequence of an insert in the pGEM-T vector, according to subject invention (Acropora millepora 10-2 in pGEM-T).

SEQ ID NO:32 is the nucleotide sequence of an insert in the pGEM-T vector, according to subject invention (Acropora millepora 11-1 in pGEM-T).

30 **SEQ ID NO:33** is the nucleotide sequence of an insert in the pGEM-T vector, according to subject invention (Acropora millepora 12-1 in pGEM-T).

SEQ ID NO:34 is the nucleotide sequence of an insert in the pGEM-T vector, according to subject invention (Acropora millepora 14-1 in pGEM-T).

SEQ ID NO:35 is the nucleotide sequence of an insert in the pGEM-T vector, according to subject invention (*Acropora nobilis* 15-1 in pGEM-T).

SEQ ID NO:36 is the nucleotide sequence of an insert in the pGEM-T vector, according to subject invention (*Acropora nobilis* 16-1 in pGEM-T).

5 **SEQ ID NO:37** is the nucleotide sequence of an insert in the pGEM-T vector, according to subject invention (*Acropora nobilis* 17-1 in pGEM-T).

SEQ ID NO:38 is the nucleotide sequence of an insert in the pGEM-T vector, according to subject invention (*Agaricia fragilis* 1 in pGEM-T).

10 **SEQ ID NO:39** is the nucleotide sequence of an insert in the pGEM-T vector, according to subject invention (*Agaricia fragilis* 2 in pGEM-T).

SEQ ID NO:40 is the nucleotide sequence of an insert in the pGEM-T vector, according to subject invention (*Agaricia fragilis* 3 in pGEM-T).

SEQ ID NO:41 is the nucleotide sequence of an insert in the pGEM-T vector, according to subject invention (*Agaricia fragilis* 4 in pGEM-T).

15 **SEQ ID NO:42** is the nucleotide sequence of an insert in the pGEM-T vector, according to subject invention (*Agaricia fragilis* 5 in pGEM-T).

SEQ ID NO:43 is the nucleotide sequence of an insert in the pGEM-T vector, according to subject invention (*Agaricia fragilis* 6 in pGEM-T).

20 **SEQ ID NO:44** is the nucleotide sequence of an insert in the pGEM-T vector, according to subject invention (*Agaricia fragilis* 8 in pGEM-T).

SEQ ID NO:45 is the amino acid sequence of a protein of the subject invention as encoded by the following construct: *Acropora aculeus* 1-1 in pGEM-T.

SEQ ID NO:46 is the amino acid sequence of a protein of the subject invention as encoded by the following construct: *Acropora aculeus* 1-2 in pGEM-T.

25 **SEQ ID NO:47** is the amino acid sequence of a protein of the subject invention as expressed by the following construct: *Acropora aculeus* 2-1 in pGEM-T.

SEQ ID NO:48 is the amino acid sequence of a protein of the subject invention as encoded by the following construct: *Acropora aculeus* 2-2 in pGEM-T.

30 **SEQ ID NO:49** is the amino acid sequence of a protein of the subject invention as encoded by the following construct: *Acropora aculeus* 3-1 in pGEM-T.

SEQ ID NO:50 is the amino acid sequence of a protein of the subject invention as encoded by the following construct: *Acropora aculeus* 5-2 in pGEM-T.

SEQ ID NO:51 is the amino acid sequence of a protein of the subject invention as encoded by the following construct: *Acropora aculeus* 6-1 in pGEM-T.

SEQ ID NO:52 is the amino acid sequence of a protein of the subject invention as encoded by the following construct: *Acropora hyacinthus* 7-1 in pGEM-T.

5 **SEQ ID NO:53** is the amino acid sequence of a protein of the subject invention as encoded by the following construct: *Acropora millepora* 8-2 in pGEM-T.

SEQ ID NO:54 is the amino acid sequence of a protein of the subject invention as encoded by the following construct: *Acropora millepora* 9-1 in pGEM-T.

10 **SEQ ID NO:55** is the amino acid sequence of a protein of the subject invention as encoded by the following construct: *Acropora millepora* 9-2 in pGEM-T.

SEQ ID NO:56 is the amino acid sequence of a protein of the subject invention as encoded by the following construct: *Acropora millepora* 10-1 in pGEM-T.

SEQ ID NO:57 is the amino acid sequence of a protein of the subject invention as encoded by the following construct: *Acropora millepora* 10-2 in pGEM-T.

15 **SEQ ID NO:58** is the amino acid sequence of a protein of the subject invention as encoded by the following construct: *Acropora millepora* 11-1 in pGEM-T.

SEQ ID NO:59 is the amino acid sequence of a protein of the subject invention as encoded by the following construct: *Acropora millepora* 12-1 in pGEM-T.

20 **SEQ ID NO:60** is the amino acid sequence of a protein of the subject invention as encoded by the following construct: *Acropora millepora* 14-1 in pGEM-T.

SEQ ID NO:61 is the amino acid sequence of a protein of the subject invention as encoded by the following construct: *Acropora nobilis* 15-1 in pGEM-T.

SEQ ID NO:62 is the amino acid sequence of a protein of the subject invention as encoded by the following construct: *Acropora nobilis* 16-1 in pGEM-T.

25 **SEQ ID NO:63** is the amino acid sequence of a protein of the subject invention as encoded by the following construct: *Acropora nobilis* 17-1 in pGEM-T.

SEQ ID NO:64 is the amino acid sequence of a protein of the subject invention as encoded by the following construct: *Agaricia fragilis* 1 in pGEM-T.

30 **SEQ ID NO:65** is the amino acid sequence of a protein of the subject invention as expressed by the following construct: *Agaricia fragilis* 2 in pGEM-T.

SEQ ID NO:66 is the amino acid sequence of a protein of the subject invention as encoded by the following construct: *Agaricia fragilis* 3 in pGEM-T.

SEQ ID NO:67 is the amino acid sequence of a protein of the subject invention as encoded by the following construct: *Agaricia fragilis* 4 in pGEM-T.

SEQ ID NO:68 is the amino acid sequence of a protein of the subject invention as encoded by the following construct: *Agaricia fragilis* 5 in pGEM-T.

5 **SEQ ID NO:69** is the amino acid sequence of a protein of the subject invention as encoded by the following construct: *Agaricia fragilis* 6 in pGEM-T.

SEQ ID NO:70 is the amino acid sequence of a protein of the subject invention as encoded by the following construct: *Agaricia fragilis* 8 in pGEM-T.

SEQ ID NO:71 is the coding region of the construct of **SEQ ID NO:45**.

10 **SEQ ID NO:72** is the coding region of the construct of **SEQ ID NO:46**.

SEQ ID NO:73 is the coding region of the construct of **SEQ ID NO:47**.

SEQ ID NO:74 is the coding region of the construct of **SEQ ID NO:48**.

SEQ ID NO:75 is the coding region of the construct of **SEQ ID NO:49**.

SEQ ID NO:76 is the coding region of the construct of **SEQ ID NO:50**.

15 **SEQ ID NO:77** is the coding region of the construct of **SEQ ID NO:51**.

SEQ ID NO:78 is the coding region of the construct of **SEQ ID NO:52**.

SEQ ID NO:79 is the coding region of the construct of **SEQ ID NO:53**.

SEQ ID NO:80 is the coding region of the construct of **SEQ ID NO:54**.

SEQ ID NO:81 is the coding region of the construct of **SEQ ID NO:55**.

20 **SEQ ID NO:82** is the coding region of the construct of **SEQ ID NO:56**.

SEQ ID NO:83 is the coding region of the construct of **SEQ ID NO:57**.

SEQ ID NO:84 is the coding region of the construct of **SEQ ID NO:58**.

SEQ ID NO:85 is the coding region of the construct of **SEQ ID NO:59**.

SEQ ID NO:86 is the coding region of the construct of **SEQ ID NO:60**.

25 **SEQ ID NO:87** is the coding region of the construct of **SEQ ID NO:61**.

SEQ ID NO:88 is the coding region of the construct of **SEQ ID NO:62**.

SEQ ID NO:89 is the coding region of the construct of **SEQ ID NO:63**.

SEQ ID NO:90 is the coding region of the construct of **SEQ ID NO:64**.

SEQ ID NO:91 is the coding region of the construct of **SEQ ID NO:65**.

30 **SEQ ID NO:92** is the coding region of the construct of **SEQ ID NO:66**.

SEQ ID NO:93 is the coding region of the construct of **SEQ ID NO:67**.

SEQ ID NO:94 is the coding region of the construct of **SEQ ID NO:68**.

SEQ ID NO:95 is the coding region of the construct of **SEQ ID NO:69**.

SEQ ID NO:96 is the coding region of the construct of SEQ ID NO:70.

Detailed Description of the Invention

5 The present invention provides novel fluorescent and colored proteins isolated from marine organisms other than *Aequorea Victoria*. In a particularly preferred embodiment, these proteins are red fluorescent proteins featuring rapid conversion from immature green to mature red under UV-A light. Specifically exemplified herein are scubRFP from *Scolymia cubensis*; and g5.2 (cyan), mc6 (green) and R7 (green) proteins, from *Montastraea cavernosa*.

10 The subject invention further provides polynucleotide sequences encoding these proteins. These polynucleotide sequences include open reading frames encoding the specific exemplified detectable proteins, as well as expression constructs for expressing these proteins, for example, in bacterial hosts.

15 The proteins of the present invention can be readily, expressed by any one of the recombinant technology methods known to those skilled in the art having the benefit of the instant disclosure. The preferred method will vary depending upon many factors and considerations, including the host, and the cost and availability of materials and other economic considerations. The optimum production procedure for a given situation will be apparent to those skilled in the art having the benefit of the
20 current disclosure.

The subject invention also concerns cells transformed with a polynucleotide of the present invention comprising a nucleotide sequences encoding a novel detectable protein. These cells may be prokaryotic or eukaryotic, plant or animal. In one embodiment, animals, such as fish, are transformed to provide them with a unique
25 color or ability to fluoresce. Polynucleotides providing the markers of the present invention are stable in a diverse range of hosts, including prokaryotic and eukaryotic organisms, and the translation products are fully functional and capable of providing assayable characteristics.

30 In another embodiment, the present invention provides methods to synthesize colored and fluorescent proteins in a recombinant cell.

In a specific embodiment, the proteins of the subject invention can be used in molecular fluorescent tagging whereby the coding region of a protein of interest is fused with the coding region for a fluorescent protein of the subject invention. The

product of such a gene shows the functional characteristics of the protein of interest, but bears the fluorescent label allowing tracing its movements. See, for example, Eichinger, L., S. S. Lee and M. Schleicher (1999) "Dictyostelium as model system for studies of the actin cytoskeleton by molecular genetics" *Microsc Res Tech* 47:124-134; Falk, M. M. and U. Lauf (2001) "High resolution, fluorescence deconvolution microscopy and tagging with the autofluorescent tracers CFP, GFP, and YFP to study the structural composition of gap junctions in living cells" *Microsc Res Tech* 52:251-262; Kallal, L. and J. L. Benovic (2000) "Using green fluorescent proteins to study G-protein-coupled receptor localization and trafficking" *Trends Pharmacol Sci* 21:175-180; and Laird, D. W., K. Jordan, T. Thomas, H. Qin, P. Fistouris and Q. Shao (2001) "Comparative analysis and application of fluorescent protein-tagged connexins" *Microsc Res Tech* 52:263-272.

In a further embodiment, the subject invention concerns polynucleotides comprising an in-frame fusion of nucleotide sequences encoding multiple genetic markers. In one embodiment, the polynucleotides encode the genetic markers GUS, and a detectable protein of the subject invention.

The subject invention helps to provide a more abundant and diverse collection of proteins, which can be used in place of a GFP protein, such that new proteins are readily available for commercial exploitation by small companies that cannot take advantage of the current technology for financial reasons.

Definitions

As used herein, the terms "nucleic acid" and "polynucleotide" refer to a deoxyribonucleotide, ribonucleotide, or a mixed deoxyribonucleotide and ribonucleotide polymer in either single- or double-stranded form, and unless otherwise limited, would encompass known analogs of natural nucleotides that can function in a similar manner as naturally-occurring nucleotides.

As used herein, "a vector" is a DNA sequence having the elements necessary for the transcription/translation of a gene. Such elements would include, for example, promoters. Various classes of promoters are well known in the art and can be obtained commercially or assembled from the sequences and methods, which are also well known in the art. A number of vectors are available for expression and/or

cloning, and include, but are not limited to, pBR322, pUC series, M13 series, and pBLUESCRIPT vectors (Stratagene, La Jolla, CA).

As used herein, the term “expression construct” refers to a combination of nucleic acid sequences that provides for transcription of an operably linked nucleic acid sequence. As used herein, the term “operably linked” refers to a juxtaposition of the components described wherein the components are in a relationship that permits them to function in their intended manner. In general, operably linked components are in contiguous relation.

Detectable Proteins

The subject invention provides novel fluorescent and/or colored proteins. These proteins are exemplified by scubRFP from *Scolymia cubensis* (SEQ ID NO. 7); and g5.2 (cyan) (SEQ ID NO. 8), mc6 (green) (SEQ ID NO. 9) and R7 (green) (SEQ ID NO. 10) proteins, from *Montastraea cavernosa*.

The novel colored and fluorescent proteins of the present invention can be detected using standard long-wave UV light sources or, preferably, optical designs appropriate for detecting agents with the excitation/emission characteristics of the proteins exemplified herein (see, for example, Figures 2-29). These proteins are referred to herein as “detectable proteins” or “marker proteins.” The interaction of two or more residues of the protein and external agents such as molecular oxygen give rise to the colored and/or fluorescent feature of the proteins.

Advantageously, the use of these proteins facilitate real-time detection *in vivo*, a substrate is not required, and the relatively small size make the proteins very advantageous.

Substitution of amino acids other than those specifically exemplified or naturally present in the genetic marker proteins of the invention are also contemplated within the scope of the present invention. Such substitutions will create “variant proteins” within the scope of the subject invention. Variants and fragments preferably have emission and excitation maxima within 10 nm of the values shown in Figures 2-29. For example, non-natural amino acids can be substituted for the amino acids of the marker proteins, so long as a marker protein having the substituted amino acids retains its ability to be detected through fluorescence and/or color. Examples of non-natural amino acids include, but are not limited to, ornithine, citrulline,

hydroxyproline, homoserine, phenylglycine, taurine, iodotyrosine, 2,4-diaminobutyric acid, α -amino isobutyric acid, 4-aminobutyric acid, 2-amino butyric acid, γ -amino butyric acid, ϵ -amino hexanoic acid, 6-amino hexanoic acid, 2-amino isobutyric acid, 3-amino propionic acid, norleucine, norvaline, sarcosine, homocitrulline, cysteic acid, τ -butylglycine, τ -butylalanine, phenylglycine, cyclohexylalanine, β -alanine, fluoro-amino acids, designer amino acids such as β -methyl amino acids, C-methyl amino acids, N-methyl amino acids, and amino acid analogues in general. Non-natural amino acids also include amino acids having derivatized side groups. Furthermore, any of the amino acids in the protein can be of the D (dextrorotary) form or L (levorotary) form. Allelic variants of a protein sequence of a detectable protein used in the present invention are also encompassed within the scope of the invention.

Amino acids can be generally categorized in the following classes: non-polar, uncharged polar, basic, and acidic. Conservative substitutions whereby a marker protein having an amino acid of one class is replaced with another amino acid of the same class fall within the scope of the subject invention so long as a marker protein having the substitution still is detectable Table 1 below provides a listing of examples of amino acids belonging to each class.

Table 1.	
Class of Amino Acid	Examples of Amino Acids
Nonpolar	Ala, Val, Leu, Ile, Pro, Met, Phe, Trp
Uncharged Polar	Gly, Ser, Thr, Cys, Tyr, Asn, Gln
Acidic	Asp, Glu
Basic	Lys, Arg, His

Polynucleotides

cDNA sequences encoding the proteins of the present invention are provided. Polynucleotides of the present invention can be composed of either RNA or DNA. Preferably, the polynucleotides are composed of DNA. The subject invention also

encompasses those polynucleotides that are complementary in sequence to the polynucleotides disclosed herein.

Specifically exemplified are DNA sequences that encode for scubRFP from *Scolymia cubensis*; and g5.2 (cyan), mc6 (green) and R7 (green) proteins, from *Montastraea cavernosa*. These DNA sequences are set forth in SEQ. ID NOS. 3-6.

Sequences of the subject invention may utilize codons preferred for expression by the selected host strains. These sequences may also have sites for cleavage by restriction enzymes, and/or initial, terminal, or intermediate DNA sequences which facilitate construction of readily expressed vectors.

Because of the degeneracy of the genetic code, a variety of different polynucleotide sequences can encode the detectable proteins of the present invention. In addition, it is well within the skill of a person trained in the art to create alternative polynucleotide sequences encoding the same, or essentially the same, detectable proteins of the subject invention. These variant or alternative polynucleotide sequences are within the scope of the subject invention. As used herein, references to "essentially the same" sequence refers to sequences which encode amino acid substitutions, deletions, additions, or insertions which do not eliminate the detectability of the polypeptide encoded by the polynucleotides of the present invention. Allelic variants of the nucleotide sequences encoding a genetic marker protein of the invention are also encompassed within the scope of the invention.

The subject invention also concerns variants of the polynucleotides of the present invention that encode detectable proteins. Variant sequences include those sequences wherein one or more nucleotides of the sequence have been substituted, deleted, and/or inserted. The nucleotides that can be substituted for natural nucleotides of DNA have a base moiety that can include, but is not limited to, inosine, 5-fluorouracil, 5-bromouracil, hypoxanthine, 1-methylguanine, 5-methylcytosine, and tritylated bases. The sugar moiety of the nucleotide in a sequence can also be modified and includes, but is not limited to, arabinose, xylulose, and hexose. In addition, the adenine, cytosine, guanine, thymine, and uracil bases of the nucleotides can be modified with acetyl, methyl, and/or thio groups. Sequences containing nucleotide substitutions, deletions, and/or insertions can be prepared and tested using standard techniques known in the art.

Polynucleotides and polypeptides of the subject invention can also be defined in terms of more particular identity and/or similarity ranges with those exemplified herein. The sequence identity will typically be greater than 60%, preferably greater than 75%, more preferably greater than 80%, even more preferably greater than 90%, and can be greater than 95%. The identity and/or similarity of a sequence can be 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% as compared to a sequence exemplified herein. Unless otherwise specified, as used herein percent sequence identity and/or similarity of two sequences can be determined using the algorithm of Karlin and Altschul (1990), modified as in Karlin and Altschul (1993). Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul *et al.* (1990). BLAST searches can be performed with the NBLAST program, score = 100, wordlength = 12, to obtain sequences with the desired percent sequence identity. To obtain gapped alignments for comparison purposes, Gapped BLAST can be used as described in Altschul *et al.* (1997). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (NBLAST and XBLAST) can be used.

The subject invention also contemplates those polynucleotide molecules having sequences that are sufficiently homologous with the polynucleotide sequences exemplified herein so as to permit hybridization with that sequence under standard stringent conditions and standard methods (Maniatis *et al.* 1982). As used herein, "stringent" conditions for hybridization refers to conditions wherein hybridization is typically carried out overnight at 20-25 C below the melting temperature (T_m) of the DNA hybrid in 6x SSPE, 5x Denhardt's solution, 0.1% SDS, 0.1 mg/ml denatured DNA. The melting temperature, T_m , is described by the following formula (Beltz *et al.*, 1983):

$$T_m = 81.5^\circ\text{C} + 16.6 \log[\text{Na}^+] + 0.41(\%G+C) - 0.61(\% \text{ formamide}) - 600/\text{length of duplex in base pairs.}$$

Washes are typically carried out as follows:

- (1) Twice at room temperature for 15 minutes in 1x SSPE, 0.1% SDS (low stringency wash).
- (2) Once at $T_m - 20^\circ\text{C}$ for 15 minutes in 0.2x SSPE, 0.1% SDS (moderate stringency wash).

The polynucleotide sequences include the DNA strand sequence that is transcribed into RNA and the strand sequence that is complementary to the DNA strand that is transcribed. The polynucleotide sequences also include both full-length sequences as well as shorter sequences derived from the full-length sequences. The polynucleotide sequence includes both the sense and antisense strands either as individual strands or in the duplex.

Recombinant Hosts

Polynucleotide molecules containing DNA sequences encoding the colored and/or fluorescent proteins of the present invention can be introduced into a variety of host cells including bacterial cells, yeast cells, fungal cells, plant cells and animal cells. Methods by which the exogenous genetic material can be introduced into such host cells are well known in the art.

In one embodiment, the invention provides a bacteria cell capable of expressing the novel colored and fluorescent proteins.

Plants, plant tissues, and plant cells bred to contain, or transformed with, a polynucleotide of the invention are also contemplated by the present invention. In one embodiment, the polynucleotide encodes a detectable polypeptide shown in SEQ ID NOS. 7-10, or a functional fragment or variant thereof. Plants within the scope of the present invention include monocotyledonous plants, such as rice, wheat, barley, oats, sorghum, maize, sugarcane, pineapple, onion, bananas, coconut, lilies, grasses, and millet; and dicotyledonous plants, such as peas, alfalfa, tomato, melon, chickpea, chicory, clover, kale, lentil, soybean, tobacco, potato, sweet potato, radish, cabbage, rape, apple trees, grape, cotton, sunflower, and lettuce; and conifers. Techniques for transforming plant cells with a gene are known in the art and include, for example, *Agrobacterium* infection, biolistic methods, electroporation, calcium chloride treatment, etc. Transformed cells can be selected, redifferentiated, and grown into plants using standard methods known in the art. The progeny of any transformed plant cells or plants are also included within the scope of the present invention.

The subject invention also concerns non-human transgenic animals which have incorporated into the host cell genome a polynucleotide of the invention. Methods for producing transgenic animals, including mice, rats, pigs, sheep, cows, fish, and the like are well known in the art.

The subject invention also concerns methods for isolating transformants expressing a transgene. In one embodiment, an expression construct of the present invention comprising a transgene of interest operably linked to a nucleotide sequence encoding a detectable marker of the present invention is used to transform a cell. Methods for transforming cells are well known in the art. Transformed cells expressing the transgene are selected by identifying those cells expressing a genetic marker of the invention.

Expression Constructs

An expression construct of the invention typically comprises a structural gene sequence (encoding a protein), an antisense sequence, or other polynucleotide sequences, or a site for insertion of such sequences, operably linked to a polynucleotide of the present invention encoding a marker. The structural gene can be a gene encoding a protein from a prokaryotic or eukaryotic organism, for example, a human, mammal, insect, plant, bacteria, or virus. Proteins that can be encoded by a gene sequence include, but are not limited to, enzymes, hormones, cytokines, interleukins, receptors, growth factors, immunoglobulins, transcription factors, and *Bacillus thuringiensis* (*B.t.*) crystal toxin proteins. Sequences encoding *B.t.* proteins which have codon usage for preferential expression in plants are described in U.S. Patent Nos. 5,380,831; 5,567,862; 5,567,600; 6,013,523; and 6,015,891. An antisense sequence is a sequence wherein the RNA transcribed from the antisense sequence is at least partially complementary to RNA transcribed from a gene encoding a protein.

Expression constructs of the invention will also generally include regulatory elements that are functional in the intended host cell in which the expression construct is to be expressed. Thus, a person of ordinary skill in the art can select regulatory elements for use in, for example, bacterial host cells, yeast host cells, plant host cells, insect host cells, mammalian host cells, and human host cells. Regulatory elements include promoters, transcription termination sequences, translation termination sequences, enhancers, and polyadenylation elements.

An expression construct of the invention can comprise a promoter sequence operably linked to a polynucleotide sequence encoding a marker of the invention. Promoters can be incorporated into a polynucleotide using standard techniques known in the art. Multiple copies of promoters or multiple promoters can be used in an

expression construct of the invention. In a preferred embodiment, a promoter can be positioned about the same distance from the transcription start site as it is from the transcription start site in its natural genetic environment. Some variation in this distance is permitted without substantial decrease in promoter activity. A transcription start site is typically included in the expression construct.

For expression in prokaryotic systems, an expression construct of the invention can comprise promoters such as, for example, alkaline phosphatase promoter, tryptophan (trp) promoter, lambda P_L promoter, β -lactamase promoter, lactose promoter, phoA promoter, T3 promoter, T7 promoter, or tac promoter (de Boer *et al.*, 1983).

Expression constructs for use in bacteria are given in SEQ ID NOS. 11-14, and the corresponding amino acid sequences are given in SEQ ID NOS. 15-18.

If the expression construct is to be provided in a plant cell, plant viral promoters, such as, for example, the cauliflower mosaic virus (CaMV) 35S (including the enhanced CaMV 35S promoter (see, for example U.S. Patent No. 5,106,739)) or 19S promoter can be used. Plant promoters, such as prolifera promoter, Ap3 promoter, heat shock promoters, T-DNA 1'- or 2'-promoter of *A. tumefaciens*, polygalacturonase promoter, chalcone synthase A (CHS-A) promoter from petunia, tobacco PR-1a promoter, ubiquitin promoter, actin promoter, alcA gene promoter, pin2 promoter (Xu *et al.*, 1993), maize WipI promoter, maize trpA gene promoter (U.S. Patent No. 5,625,136), maize CDPK gene promoter, and RUBISCO SSU promoter (U.S. Patent No. 5,034,322) can also be used. Seed-specific promoters such as the promoter from a β -phaseolin gene (of kidney bean) or a glycinin gene (of soybean), and others, can also be used. Constitutive promoters (such as the CaMV, ubiquitin, actin, or NOS promoter), tissue-specific promoters (such as the E8 promoter from tomato), developmentally-regulated promoters, and inducible promoters (such as those promoters that can be induced by heat, light, hormones, or chemicals) are contemplated for use with the polynucleotides of the invention.

For expression in animal cells, an expression construct of the invention can comprise suitable promoters that can drive transcription of the polynucleotide sequence. If the cells are mammalian cells, then promoters such as, for example, actin promoter, metallothionein promoter, NF-kappaB promoter, EGR promoter, SRE promoter, IL-2 promoter, NFAT promoter, osteocalcin promoter, SV40 early

promoter and SV40 late promoter, Lck promoter, BMP5 promoter, TRP-1 promoter, murine mammary tumor virus long terminal repeat promoter, STAT promoter, or an immunoglobulin promoter can be used in the expression construct. The baculovirus polyhedrin promoter can be used with an expression construct of the invention for
5 expression in insect cells. Promoters suitable for use with an expression construct of the invention in yeast cells include, but are not limited to, 3-phosphoglycerate kinase promoter, glyceraldehyde-3-phosphate dehydrogenase promoter, metallothionein promoter, alcohol dehydrogenase-2 promoter, and hexokinase promoter.

Expression constructs of the invention may optionally contain a transcription
10 termination sequence, a translation termination sequence, signal peptide sequence, and/or enhancer elements. Transcription termination regions can typically be obtained from the 3' untranslated region of a eukaryotic or viral gene sequence. Transcription termination sequences can be positioned downstream of a coding sequence to provide for efficient termination. Signal peptides are a group of short
15 amino terminal sequences that encode information responsible for the relocation of an operably linked mature polypeptide to a wide range of post-translational cellular destinations, ranging from a specific organelle compartment to sites of protein action and the extracellular environment. Targeting marker gene products to an intended cellular and/or extracellular destination through the use of operably linked signal
20 peptide sequence is contemplated for use with the polypeptides of the invention. Enhancers are cis-acting elements that increase activity of a promoter and can also be included in the expression construct. Enhancer elements are known in the art, and include, but are not limited to, the CaMV 35S enhancer element, maize shrunken-1 enhancer element, cytomegalovirus (CMV) early promoter enhancer element, and the
25 SV40 enhancer element.

DNA sequences which direct polyadenylation of the mRNA encoded by the structural gene can also be included in the expression construct. The expression constructs of the invention can also include a polynucleotide sequence that directs transposition of other genes, *i.e.*, a transposon.

Applications

There are many ways in which the novel proteins of the subject invention can be used. In one embodiment, the proteins can be used to identify cells. In these

methods the proteins can be used to express fluorescence in a cell. One use for this method is in pre-labeling isolated cells or a population of similar cells prior to exposing the cells to an environment in which different cell types are present. Detection of fluorescence in only the original cells allows the location of such cells to be determined and compared with the total population.

A second group of methods concerns the identification of cells that have been transformed with exogenous DNA of interest. Identifying cells transformed with exogenous DNA is required in many *in vitro* procedures as well as in *in vivo* applications such as gene therapy.

In one embodiment of the subject invention, a polynucleotide sequence encoding a protein of the subject invention is fused to a DNA sequence encoding a selected protein in order to directly label the encoded protein. Expressing such a fluorescent and/or colored protein in a cell results in the production of labeled proteins that can be readily detected. This is useful in confirming that a protein is being produced by a chosen host cell. It also allows the location of the selected protein to be determined.

Cells that have been transformed with exogenous DNA can also be identified without creating a fusion protein. Here, the method relies on the identification of cells that have received a plasmid or vector that comprises at least two transcriptional or translational units. A first unit encodes and directs expression of the desired protein, while the second unit encodes and directs expression of the detectable protein. Co-expression of the detectable protein from the second transcriptional or translational unit ensures that cells containing the vector are detected and differentiated from cells that do not contain the vector.

In methods to produce fluorescent molecular weight markers, a gene sequence is generally fused to one or more DNA sequences that encode proteins having defined amino acid sequences and the fusion proteins are expressed from an expression vector. Expression results in the production of fluorescent proteins of defined molecular weight or weights that may be used as markers (following calculation of the size of the complete amino acid sequence).

Amino acid replacements that produce different color forms permit simultaneous use of multiple reporter genes. Different colored proteins can be used to identify multiple cell populations in a mixed cell culture or to track multiple cell

types, enabling differences in cell movement or migration to be visualized in real time without the need to add additional agents or fix or kill the cells.

Other options include tracking and determining the ultimate location of multiple proteins within a single cell, tissue or organism; differential promoter analysis in which gene expression from two different promoters is determined in the same cell, tissue or organism; and FACS sorting of mixed cell populations.

The techniques that can be used with spectrally separable proteins are exemplified by confocal microscopy, flow cytometry, and fluorescence activated cell sorting (FACS) using modular flow, dual excitation techniques.

In one embodiment, the subject invention concerns polynucleotides comprising an in-frame fusion of nucleotide sequences encoding multiple genetic markers. For example, a polynucleotide of the invention may comprise a first nucleotide sequence that is operably linked in-frame to a second nucleotide sequence. The polynucleotide encodes the amino acid sequences of the detectable protein and another genetic marker such that the genetic markers are in direct contact with one another, *i.e.*, where the last amino acid of the fluorescent genetic marker is immediately contiguous with the first amino acid of the other genetic marker, or they can be separated by a peptide linker sequence, for example, as described in U.S. Patent Nos. 5,891,680 and Li *et al.*, 2001, that do not substantially alter functional activity of the genetic markers.

The subject invention also concerns kits comprising in one or more containers and a polynucleotide and/or protein of the present invention.

Additional useful applications of the technology described herein include, but are not limited to, the following:

FRET – Fluorescence Resonant Energy Transfer: This technique allows observation and quantification of molecular interactions. It requires at least two fluorescent proteins of different colors. Currently the most widely used pair is CFP and YFP (mutated variants of GFP); the proteins of the subject invention may be substituted for either or both of them.

References:

1. Hanson, M. R. and R. H. Kohler. 2001. GFP imaging: methodology and application to investigate cellular compartmentation in plants. *J Exp Bot* 52: 529-539.
2. Pollok, B. A. and R. Heim. 1999. Using GFP in FRET-based applications. *Trends Cell Biol* 9: 57-60.
3. Schuttrigkeit, T. A., U. Zachariae, T. von Feilitzsch, J. Wiehler, J. von Hummel, B. Steipe and M. E. Michel-Beyerle. 2001. Picosecond time-resolved FRET in the fluorescent protein from *Discosoma Red* (wt-DsRed). *Chemphyschem* 2: 325-328.
4. Hillisch, A., M. Lorenz and S. Diekmann. 2001. Recent advances in FRET: distance determination in protein-DNA complexes. *Curr Opin Struct Biol* 11: 201-207.

FRAP – Fluorescence Redistribution After Photobleaching: This technique quantifies the dynamics of tagged molecules or the reporter molecules themselves. It involves in photobleaching (burning out) of all the fluorescent molecules within a small area by intense excitation light and monitoring the process of fluorescence recovery within this area (due to migration of tagged molecules from adjacent areas).

References:

1. Reits, E. A. and J. J. Neefjes. 2001. From fixed to FRAP: measuring protein mobility and activity in living cells. *Nat Cell Biol* 3: E145-147.
2. Houtsmuller, A. B. and W. Vermeulen. 2001. Macromolecular dynamics in living cell nuclei revealed by fluorescence redistribution after photobleaching. *Histochem Cell Biol* 115: 13-21.

“Fluorescent timer” applications: one of the proteins exemplified herein – scubRFP – due to its natural spectroscopic properties, can be used as a reporter that changes color with time. Such reporters make it possible to estimate the time elapsed since the reporter protein was synthesized by quantifying its color. In addition, since the maturation speed (the rate of conversion from green to red) in scubRFP can be increased by UV-A light, it is possible to adjust its timing scale: experiments that need timing in shorter intervals may use appropriate background UV illumination to speed up the green-to-red conversion.

References:

1. Terskikh, A. V., A. Fradkov, A. Zarauskiy, A. V. Kajava, M. Matz, S. Kim, I. Weissman and P. Siebert. 2000. "Fluorescent timer": Protein that changes color over time. *Molecular Biology of the Cell* 11: 648.
- 5 2. Verkhusha, V. V., H. Otsuna, T. Awasaki, H. Oda, S. Tsukita and K. Ito. 2001. An enhanced mutant of red fluorescent protein DsRed for double labeling and developmental timer of neural fiber bundle formation. *Journal of Biological Chemistry* 276: 29621-29624.

10 "Light-inducible fluorescence": since the red fluorescence of scubRFP can be induced by exposure to UV-A light, it is possible to use this protein as a light-inducible reporter. Such a reporter can be used for studying molecular dynamics, in a way that is analogous to FRAP (see above). A small area can be irradiated by the fluorescence-inducing light, after which the process of redistribution of active fluorescent
15 molecules from the irradiated spot can be followed.

References:

1. Ando, R., H. Hama, M. Yamamoto-Hino, H. Mizuno and A. Miyawaki. 2002. An optical marker based on the UV-induced green-to-red photoconversion of a fluorescent protein. *Proceedings of the National Academy of Sciences of the*
20 United States of America 99: 12651-12656.
2. Patterson, G. H. and J. Lippincott-Schwartz. 2002. A photoactivatable GFP for selective photolabeling of proteins and cells. *Science* 297: 1873-1877.
3. Chudakov, D. M., V. V. Belousov, A. G. Zarausky, V. V. Novoselov, D. B. Staroverov, D. B. Zorov, S. Lukyanov and K. A. Lukyanov. 2003. Kindling
25 fluorescent proteins for precise in vivo photolabeling (vol 21, pg 191, 2003). *Nature Biotechnology* 21: 452-452.

30 Coloring of biological objects for decorative and other non-scientific purposes. Examples: producing decorative fish for aquariums; coloring of fur, wool and milk by means of genetic modifications of appropriate animals; and coloring of decorative plants. Such uses can be implemented by a person skilled in the art having the benefit of the teachings of the current disclosure.

All patents, patent applications, provisional applications, and publications referred to or cited herein are incorporated by reference in their entirety, including all figures and tables, to the extent they are not inconsistent with the explicit teachings of this specification.

5

Following are examples which illustrate procedures for practicing the invention. These examples should not be construed as limiting. All percentages are by weight and all solvent mixture proportions are by volume unless otherwise noted.

10 Example 1 — Bacterial Expression Construct

As illustrated in Figure 1, to prepare a bacterial expression construct, the ORF of the target detectable protein was amplified by means of polymerase chain reaction (PCR), using primers corresponding to the beginning and end of the protein's ORF. The upstream primer carried a 5'-heel **ttgattgattgaaggagaaat**atcATG (SEQ ID NO:1),
15 which encoded three termination codons in three frames (bold), followed by the ribosome binding site (underlined), 6 spacer bases and initiation ATG codon.

The downstream primer encoded a 6xHis tag in place of the original termination codon (the heel sequence was 5'-tta tta gtg atg gtg atg gtg atg (SEQ ID NO:2)), to facilitate protein purification by means of metal-affinity chromatography.

20 The products of amplification were cloned into pGEM-T vector (Promega) using manufacturer-provided reagents and protocol. The expressing clones were identified after overnight growth of the colonies by their fluorescent appearance.

Example 2 — Additional Proteins and Polynucleotides

25 The subject invention also provides proteins from *Acropora* ("staghorn corals") and *Agarica fragilis* ("fragile saucer coral"), as well as polynucleotides encoding these proteins.

In one embodiment, the invention provides nucleotide sequences of the inserts in pGEM-T vector (Promega), the conceptual translations of these inserts, and special
30 properties of purified protein products.

The vector constructs are shown in SEQ ID NOs.:19-44. The encoded proteins are shown in SEQ ID NOs.:45-70. The open reading frames encoding the

proteins of SEQ ID NOs.: 45-70 are shown in SEQ ID NOs.:71-96. The spectral characteristics of the proteins are shown in Figures 4-29.

Example 3 — Excitation and emission spectra of the detectable proteins

5 The excitation spectra were measured from the proteins purified after bacterial expression. The spectra are shown in Figures 2-29. Emission spectra (dotted lines) were measured using USB2000 uv-vis spectrometer (Ocean Optics), excitation spectra (solid lines) – using spectrofluorometer LS-50B (Perkin Elmer). The indicated positions of excitation and emission maxima are accurate within 5 nm.

Example 4 — Multiple Marker Constructs

10 There are several advantages associated with the use of fusion markers, including: 1) achievement of combined functionalities in a single transcription unit, 2) reduced usage of genetic elements, such as promoters and terminators, for expressing multiple marker genes, 3) reduced overall length of insertion sequences that may lead to increased transformation efficiency, and most importantly 4) elimination of molecular interactions between adjacent genetic elements. Such unwanted interactions are frequently encountered when multiple expression units associated with different marker genes are used simultaneously and often complicate the interpretation of expression results.

20 In an effort to improve marker functionality and versatility, several translational fusions between two genetic markers have been developed. Datla *et al.* (1991; U.S. Patent No. 5,639,663) created a bifunctional fusion between GUS and neomycin phosphotransferase (NPTII) to provide a biochemically assayable reporter activity and a conditionally selectable growth advantage for use in plant transformation. Another bifunctional fusion, between GUS and GFP, was also developed to provide both indicative and assayable reporter activities for monitoring transient and stable transgene expression in plant cells (Quaedvlieg *et al.*, 1998). More recently, Li *et al.* (2001) constructed a bifunctional fusion between GFP and NPTII and successfully used this marker for continuous analysis of promoter activity and transgene expression in transgenic grape plants throughout the entire process of plant development.

Small portions of a protein that provide unique functions such as protein/DNA/substrate binding activity can be inserted into another heterologous protein to create a hybrid fusion with enhanced functionality and utility. In other cases, an entire gene or protein of interest has been fused in-frame to another heterologous gene or protein to form a double fusion to provide combined functionalities. Production of multiple proteins using fusion constructs composed of two genes from transgenic plants has been demonstrated previously (U.S. Patent No. 6,455,759).

In one embodiment, the subject invention provides cells transformed with a polynucleotide of the present invention comprising an in-frame fusion of nucleotide sequences encoding multiple markers. Preferably, the polynucleotide sequence is provided in an expression construct of the invention. The transformed cell can be a prokaryotic cell, for example, a bacterial cell such as *E. coli* or *B. subtilis*, or the transformed cell can be a eukaryotic cell, for example, a plant or animal cell. Animal cells include human cells, mammalian cells, avian cells, fish cells and insect cells. Mammalian cells include, but are not limited to, COS, 3T3, and CHO cells.

Genetic markers that can be used in conjunction with the detectable proteins of the present invention are known in the art and include, for example, polynucleotides encoding proteins that confer a conditionally selective growth advantage, such as antibiotic resistance and herbicide-resistance; polynucleotides encoding proteins that confer a biochemically assayable reporter activity; and polynucleotides encoding proteins that confer an indicative reporter activity. Examples of polynucleotides encoding proteins providing antibiotic resistance include those that can provide for resistance to one or more of the following antibiotics: hygromycin, kanamycin, bleomycin, G418, streptomycin, paromomycin, and spectinomycin. Kanamycin resistance can be provided by neomycin phosphotransferase (NPTII). Examples of polynucleotides encoding proteins providing herbicide resistance include those that can provide for resistance to phosphinothricin acetyltransferase or glyphosate. Examples of genetic markers that confer assayable or indicative reporters activity that can be used in the present invention include, but are not limited to, polynucleotides encoding β -glucuronidase (GUS), β -galactosidase, chloramphenicol acetyltransferase (CAT), luciferase, nopaline synthase (NOS), and green fluorescence protein (GFP).

It should be understood that the examples and embodiments described herein are for illustrative purposes only and that various modifications or changes in light thereof will be suggested to persons skilled in the art and are to be included within the spirit and purview of this application.

Claims

We claim:

1. A protein comprising an amino sequence selected from the group consisting of SEQ. ID NOs: 7-10, SEQ ID NOs: 45-70, fragments of these sequences, and variants of these sequences and fragments; wherein the amino acid sequence of a variant is at least 90% identical to at least one of said SEQ ID NOs.:7-10 and 45-70 or a fragment of one of said sequences; and wherein said fragments and said variants have emission and excitation maxima there are within ± 10 nm of the emission and excitation maxima for at least one of SEQ ID NOs.: 7-10 and SEQ ID NOs. 45-70.

2. The protein, according to claim 1, wherein said protein has an amino acid sequence selected from the group consisting of SEQ. ID NOs: 7-10 and SEQ ID NOs: 45-70.

3. The protein, according to claim 1, wherein said protein has an amino acid sequence selected from the group consisting of SEQ. ID NOs: 7-10.

4. The protein, according to claim 1, wherein said protein has SEQ ID NO:10.

5. A polynucleotide sequence that encodes a protein comprising an amino sequence selected from the group consisting of SEQ. ID NOs: 7-10, SEQ ID NOs: 45-70, fragments of these sequences, and variants of these sequences and fragments; wherein the amino acid sequence of a variant is at least 90% identical to at least one of said SEQ ID NOs.:7-10 and 45-70, or a fragment of one of said sequences; and wherein said fragments and said variants have emission and excitation maxima there are within ± 10 nm of the emission and excitation maxima for at least one of SEQ ID NOs.: 7-10 and SEQ ID NOs. 45-70.

6. The polynucleotide sequence, according to claim 5, wherein said polynucleotide has a sequence is selected from the group consisting of SEQ. ID NOs: 3-6 and SEQ ID NOs: 71-96.

7. A polynucleotide sequence selected from the group consisting of SEQ ID NOs: 11-14 and SEQ ID NOs: 19-44.

8. A protein selected from the group consisting of the proteins expressed when a bacterium is transformed with a polynucleotide sequence selected from the group consisting of SEQ ID NOs: 11-14 and SEQ ID NOs: 19-44.

9. Use of a protein, wherein said protein comprises a protein comprising an amino sequence selected from the group consisting of SEQ. ID NOs: 7-10, SEQ ID NOs: 45-70, fragments of these sequences, and variants of these sequences and fragments; wherein the amino acid sequence of a variant is at least 90% identical to at least one of said SEQ ID NOs.:7-10 and 45-70, or a fragment of one of said sequences; and wherein said fragments and said variants have emission and excitation maxima there are within ± 10 nm of the emission and excitation maxima for at least one of SEQ ID NOs.: 7-10 and SEQ ID NOs. 45-70, for monitoring gene expression; as a tag for tracing the location of proteins; as a reporter molecule in a protein-based biosensor; or as a pigment for modifying the color, or fluorescence, or both, of living tissue.

10. The use, according to claim 9, wherein a polynucleotide that encodes said protein is fused with a polynucleotide that encodes a protein of interest.

11. A cell transformed to express a heterologous polynucleotide wherein said heterologous polynucleotide encodes a protein comprising an amino sequence selected from the group consisting of SEQ. ID NOs: 7-10, SEQ ID NOs: 45-70, fragments of these sequences, and variants of these sequences and fragments; wherein the amino acid sequence of a variant is at least 90% identical to at least one of said SEQ ID NOs.:7-10 and 45-70 or a fragment of one of said sequences; and wherein said fragments and said variants have emission and excitation maxima there are within ± 10 nm of the emission and excitation maxima for at least one of SEQ ID NOs.: 7-10 and SEQ ID NOs. 45-70.

12. The cell, according to claim 11, wherein said cell is a plant cell.

13. The cell, according to claim 11, wherein said cell is a fish cell.

14. A polynucleotide encoding multiple markers wherein at least one of said markers is selected from the group consisting of a protein comprising an amino sequence selected from the group consisting of SEQ. ID NOs: 7-10, SEQ ID NOs: 45-70, fragments of these sequences, and variants of these sequences and fragments; wherein the amino acid sequence of a variant is at least 90% identical to at least one of said SEQ ID NOs.:7-10 and 45-70 or a fragment of one of said sequences; and wherein said fragments and said variants have emission and excitation maxima there are within ± 10 nm of the emission and excitation maxima for at least one of SEQ ID NOs.: 7-10 and SEQ ID NOs. 45-70.

15. The polynucleotide, according to claim 14, wherein one of said markers is GUS.

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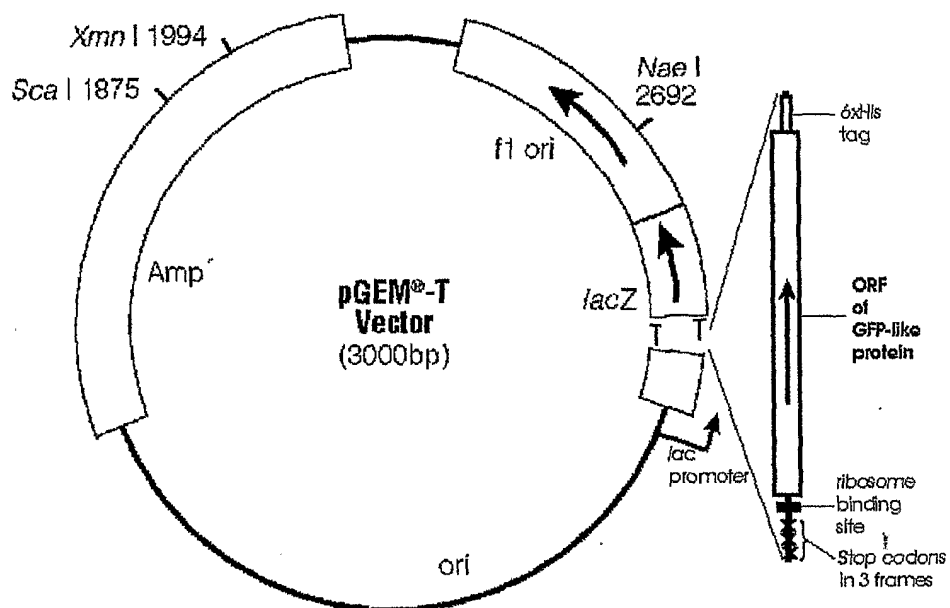


FIG. 1

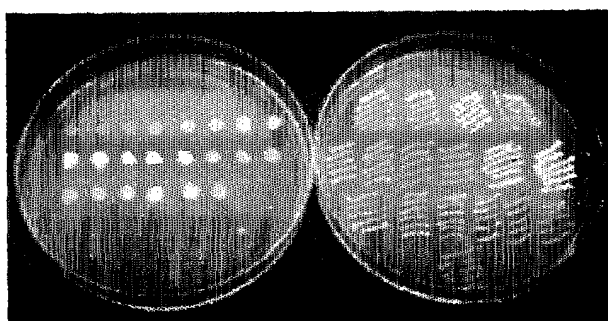


FIG. 2

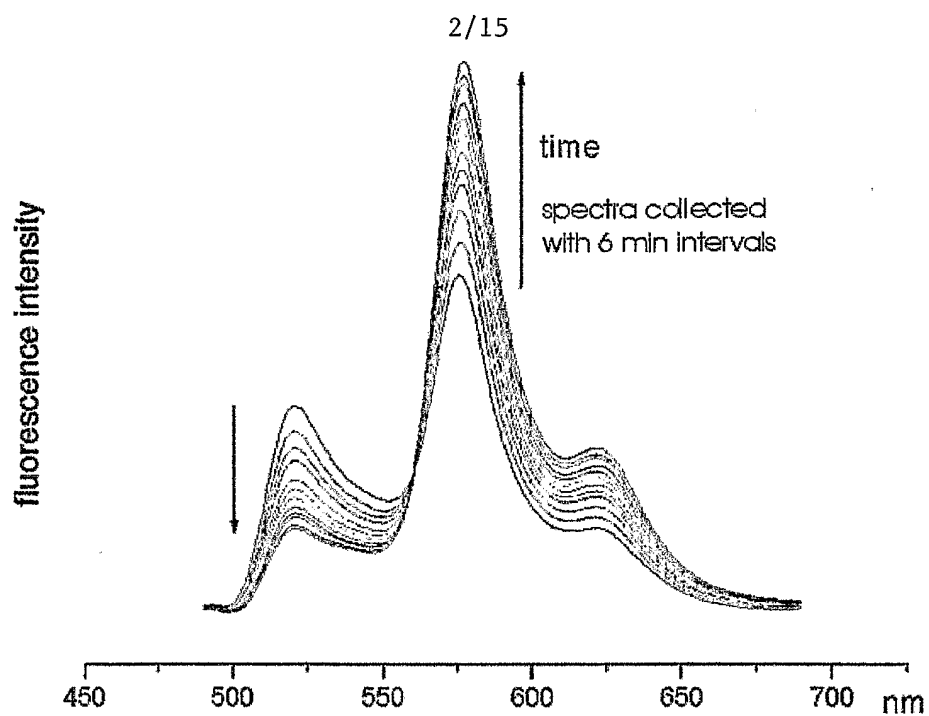


FIG. 3A

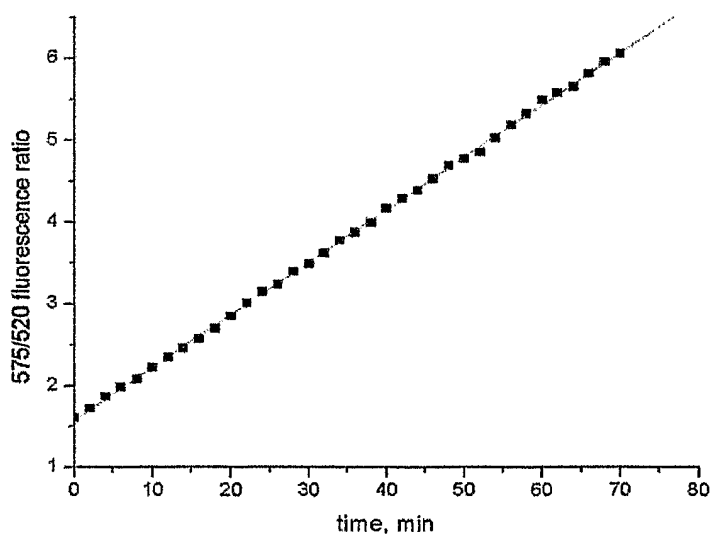


FIG. 3B

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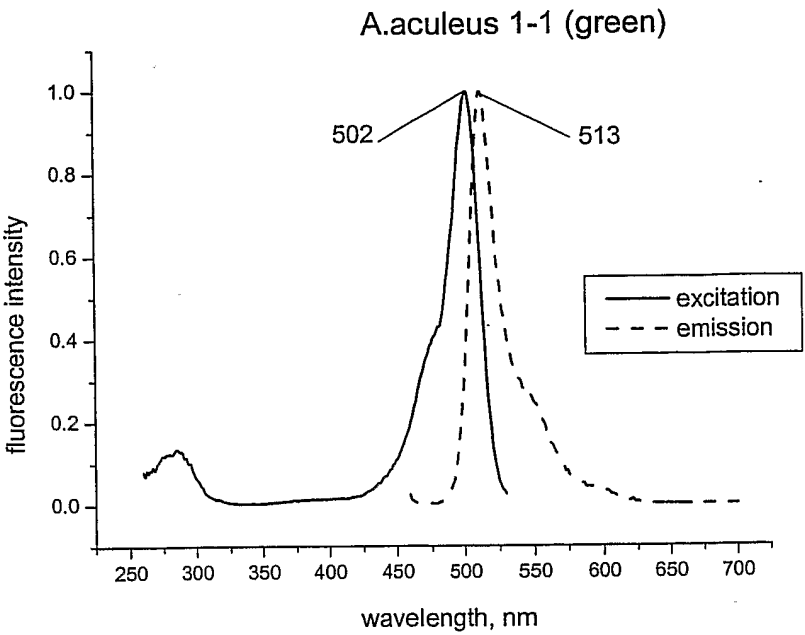


FIG. 4

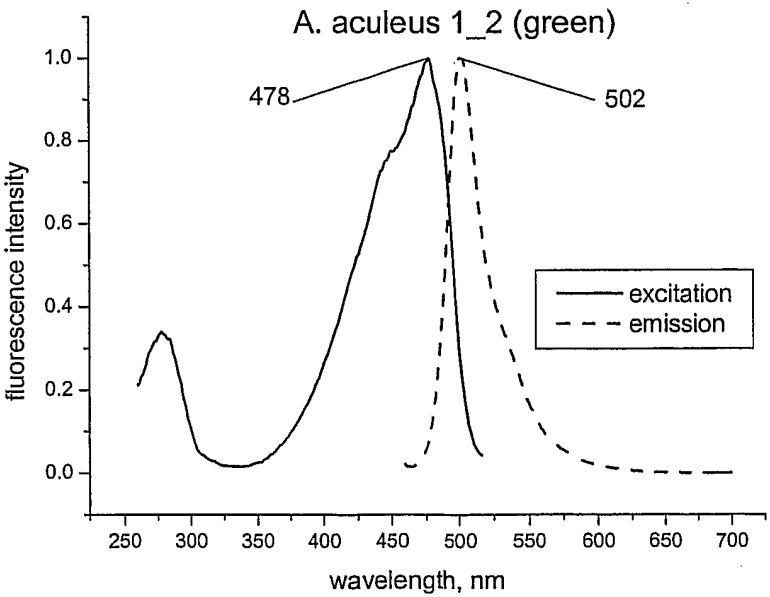


FIG. 5

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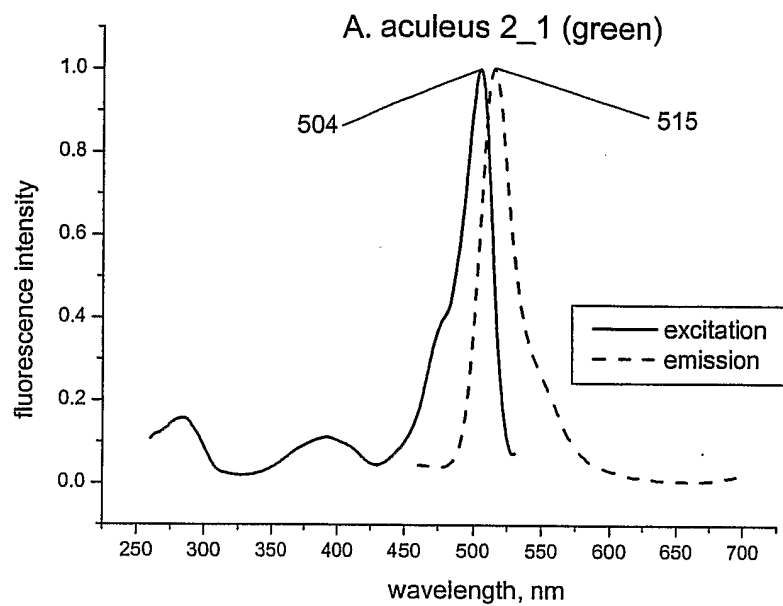


FIG. 6

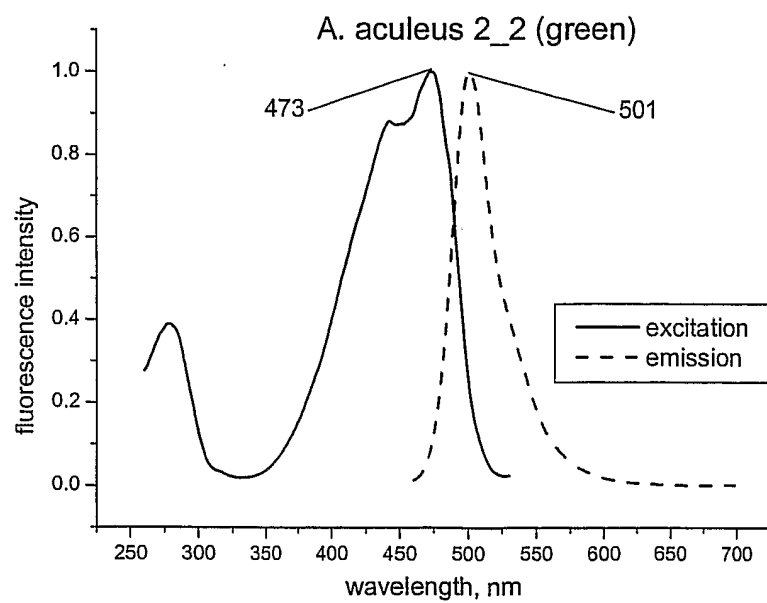


FIG. 7

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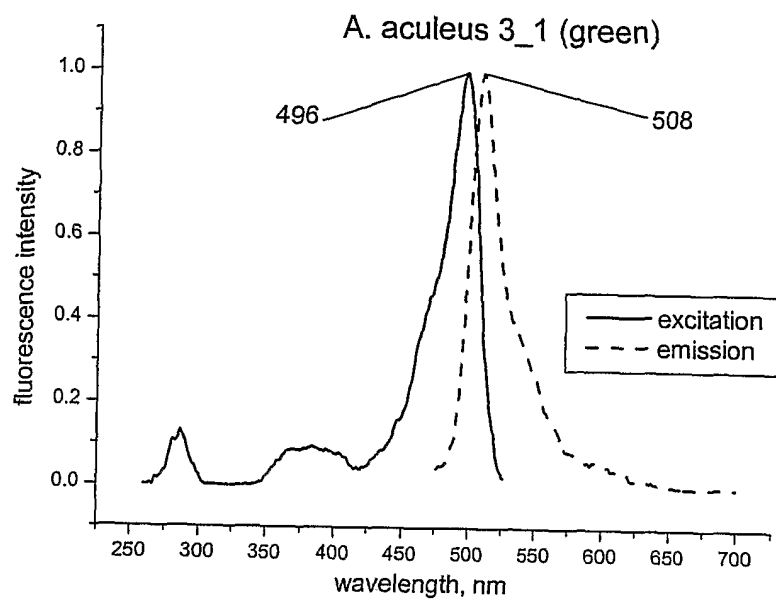


FIG. 8

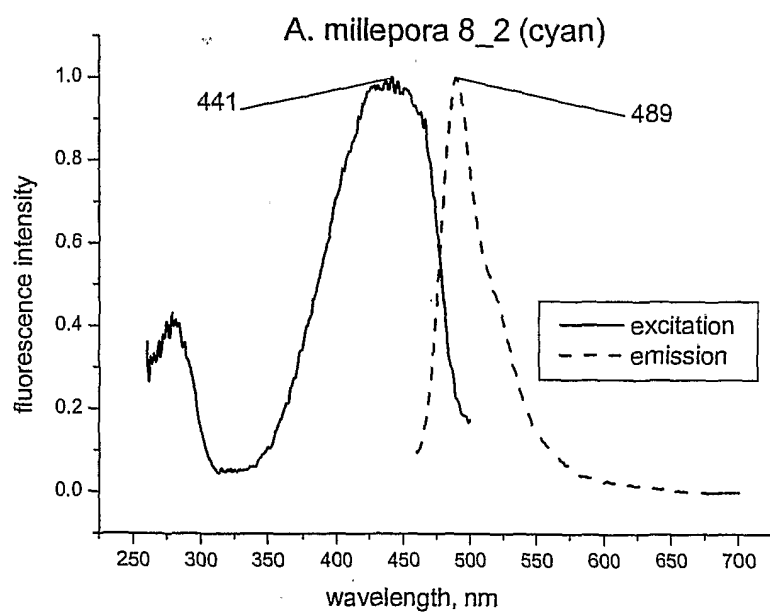


FIG. 9

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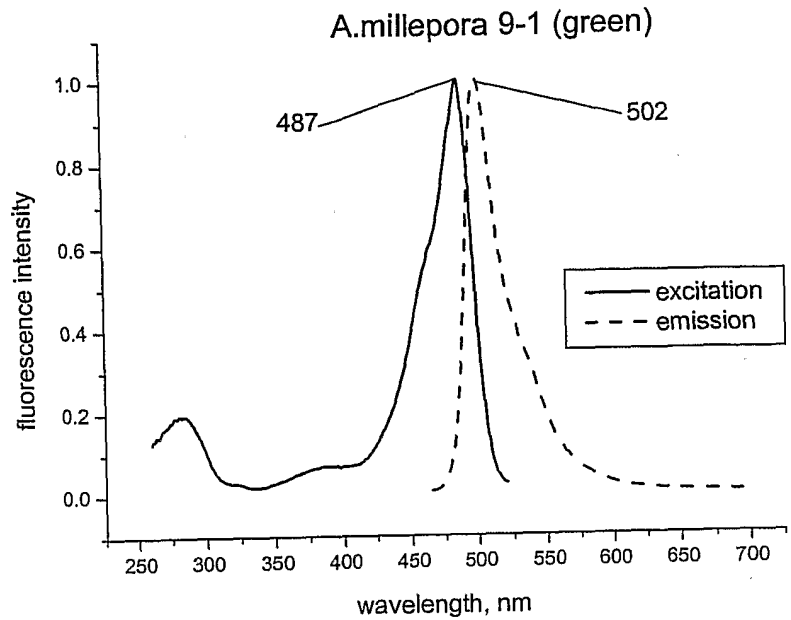


FIG. 10

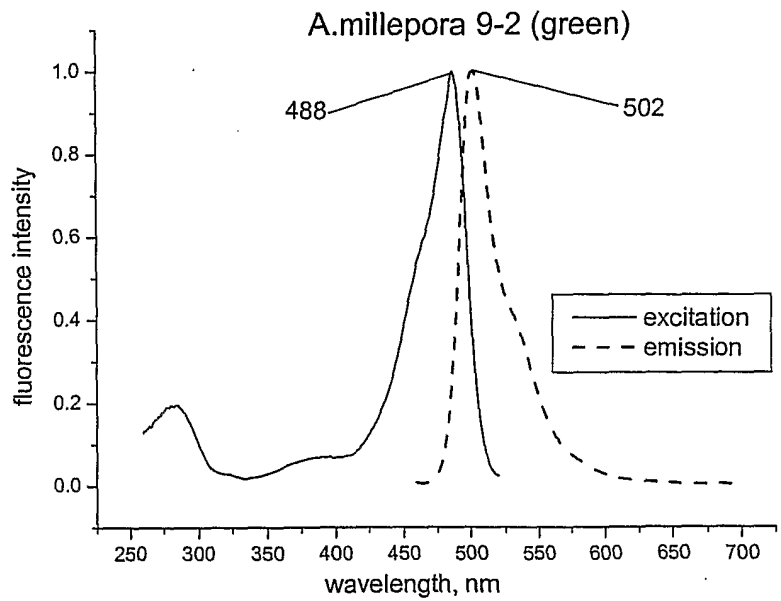


FIG. 11

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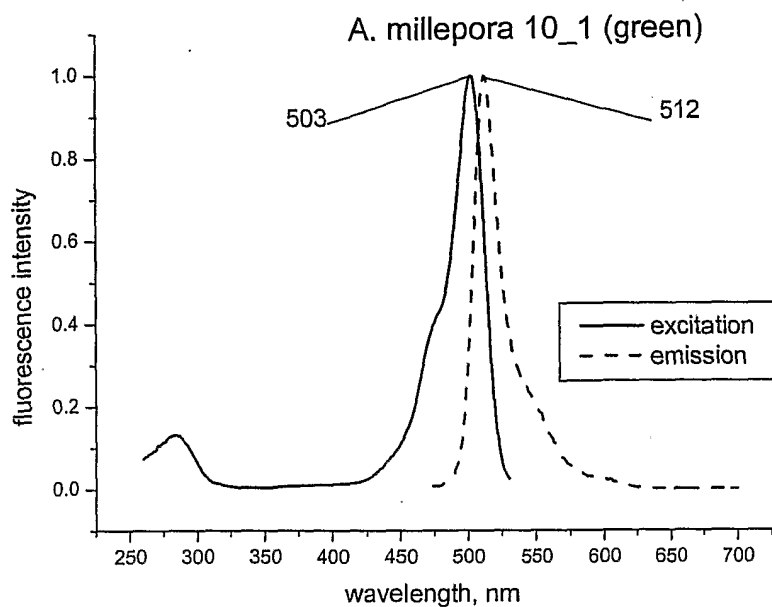


FIG. 12

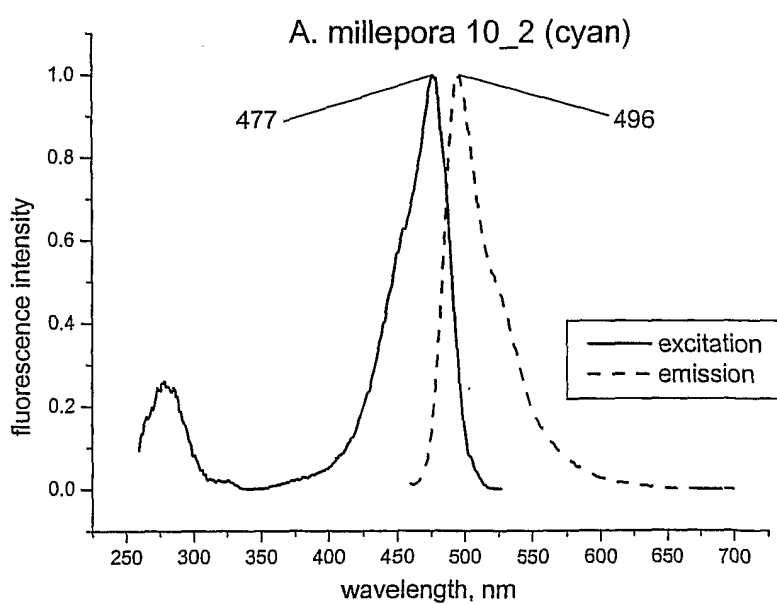


FIG. 13

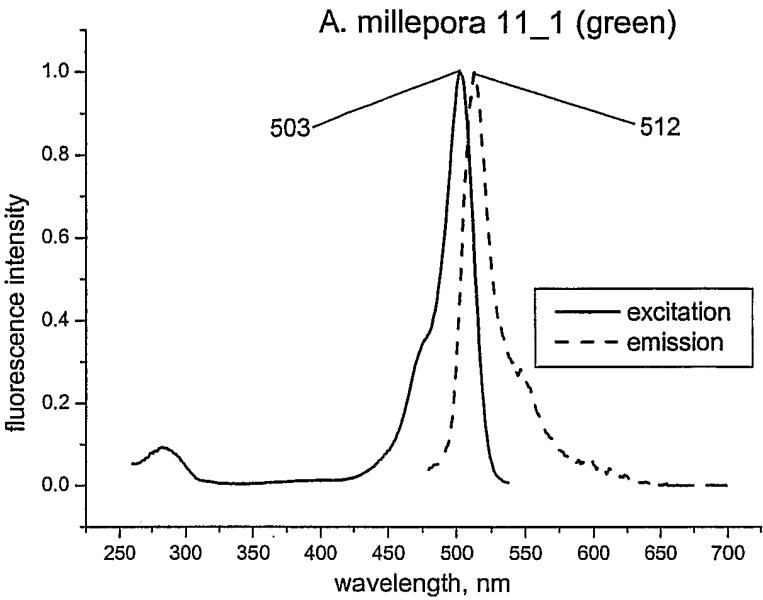


FIG. 14

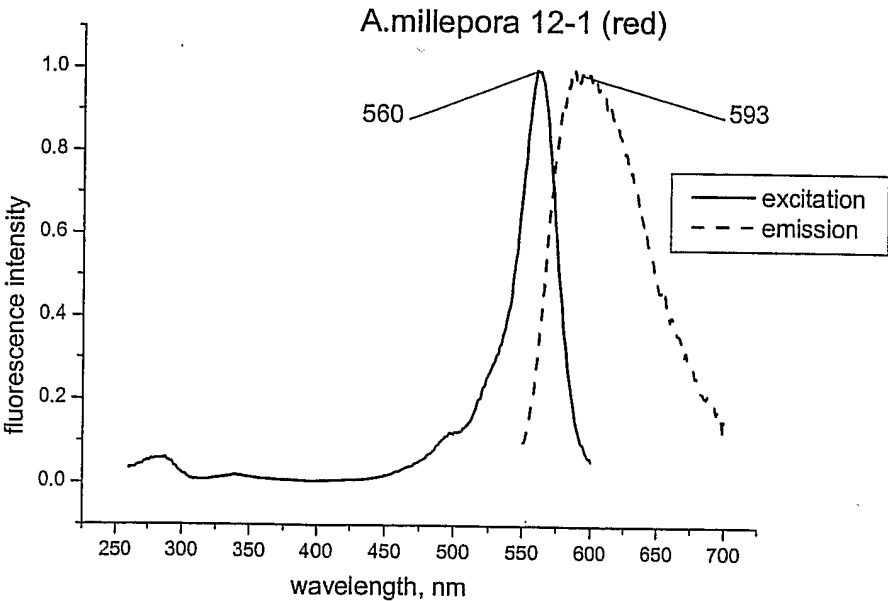


FIG. 15

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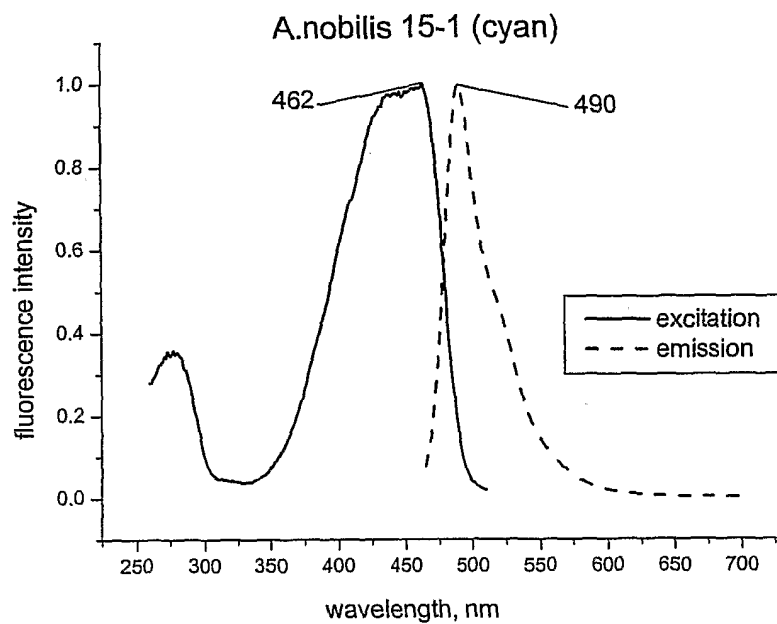


FIG. 16

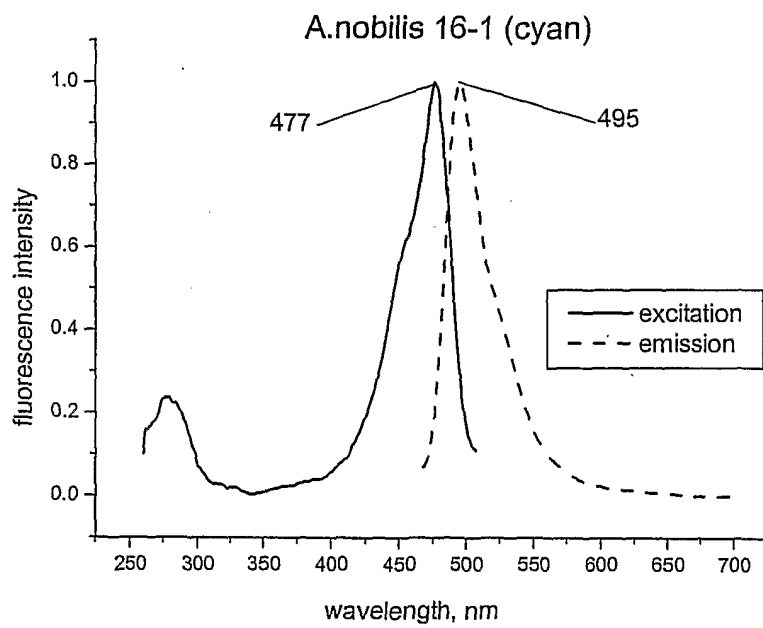


FIG. 17

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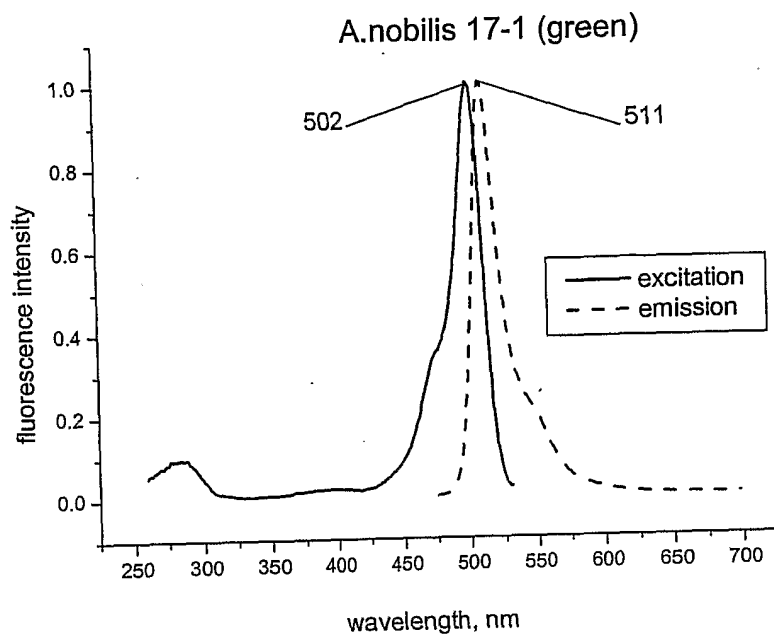


FIG. 18

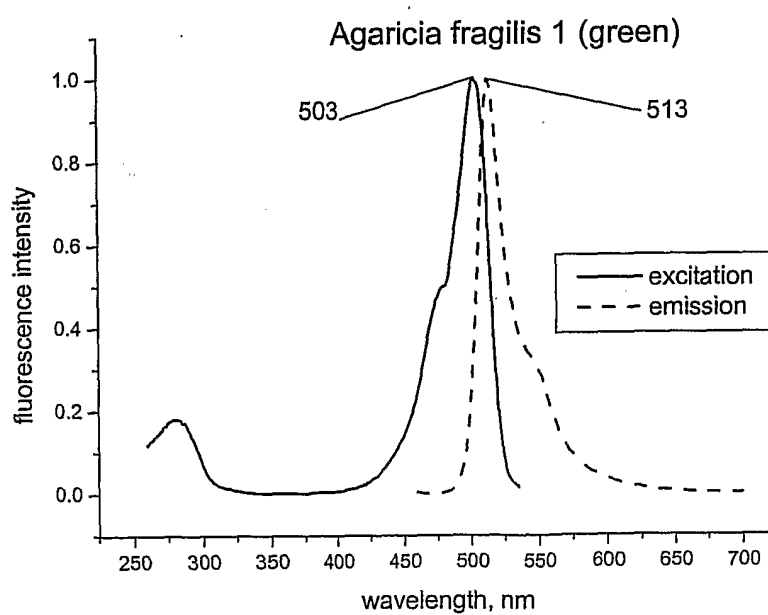


FIG. 19

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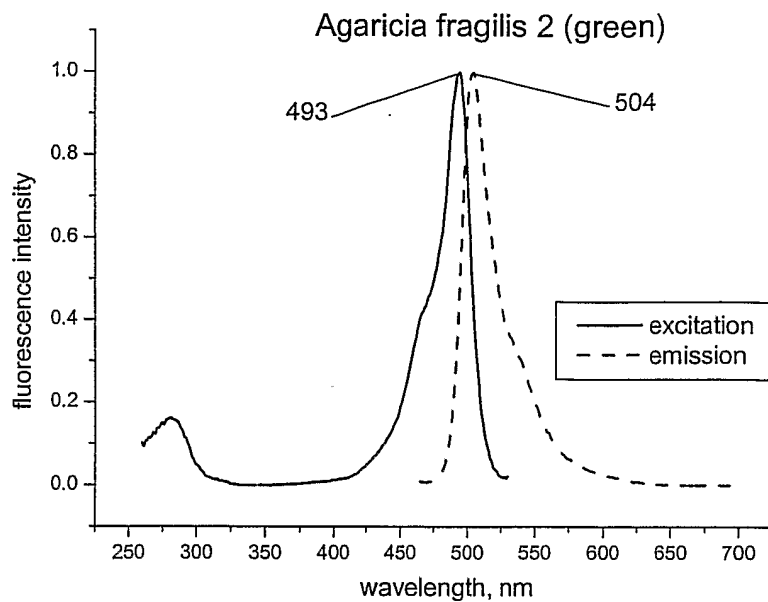


FIG. 20

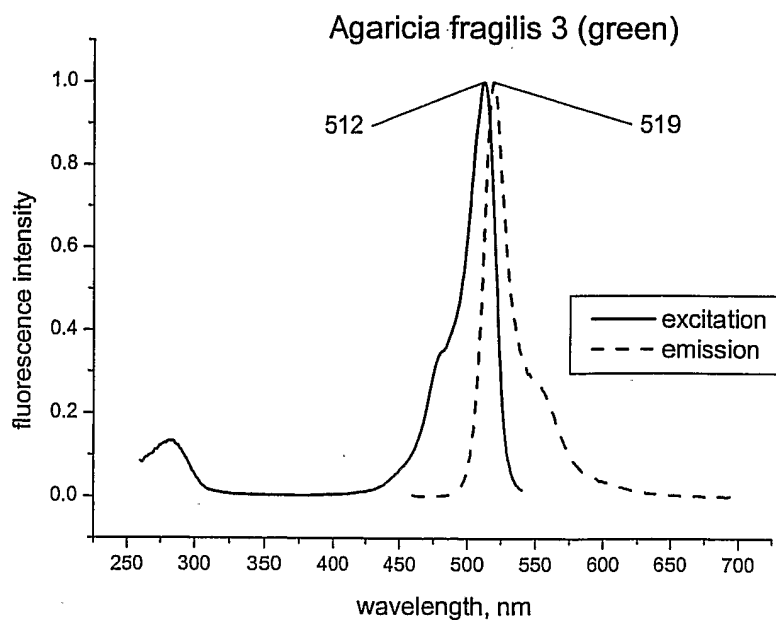


FIG. 21

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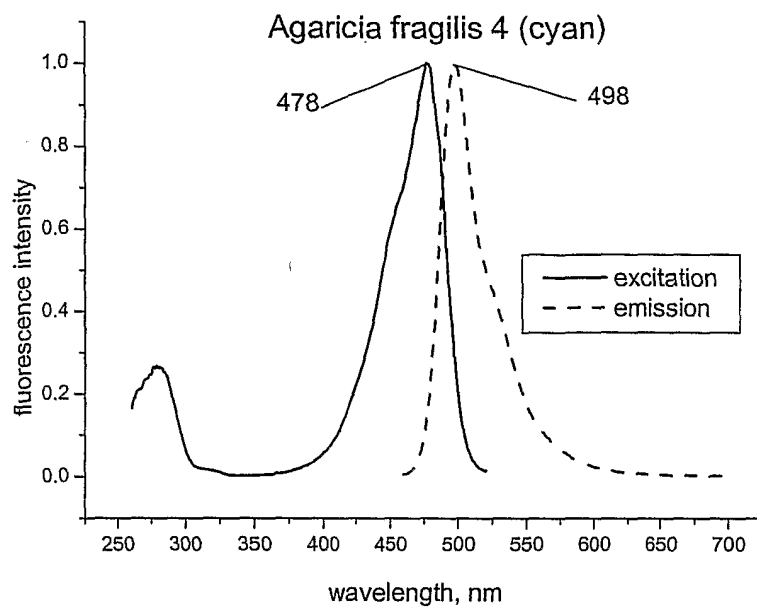


FIG. 22

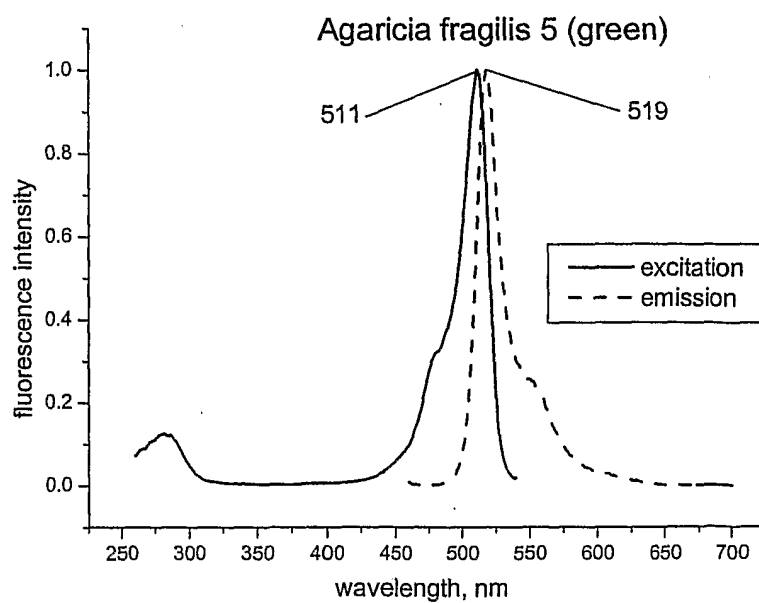


FIG. 23

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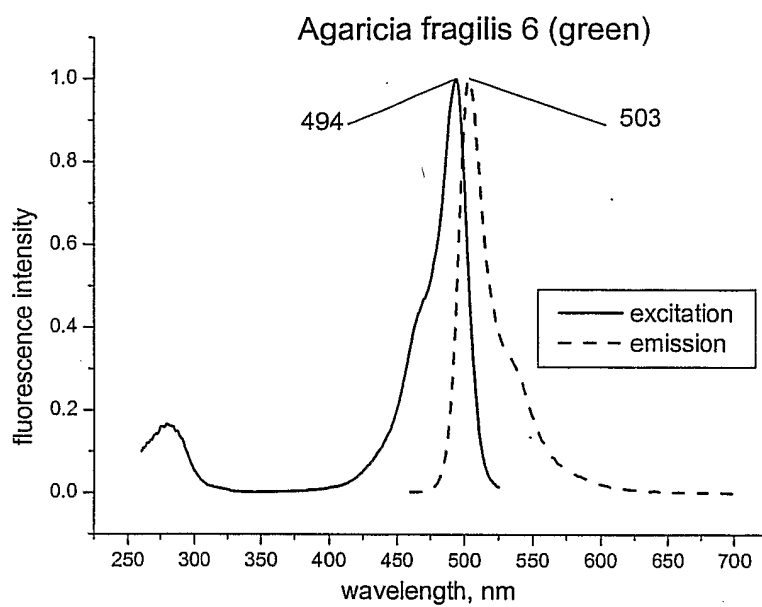


FIG. 24

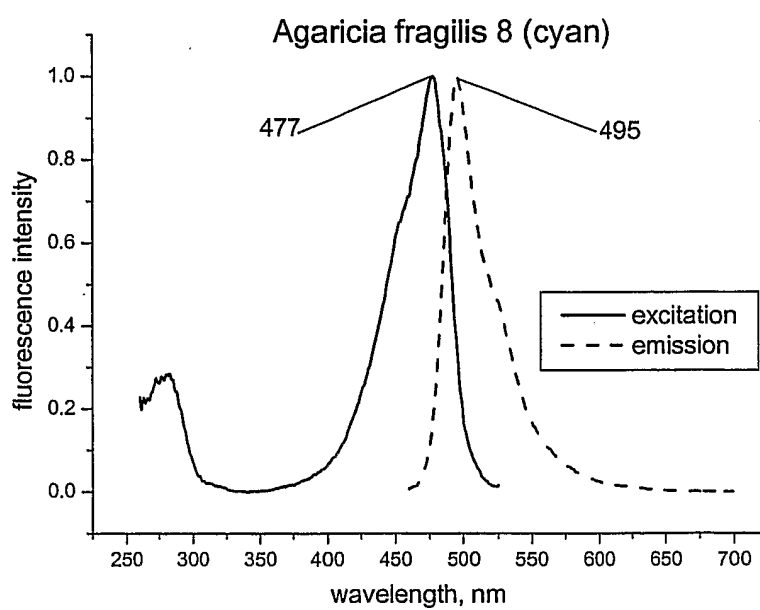


FIG. 25

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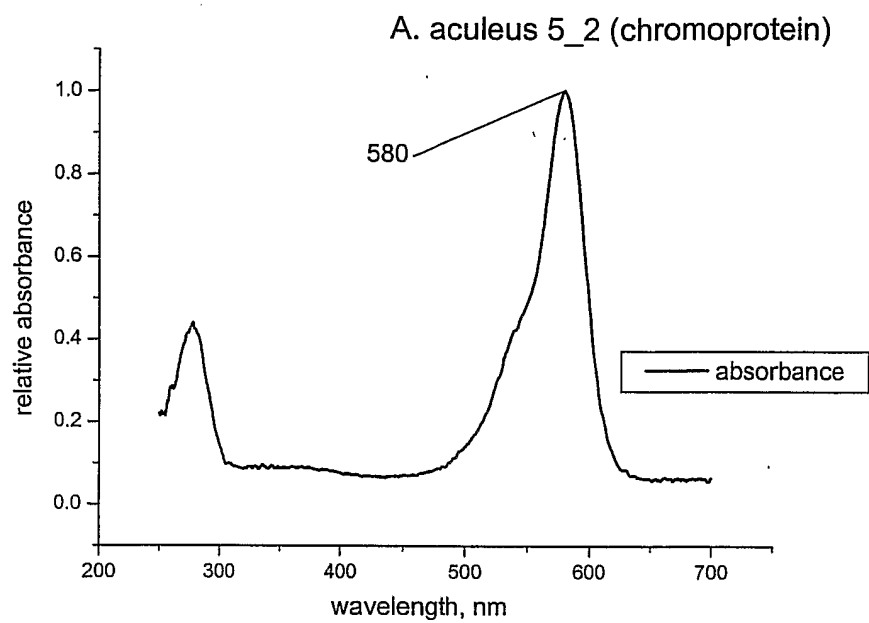


FIG. 26

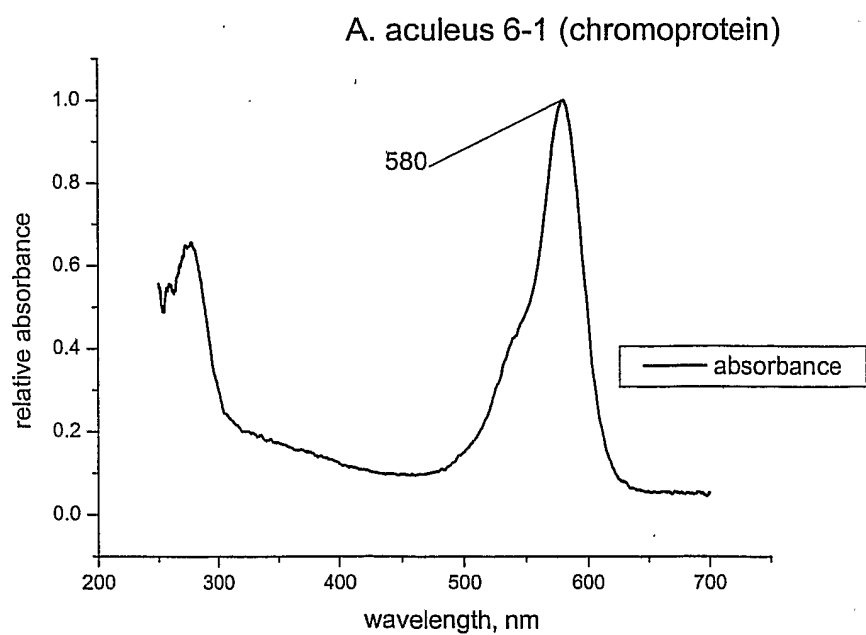


FIG. 27

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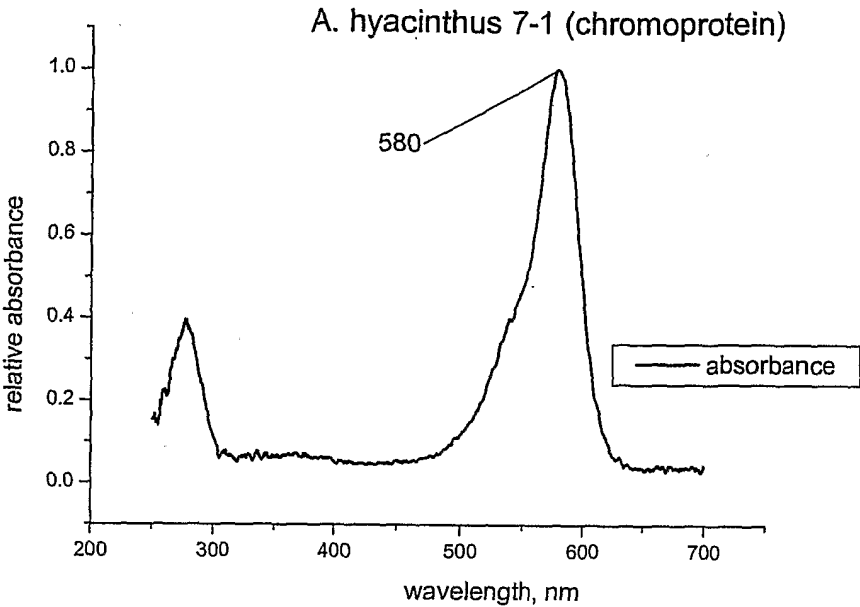


FIG. 28

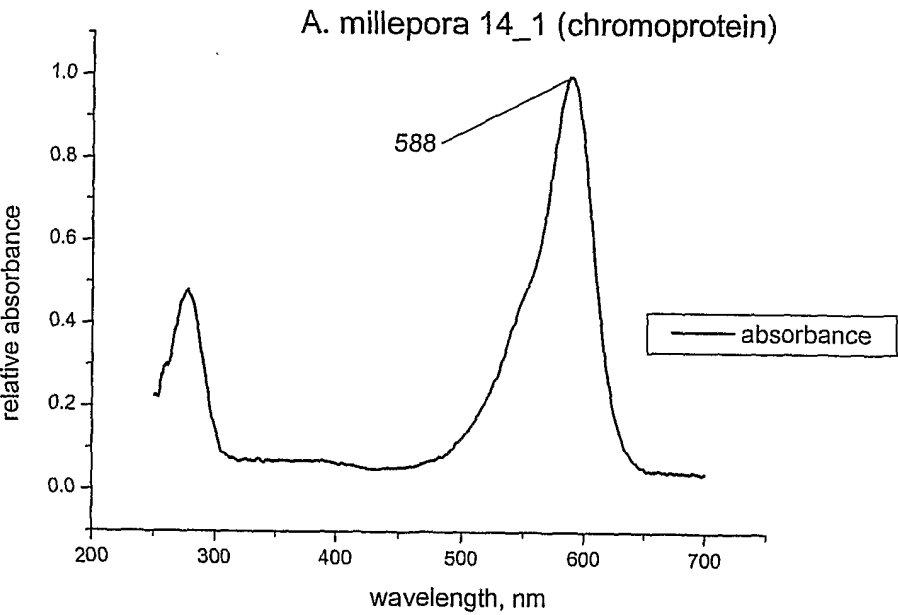


FIG. 29

SEQUENCE LISTING

<110> University of Florida Research Foundation, Inc.
Matz, Mikhail
Kelmanson, Ilya
Salih, Anya
Meleshkevitch, Ella

<120> Novel Fluorescent and Colored Proteins, and Polynucleotides that
Encode These Proteins

<130> UF-364XC1

<150> US 60/472,196
<151> 2003-05-20

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Asn Arg Val Phe Thr Lys Tyr Pro Arg Asp Ile Pro Asp Tyr Phe Lys
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Gln Ser Phe Pro Glu Gly Tyr Ser Trp Glu Arg Ser Met Thr Phe Glu
85 90 95

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

Cys Phe Phe Tyr Glu Ile Arg Phe Tyr Gly Val Asn Phe Pro Ser Asn
115 120 125

Gly Pro Val Met Gln Lys Lys Thr Leu Lys Trp Glu Pro Ser Thr Glu
130 135 140

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

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 115 120 125
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tgctttatct atgaaattcg atatgatggg gtgaactttc cccaagtgg tccagttatg      420
caaaagaaga cgctgaaatg ggagccatcc actgagaaaa tgtatgtgcg tgatggagtg      480
ctgaaggggtg atgttaacat ggctctgttg cttgaaggag gtggccatta ccgatgtgac      540
tttcgaagta cttacaaagc gaagaaacgt gttcagttgc cagactatca ctttgtggac      600
caccgcattg agattttgag ccatgacaat gactacaaca ccgtaaagct gtctgagaat      660
gccgaggtc gctattctat gctgccgagt caggccaagg aaagtgcaca tcaccatcac      720
catcactaa                                     729

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<210> 13

<211> 729

<212> DNA

<213> Montastraea cavernosa

<400> 13

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ttgattgatt gaaggagaaa tatcatgagt gtgattaaac cagatatgaa gatcaagctg      60
cgtatgcaag gcgttgtaaa cgggcacaag ttcgtgatta aaggagaagg agagggcaag      120
cctttcgagg gaacgcagac tataaacctt acagtcaaag aaggcgcacc tctccctttt      180
gcttacgaca tcttgacatc agcattccag tatggcaaca gggcattcac caaatatcca      240
gacgatatac cagactattt caagcagacg tttcctgaag ggtattcgtg ggagcgaatc      300
atggcttatg aagaccagag tatttgcacg gccacaagcg acataaaaat ggaaggcgac      360
tgttttatct acgaaattca atttcatggg gtgaactttc caccaatgg tccagttatg      420
cagaagaaga cgctgaaatg ggaaccatcc accgagaaaa tgtatgtgcg tgatggagtg      480
ctgaaggggtg atgttaacat ggctctgttg cttgaaggag gtggccatta ccgatgtgac      540
ttcagaagta cttacaaagc gaagaaggat gttcatttgc cagactatca ctacgtggac      600
caccgcattg agattttgag ccatgacaaa gattacaaaa atgttacgct gtatgagcat      660
gccaaagctc gctattctat gctgccgagt aaggccaagg aaagtgcaca tcaccatcac      720

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catcactaa

729

<210> 14

<211> 741

<212> DNA

<213> Scolymia cubensis

<400> 14

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ttgattgatt gaaggagaaa tatcatgtct gccatcaaga ctgtggtaaa gcaattcatg      60
aagatcaaga tgtcttttga aggcactgta aacgggcact acttcaagat tgtaggagag      120
ggtgatggca ctccctttga gggaaaacag actttacacc tcaaggtcaa agagggcgca      180
cctctgcctt ttgcctacga taccctgaca acagctcttc attacggaaa cagggtattc      240
gtcgaatacc cagaaaacat cccagactat ttcaagcagt cgttccttaa gggatattca      300
tggaagaa gacctacttt cgaagacggg ggaatttgca tcgccagaag cgacatcaaa      360
atggttggcg acactttcca taacgaggtt caattttacg gggtaaactt tcccccaat      420
ggtcctgtta tgcagaggca cacgggtgaa tgggagccat cactgagaa gatttatgtg      480
cgtgatggag tgttgacggg tgatattacc atggctctgt tgcttaaagg aggtacccat      540
taccgatgtg acttcagaac tacttataaa gctaaggaga aggggtccaa gttcccaggc      600
tatcaccttg tcgatcattg tattgagatt acaagccatg acaaagatta caacgtgggt      660
gagctgtatg agcatgccgt cgctcattct ggattgccgg acagtgccaa tcgattgatt      720
gattgaagga gaaatatcta a                                     741

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<210> 15

<211> 234

<212> PRT

<213> Montastraea cavernosa

<400> 15

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Met Ser Val Ile Lys Ser Asp Met Lys Ile Lys Leu Pro Met Glu Gly
1           5           10           15

Thr Val Asn Gly His Lys Phe Val Ile Thr Gly Glu Gly Glu Gly Lys
          20           25           30

Pro Phe Gln Gly Thr His Thr Ile Thr Leu Lys Val Lys Glu Gly Gly
          35           40           45

Pro Leu Pro Phe Pro Tyr Asp Ile Leu Thr Thr Ala Phe Gln Tyr Gly
          50           55           60

Asn Arg Val Phe Thr Lys Tyr Pro Arg Asp Ile Pro Asp Tyr Phe Lys
65           70           75           80

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<210> 16
<211> 234
<212> PRT
<213> Montastraea cavernosa
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<400> 16

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

Cys Phe Ile Tyr Glu Ile Arg Tyr Asp Gly Val Asn Phe Pro Pro Ser
 115 120 125
 Gly Pro Val Met Gln Lys Lys Thr Leu Lys Trp Glu Pro Ser Thr Glu
 130 135 140
 Lys Met Tyr Val Arg Asp Gly Val Leu Lys Gly Asp Val Asn Met Ala
 145 150 155 160
 Leu Leu Leu Glu Gly Gly Gly His Tyr Arg Cys Asp Phe Arg Ser Thr
 165 170 175
 Tyr Lys Ala Lys Lys Arg Val Gln Leu Pro Asp Tyr His Phe Val Asp
 180 185 190
 His Arg Ile Glu Ile Leu Ser His Asp Asn Asp Tyr Asn Thr Val Lys
 195 200 205
 Leu Ser Glu Asn Ala Glu Ala Arg Tyr Ser Met Leu Pro Ser Gln Ala
 210 215 220
 Lys Glu Ser Ala His His His His His His
 225 230

<210> 17
 <211> 234
 <212> PRT
 <213> Montastraea cavernosa
 <400> 17

Met Ser Val Ile Lys Pro Asp Met Lys Ile Lys Leu Arg Met Gln Gly
 1 5 10 15
 Val Val Asn Gly His Lys Phe Val Ile Lys Gly Glu Gly Glu Gly Lys
 20 25 30
 Pro Phe Glu Gly Thr Gln Thr Ile Asn Leu Thr Val Lys Glu Gly Ala
 35 40 45
 Pro Leu Pro Phe Ala Tyr Asp Ile Leu Thr Ser Ala Phe Gln Tyr Gly
 50 55 60
 Asn Arg Val Phe Thr Lys Tyr Pro Asp Asp Ile Pro Asp Tyr Phe Lys
 65 70 75 80
 Gln Thr Phe Pro Glu Gly Tyr Ser Trp Glu Arg Ile Met Ala Tyr Glu
 85 90 95
 Asp Gln Ser Ile Cys Thr Ala Thr Ser Asp Ile Lys Met Glu Gly Asp
 100 105 110
 Cys Phe Ile Tyr Glu Ile Gln Phe His Gly Val Asn Phe Pro Pro Asn
 115 120 125
 Gly Pro Val Met Gln Lys Lys Thr Leu Lys Trp Glu Pro Ser Thr Glu
 130 135 140

Lys Met Tyr Val Arg Asp Gly Val Leu Lys Gly Asp Val Asn Met Ala
145 150 155 160

Leu Leu Leu Glu Gly Gly Gly His Tyr Arg Cys Asp Phe Arg Ser Thr
165 170 175

Tyr Lys Ala Lys Lys Asp Val His Leu Pro Asp Tyr His Tyr Val Asp
180 185 190

His Arg Ile Glu Ile Leu Ser His Asp Lys Asp Tyr Lys Asn Val Thr
195 200 205

Leu Tyr Glu His Ala Lys Ala Arg Tyr Ser Met Leu Pro Ser Lys Ala
210 215 220

Lys Glu Ser Ala His His His His His His
225 230

<210> 18

<211> 238

<212> PRT

<213> Scolymia cubensis

<400> 18

Met Ser Ala Ile Lys Thr Val Val Lys Gln Phe Met Lys Ile Lys Met
1 5 10 15

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

Gly Asp Gly Thr Pro Phe Glu Gly Lys Gln Thr Leu His Leu Lys Val
35 40 45

Lys Glu Gly Ala Pro Leu Pro Phe Ala Tyr Asp Ile Leu Thr Thr Ala
50 55 60

Leu His Tyr Gly Asn Arg Val Phe Val Glu Tyr Pro Glu Asn Ile Pro
65 70 75 80

Asp Tyr Phe Lys Gln Ser Phe Pro Lys Gly Tyr Ser Trp Glu Arg Ser
85 90 95

Leu Thr Phe Glu Asp Gly Gly Ile Cys Ile Ala Arg Ser Asp Ile Lys
100 105 110

Met Val Gly Asp Thr Phe His Asn Glu Val Gln Phe Tyr Gly Val Asn
115 120 125

Phe Pro Pro Asn Gly Pro Val Met Gln Arg His Thr Val Lys Trp Glu
130 135 140

Pro Ser Thr Glu Lys Ile Tyr Val Arg Asp Gly Val Leu Thr Gly Asp
145 150 155 160

Ile Thr Met Ala Leu Leu Leu Lys Gly Gly Thr His Tyr Arg Cys Asp
165 170 175

Phe Arg Thr Thr Tyr Lys Ala Lys Glu Lys Gly Pro Lys Phe Pro Gly
 180 185 190
 Tyr His Leu Val Asp His Cys Ile Glu Ile Thr Ser His Asp Lys Asp
 195 200 205
 Tyr Asn Val Val Glu Leu Tyr Glu His Ala Val Ala His Ser Gly Leu
 210 215 220
 Pro Asp Ser Ala Asn Arg Gln Ser His His His His His His
 225 230 235

<210> 19
 <211> 765
 <212> DNA
 <213> Acropora aculeus

<400> 19
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 aagcagggca tcgtacaaga aatgaagacg aaataccgta tggaaggcag tgtcaatggc 120
 catgaattca cgatcgaagg tgtaggaact gggtagcctt acgaaggga acagatgtcc 180
 gaattagtga tcatcaagcc taagggaaa ccccttccat tctcctttga catactgtca 240
 tcagtctttc aatatggaaa caggtgcttc acaaagtacc ctgcagacat gcctgactat 300
 ttcaagcaag cattcccaga tggaatgtca tatgaaaggc catttctatt tgaggatgga 360
 gcagttgcta cagccagctg gaacattcgt ctcgaaggaa attgcttcat ccacaattcc 420
 atctttcatg gcgtaaaact tcccgatgat ggacccgtaa tgaaaaagaa gacaattggc 480
 tgggataagt ccttcgaaaa aatgactgtg tctaaagagg tgttaagagg tgatgtgact 540
 atgtttctta tgctcgaagg aggtgggttac cacagatgcc agtttcactc cacttacaaa 600
 acagagaagc cggtcgaact gccccgaat catgtcgtag aacatcaa atgtgaggacc 660
 gaccttgccc aaagtgcaaa aggcttcacg gtcaagctgg aagcacatgc tgcggctcat 720
 gttaaccctt tgaaggttca acagcaccat caccatcact aataa 765

<210> 20
 <211> 765
 <212> DNA
 <213> Acropora aculeus

<400> 20
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 aagcatggca tcacacaaga aatgccgacg aaataccata tgaaaggcag tgtcaatggc 120
 catgaattcg agatcgaagg tgtaggaact ggacaccctt acgaaggga acacatggcc 180
 gaattagtga tcataaagcc tgcgggaaaa ccccttccat tctcctttga catactgtca 240

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acagtcattc aatacggaaa cagatgcttc actaagtacc ctgcagacct gcctgactat   300
ttcaagcaag catacccagg tggaatgtca tatgaaaggt catttgtgta tcaggatgga   360
ggaattgcta cagcgagctg gaacgttagt ctcgagggaa attgcttcat ccacaaatcc   420
acctatcttg gtgtaaactt tcctgctgat ggacccgtaa tgacaaagaa gacaattggc   480
tgggataaag cctttgaaaa aatgactggg ttcaatgagg tgttaagagg tgatgtgact   540
gagtttctta tgctcgaagg aggtgggttac cattcatgcc agtttcactc cacttacaaa   600
ccagagaagc cggtcgaact gccccgaat catgtcatag aacatcacat tgtgaggacc   660
gaccttggca agactgcaaa aggcttcatg gtcaagctgg tacaacatgc tgcggctcat   720
gttaacactt tgaaggttca acatcaccat caccatcact aataa                   765

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<210> 21
<211> 716
<212> DNA
<213> Acropora aculeus

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<400> 21
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agtgtcaatg gccatgaatt cacgatcgaa ggtgtaggaa ctgggtaccc ttacgaaggg   120
aagcagatgt ccgaattagt gatcgtcaag cctaagggaa agccccttcc attctccttt   180
gacatactgt catcagtctt tcaatatgga aacaggtgct tcacaaagta ccctgcagac   240
atgcctgact atttcaagca agcattccca gatggaatgt catatgaaag gtcattttcta   300
tttgaggatg gagcagttgc tacagccagc tggaacattc gtctcgaagg aaattgcttc   360
atccacaatt ccatctttca tggcgtaaac tttcccgctg atggaccctg aatgaaaaag   420
aagacaattg gctgggataa gtccttcgaa aaaatgactg tgtctaaaga ggtgttaaga   480
ggtgatgtga ctatgtttct tatgctcgaa ggaggtgggt accacagatg ccagtttcac   540
tccacttaca aaacagtga gccggtcgaa ctgccccga atcatgtcgt agaacatcaa   600
attgtgagga ccgaccttgg ccaaagtgc aaaggcttca cagtcaagct ggaagcacat   660
gctgcggctc atgtaaccct ttgaagggtc aacatcacca tcaccatcac taataa       716

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<210> 22
<211> 765
<212> DNA
<213> Acropora aculeus

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<400> 22
ttgattgatt gaaggagaaa tatcatgatc aagccatcta tcctcaacat gtctctttca   60

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aagcatggca tcacacaaga aatgccgacg aaataccata tgaaaggcag tgtcaatggc 120
catgaattcg agatcgaagg tgtaggaact ggacaccctt acgaagggaac acacatggcc 180
gaattagtga tcataaagcc tgcgggaaaa ccccttccat tctcctttga catactgtca 240
acagtcattc aatacggaaa cagatgcttc actaagtacc ctgcagacct gcctgactat 300
ttcaagcaag catacccagg tggaatgtca tatgaaaggt catttgtatt tcaggatgga 360
ggaattgcta cagcgagctg gaacgtcggg ctcgaggga attgcttcat ccacaaatcc 420
acctatcttg gtgtaaaactt tcctgctgat ggaccgtaa tgacaaagaa gacaattggc 480
tgggataaag cctttgaaaa aatgactggg ttcaatgagg tgttaagagg tgatgtgact 540
gagtttctta tgctcgaagg aggtgggttac cattcatgcc agtttcactc cacttacaaa 600
ccagagaagc cggtaaaact gccccgaat catgtcatag aacatcacat tgtgaggacc 660
gaccttggca agactgcaaa aggcttcatg gtcaagctgg tacaacatgc tgcggctcat 720
gttaaccctt tgaaggttca acatcaccat caccatcact aataa 765

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<210> 23
<211> 765
<212> DNA
<213> Acropora aculeus

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<400> 23
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aagcatggca tcacacaaga aatgccgacg aaataccata tgaaaggcaa tgtcaatggc 120
catgaattcg agatcgaagg tgtaggaact ggacaccctt acgaagggaac acacatggcc 180
gaattagtga tcataaagcc tgcgggaaaa ccccttccat tctcctttga catactgtca 240
acagtcattc aatacggaaa cagatgcttc actaagtacc ctgcagacct gcctgactat 300
ttcaagcaag cgtacccagg tggaatgtca tatgaaaggt catttgtatt tcaggatgga 360
ggaattgcta cagcgagctg gaacgttggg ctcgaggga attgcttcat ccacaaatcc 420
acctatcttg gtgtaaaactt tcctgctgat ggaccgtaa tgacaaagaa gacaattggc 480
tgggataaag cctttgaaaa aatgactggg ttcaatgagg tgttaagagg cgatgtgact 540
gggtttctta tgctcgaagg aggtgggttac cattcatgcc agtttcactc cacttacaaa 600
ccagagaagc cggtaaaact gccccgaat catgtcatag aacatcacat tgtgaggacc 660
gaccttggca agactgcaaa aggcttcatg gtcaagctgg tacaacatgc tgcggctcat 720
gtgaaccctt tgaaggttca acatcaccat caccatcact aataa 765

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<210> 24

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<211> 711
 <212> DNA
 <213> *Acropora aculeus*

<400> 24
 ttgattgatt gaaggagaaa tatcatgagt gtgatcgcta aacaaatgac ctacaagggt 60
 tatatgtcag gcacggtcaa tggacattac tttgagggtcg aaggcgatgg aaaaggaaag 120
 ccttacgagg gggagcagac ggtgaagctc actgtcacca agggaggacc tctgccattt 180
 gcttgggata ttttatcacc acagtccacag tacggaagca taccattcac caaataccct 240
 gacgacatcc ctgactatgt aaagcagtca ttcccgagg gatatabatg ggagaggatc 300
 atgaactttg aagatggtgc agtgtgtact gtcagcaatg attccagcat ccaaggcaac 360
 tgtttcatct acaatgtcaa gttctctggt ttgaactttc ctccaatgg accggttatg 420
 cagaagaaga cacagggctg ggaaccaac actgagcgtc tctttgcacg agatggaatg 480
 ctgataggaa acaactttat ggctctgaag ttagaaggag gtggtcacta tttgtgtgaa 540
 ttcaaactta cttacaaggc aaagaagcct gtgaggatgc cagggtatca ctatgttgac 600
 cgcaaaactgg atgtaaccaa tcacaacagg gattacactt ccgttgagca gcgtgaaatt 660
 tccattgcac gcaaacctgt ggtcgcccat caccatcacc atcactaata a 711

<210> 25
 <211> 735
 <212> DNA
 <213> *Acropora aculeus*

<400> 25
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 gctaaacaaa tgacctacaa ggtttatatg tcaggcacgg tcaatggaca ttactttgag 120
 gtcgaaggcg atggaaaagg aaagccttac gagggggagc agacggtgaa gctcactgtc 180
 accaaggagg gacctctgcc atttgcttgg gatattttat caccgcagtc acgtacgga 240
 agcataccat tcaccaaata ccctgacgac atccctgact atgtaaagca gtcattcccg 300
 gagggatata catgggagag gatcatgaac tttgaggatg gtgcagtgtg tactgtcagc 360
 aatgattcca gcatccaagg caactgtttc atctacaatg tcaagttctc tggtttgaac 420
 tttcctccca atggaccggt tatgcggaag aagacacggg gctgggaacc caaactgag 480
 cgtctctttg cacgggatgg aatgctgata ggaaacaact ttatggctct gaagttagaa 540
 ggagggtggc actatttgtg tgaattcaaa tctacttaca aggcaaagaa gcctgtgagg 600
 atgccagggt atcactatgt tgaccgcaa ctggatgtaa ccaatcaca cagggttac 660
 acttccgttg agcagtgtga aatttccatt gcacgcaaac ctgtggtcgc ccatcaccat 720

caccatcact aataa 735

<210> 26
 <211> 711
 <212> DNA
 <213> Acropora hyacinthus

<400> 26
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 tatatgtcag gcacgggtcaa tggacactac tttgagggtcg aaggcgatgg aaaaggaaag 120
 ccttacgagg gggagcaaac ggtaaggctg actgtcacca agggcgagacc tctgccgttt 180
 gcttgggata ttttatcacc acagtcacag tacggaagca taccattcac caagtaccct 240
 gaagacatcc ctgactatgt gaagcagtca ttcccggagg gatatacatg ggagaggatc 300
 atgaactttg aagatggtgc agtgtgtact gtcagcaatg attccagcat ccaaggcaac 360
 tgtttcatct accatgtcaa gttctctggg ttgaactttc ctcccaatgg acctgttatg 420
 cagaagaaga cacagggctg ggaacccaac actgagcgtc tctttgcacg agatggagtt 480
 ctgataggaa acaactttat ggccctgaag ttagaaggag gtgggtcacta tttgtgtgaa 540
 ttcaaactcta cttacaaggc aaagaagcct gtgaagatgc ctgggtatca ctttgttgac 600
 cgcaaactgg atgtaaccaa tcacaacaag gattacactt ctgttgagca gcgtgaaatt 660
 tccattgcac gcaaacctgt ggtcgccac caccatcacc atcactaata a 711

<210> 27
 <211> 741
 <212> DNA
 <213> Acropora millepora

<400> 27
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 aagacgaaat accatatgga aggcagtgtc aatggccatg aattcacgat cgaagggtga 120
 ggaactggaa acccttacga aggcacacag atgtccgaat tagtgatcac cgagcctgca 180
 ggaaaacccc ttccattctc ctttgacatt ctgtcaacag tctttcagta tggaaacagg 240
 tgcttcacaa agtaccctga aggaatgact gactatttca agcaagcatt cccagatgga 300
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 attcgtcttg agagagattg cttcatccac aaatccatct atcatggcgt taactttccc 420
 gctgatggac ccgtaatgaa aaagaagacc attgggtggg ataaagcctt cgaaaaaatg 480
 actgtgtcca aagacgtttt aagaggatgat gtgactgagt ttcttatgct cgaaggaggt 540

ggttaccaca gctgccagtt tcaactccact tacaaccag agaagccggt tacactgccc 600
 cctaatactg tcgtggaaca tcacattgtg aggactgacc ttggccaaac tgcaaaaggc 660
 ttcacagtca agctggaaga acatgctgcg gctcatgtta accctttgaa gggtcaccat 720
 caccatcacc atcactaata a 741

<210> 28
 <211> 726
 <212> DNA
 <213> Acropora millepora

<400> 28
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 gaattcacga tcgaagggtg aggaactggg tacccttacg aagggaaca gatatccgaa 180
 ttagtgatca tcaagcctgc gggaaaaccc cttccattct cctttgacat actgtcatca 240
 gtctttcaat atggaaacag gtgcttcaca aagtaccctg cagacatgcc tgactatttc 300
 aagcaagcat tcccagatgg aatgtcatat gaaaggatcat ttctatttga ggatggagca 360
 gttgccacag ccagctggaa cattcgtctc gaaggaaatt gcttcatcca caaatccatc 420
 tttcatggcg taaactttcc cgctgatgga cccgtaatga aaaagaagac aattgactgg 480
 gataagtcct tcgaaaaaat gactgtgtct aaagagggtgc taagagggtga cgtgactatg 540
 tttcttatgc tcgaaggagg tggttctcac agatgccaat ttactccac ttacaaaaca 600
 gagaagccgg tcacactgcc cccgaatcat gtcgtagaac atcaaattgt gaggaccgac 660
 cttggccaaa ctgcaaaagg cttcacagtc aagctggaag aacatgctgc ggctcatgtt 720
 agccta 726

<210> 29
 <211> 761
 <212> DNA
 <213> Acropora millepora

<400> 29
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 caaggcatcg tacaagaaat gaagacgaaa taccatatgg aaggcagtgt caatggccat 120
 gaattcacga tcgaagggtg aggaactggg tacccttacg aagggaaca gatgtccgaa 180
 ttagtgatca tcaagcctgc gggaaaaccc cttccattct cctttgacat actgtcatca 240
 gtctttcaat atggaaacag gtgcttcaca aagtaccctg cagacatgcc tgactatttc 300

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aagcaagcat tcccagatgg aatgtcatat gaaaggtcat ttctatttga ggatggagca 360
gttgccacag ccagctggaa cattcgtctc gaaggaaatt gcttcatcca caaatccatc 420
tttcatggcg taaactttcc cgctgatgga cccgtaatga aaaagaagac aattgactgg 480
gataagtcct tcgaaaaaat gactgtgtct aaagaggtgc taagaggtga cgtgactatg 540
tttcttatgc tcgaaggagg tggttctcac agatgccaat ttcactccac ttacaaaaca 600
gagaagccgg tcacactgcc cccgaatcat gtcgtagaac atcaaattgt gaggaccgac 660
cttggccaaa ctgcaaaagg cttcacagtc aagctggaag aacatgctgc ggctcatgta 720
accctttgaa ggttcaacat caccatcacc atcactaata a 761

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<210> 30
<211> 762
<212> DNA
<213> Acropora millepora

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<400> 30
ttgattgatt gaaggagaaa tatcatgagg caatctatcc tcaacatgtc ttattcaaag 60
cagggcatcg tacaagaaat gaagacgaaa taccgtatgg aaggcagtgt caatggccat 120
gaattcacga tcgaagggtgt aggaactggg tacccttacg aagggaagca gatgtccgaa 180
ttagtgatcg tcaagcctaa gggaaagccc cttccattct cctttgacat actgtcatca 240
gtctttcaat atggaaacag gtgcttcaca aagtaccctg cagacatgcc tgactatttc 300
aagcaagcat tcccagatgg aatgtcatat gaaaggtcat ttctatttga ggatggagca 360
gttgctacag ccagctggaa cattcgtctc gaaggaaatt gcttcatcca caattccatc 420
tttcatggcg taaactttcc cgctgatgga cccgtaatga aaaagaagac aattggctgg 480
gataagtcct tcgaaaaaat gactgtgtct aaagaggtgt taagaggtga tgtgactatg 540
tttcttatgc tcgaaggagg tggttaccac agatgccagt ttcactccac ttacaaaaca 600
gtgaagccgg tcgaactgcc cccgaatcat gtcgtagaac atcaaattgt gaggaccgac 660
cttggccaaa gtgcaaaagg cttcacagtc aagctggaag cacatgctgc ggctcatgtt 720
aaccctttga aggttcaaca tcaccatcac catcactaat aa 762

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<210> 31
<211> 762
<212> DNA
<213> Acropora millepora

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<400> 31
ttgattgatt gaaggagaaa tatcatgaag ccatctatcc tcaacatgtc tcattcaaag 60

```

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caaggcatcg cacaagtaat gaagacgaaa taccatatgg aaggcagtgt caatggccat      120
gaattcacga tcgaaggtgt aggaactgga aacccttacg aaggctcaca gatgtccgag      180
ttagtgatca ccaagcctgc aggaaaaccc cttccattct cctttgacat tctctcaaca      240
gtctttcaat atggaaacag gtgcttcaca aagtaccctg aaggaatgac tgactatttc      300
aagcaagcat tcccagatgg aatgtcatat gaaaggctcat ttctatatga ggatggagga      360
gttgctacag ccagctggaa cattcgtctt gagagagggt gcttcatcca caaatccatc      420
tatcatggcg ttaactttcc cgctgatgga ccgtaatga aaaagaagac cattggctgg      480
gataaggcct tcgaaaaaat gactgtgtcc aaagacgtgt taagagggtga tgtgactggg      540
tttcttatgc tcgaaggagg tggttaccac aactgccagt ttactccac ttacaaacca      600
gaaaagccgg ttacactgcc ccggaatcat gtcgtggaac atcacattgt gaggactgac      660
cttggccaaa ctgcaaaagg cttcacagcc aagctggaag aacatgctgc ggctcatgta      720
aaccctttga aggttcaaca tcaccatcac catcactaat aa                          762

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<210> 32
<211> 741
<212> DNA
<213> Acropora millepora

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<400> 32
ttgattgatt gaaggagaaa tatcatgtct tattcaaagc agggcatcgt acaagaaatg      60
aagacgaaat accatatgga aggcagtgtc aatggccatg aattcacgat cgaagggtgta      120
ggaactgggt acccttacga agggaaacag atgtccgaat tagtgatcat caagcctgcg      180
ggaaaacccc ttccattctc ctttgacata ctgtcatcag tctttcaata tggaaacagg      240
tgcttcacaa agtaccctgc agacatgcct gactatttca agcaagcatt cccagatgga      300
atgtcatatg aaaggtcatt tctattttgag gatggagcag ttgctacagc cagctggaac      360
attcgtctcg aaggaaattg cttcatccac aaatccatct ttcatggcgt aaactttccc      420
gctgatggac ccgtaatgaa aaagaagaca attgactggg ataagtcctt cgaaaaaatg      480
actgtgtcta aagagggtgct aagagggtgac gtgactatgt ttcttatgct cgaaggaggt      540
ggttttcaca gatgccatt tcactccact taaaaacag agaagccggg cacactgccc      600
ccgaatcatg tcgtagaaca tcaaattgtg aggaccgacc ttggccaaag tgcaaaaggc      660
tttacagtca agctggaagc acatgctgcg gctcatgtta accctttgaa ggttaaacad      720
caccatcacc atcactaata a                          741

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<210> 33

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<211> 744
 <212> DNA
 <213> *Acropora millepora*

<400> 33
 ttgattgatt gaaggagaaa tatcatggct ctgtcaaagc acggtttaac aaaggacatg 60
 acgatgaaat accacatgga agggctctgtc gatgggcata aatttgtgat cacggggccac 120
 ggcaatggaa atccttttcga agggaaacag actatgaatc tgtgtgtggt tgaaggggga 180
 cccctgccat tctccgaaga ctttttgtct gctacgtttg actacggaaa cagggctcttc 240
 actgaatatc ctcaaggcat gggttgacttt ttcaagaatt catgtccagc tggatacaca 300
 tggcacaggt ctttactctt tgaagatgga gcagtttgca caactagtgc agatataaca 360
 gtgagtgttg aggagaactg cttttatcac aattccaagt ttcattggagt gaactttcct 420
 gctgatggac ctgtgatgaa aaagatgaca actaattggg agccatcctg cgagaaaatc 480
 ataccagtac ctagacaggg gatattgaaa ggggatattg ccatgtacct ctttctgaag 540
 gatggtgggc gttatcgggtg ccagttcgac acaatttaca aagcaaagtc tgacccgaaa 600
 gagatgccgg agtggcactt catccaacat aagctcaccg ggggaagaccg cagcgatgct 660
 aagaaccaga aatggcaact ggtagaacat gctgttgctt cccgatccgc attgcccgga 720
 catcaccatc accatcacta ataa 744

<210> 34
 <211> 711
 <212> DNA
 <213> *Acropora millepora*

<400> 34
 ttgattgatt gaaggagaaa tatcatgagt gtgatcgcta aacaaatgac ctacaagggtt 60
 tatatgtcag gcacgggtcaa tggacactac tttgaggtcg aaggcgatgg aaaaggtaag 120
 ccctacgagg gggagcagac ggtaaagctc actgtcacca agggcggacc tctgccattt 180
 gcttgggata ttttatcacc acagtgtcag tacggaagca taccattcac caagtaccct 240
 gaagacatcc ctgactatgt aaagcagtca ttcccggagg gctatacatg ggagaggatc 300
 atgaactttg aagatggtgc agtgtgtact gtcagcaatg attccagcat ccaaggcaac 360
 tgtttcatct accatgtcaa gttctctggt ttgaactttc ctcccaatgg acctgtcatg 420
 cagaagaaga cacagggctg ggaaccaac actgagcgtc tctttgcacg agatggaatg 480
 ctgctaggaa acaactttat ggctctgaag ttagaaggag gcggtcacta tttgtgtgaa 540
 ttcaaaacta cttacaaggc aaagaagcct gtgaagatgc cagggatatca ctatgttgac 600
 cgcaaactgg atgtaaccaa tcacaacaag gattacactt cggttgagca gtgtgaaatt 660

tccattgcac gcaaacctgt ggtcgcccat caccatcacc atcactaata a 711

<210> 35

<211> 765

<212> DNA

<213> Acropora nobilis

<400> 35

ttgattgatt gaaggagaaa tatcatgatc aagccatcta tcctcaacat gtcttattca 60
aagcaaggca tcgcacaagt aatgaagacg aaataccata tggaaggcag tgtcaatggc 120
catgaattca cgatcgaagg tgtaggaact ggaaaccctt acgaaggcac acagatgtcc 180
gaattagtga tcaccaagcc tgcaggaaaa ccccttccat tctcctttga cattctgtca 240
acagtctttc aatatggaaa cagggtgcttc acaaagtacc ctgaaggaat gactgactat 300
ttcaagcaag cattcccaga tggaatgtca tgtgaaaggc catttctata tgaggatgga 360
ggagttgcta cagccagctg gaacattcgt cttgagagag attgcttcat ccacaaatcc 420
atctatcatg gcgttaactt tcccgtgat ggaccgtaa tgaaaaagaa gaccattggc 480
tgggataaag ccttcgaaaa aatgactgtg tccaaagacg tgttaagagg tgatgtgact 540
gagtttctta tgctcgaagg aggtggttac cacagctgcc agtttctctc cacttacaaa 600
ccagaaaagc cggctgcact gccccgaat catgtcgtag aacatcacat tgtgaggact 660
gaccttggcc aaagtgcaaa aggcttcaca gtcaagctgg aagaacatgc tgcggctcat 720
gttaaccctt tgaaggttca acatcaccat caccatcact aataa 765

<210> 36

<211> 741

<212> DNA

<213> Acropora nobilis

<400> 36

ttgattgatt gaaggagaaa tatcatgtct tattcaaagc agggcatcgc acaagtaatg 60
aagacgaaat accatatgga aggcagtgtc aatggccatg aattcacgat cgaagggtga 120
ggaactggaa acccttacga aggcacacag atgtccgaat tggatgatcac caagcctgca 180
ggaaaacccc ttccattctc ctttgacatt ctgtcaacag tctttcaata tggaaacagg 240
tgcttcacaa agtaccctga aggaatgact gactatttca agcaagcatt ccagatgga 300
atgtcatatg aaaggtcatt tctatatgag gatggaggag ttgctacagc cggctggaac 360
attcgtcttg agagagattg cttcatccac aaatccatct atcatggcgt taactttccc 420
gctgatggac ccgtaatgaa gaagaagacc attggctggg ataaagcctt cgaaaaaatg 480

actgtgtcca aagacgtggt aagaggtgat gtgactgggt ttcttatgct cgaaggaggt 540
 ggttaccaca gctgccagtt tcactccact taaaaaccag aaaagccggc tgcactgccc 600
 ccgaatcatg tcgtagaaca tcacattgtg aggactgacc ttggccaaag tgcaaaaggc 660
 ttcacagtca agctggaaga acatgctgcg gctcatgtta accctttgaa ggttcaacat 720
 caccatcacc atcactaata a 741

<210> 37
 <211> 741
 <212> DNA
 <213> *Acropora nobilis*

<400> 37
 ttgattgatt gaaggagaaa tatcatgtct tattcaaagc agggcatcgc acaagaaatg 60
 aagacgaaat accatatgga aggcagtgtc aatggccatg aattcacggc cgaagggtga 120
 gggactgggt acccttacga aggggaacag atgtccgaat tagtgatcat cgagcctgcg 180
 ggaaaacccc ttccattctc ctttgacata ctgtcatcag tctttcagta tggaaacagg 240
 tgcttcacaa aataccctgc agacatgcct gactatttca agcaagcatt tccagatgga 300
 atgtcatatg aaaggtcatt tctatttgag gatggagcag ttgctacagc cagctggaaa 360
 attcgtctcg aaggaaattg cttcatccac aactccatct ttaatggcgt aaactttccc 420
 gctgatggac ccgtaatgga aaagaagaca attggtctggg ataagtcctt cgaaaaaatg 480
 actgtgtcta aagaggtgct aagaggtgat gtgactatgt ttcttatgct cgaaggaggt 540
 ggttctcaca gatgccagtt tcactccact taaaaacag agaagccggc cacactgccc 600
 ccgaatcatg tcgtagaaca tcaaattgtg aggaccgacc ttggccaaag tgcaaaaggc 660
 tttacagtca agctggaagc acatgctgcg gctcatgtta accctttgaa ggttaaacad 720
 caccatcacc atcactaata a 741

<210> 38
 <211> 726
 <212> DNA
 <213> *Agaricia fragilis*

<400> 38
 ttgattgatt gaaggagaaa tatcatgagt gtgattgtaa aggaaatgat gactaagcta 60
 cacatggaag gtactgttaa cgggcacgcc cttacaattg aaggcaaagg aaaaggcgat 120
 ccttacaatg gagtgcagtc tatgaacctt gacgtcaaag gcggtgcgcc tttgccgttc 180
 tctttcgatc tcttgacgcc agcattcatg tacggcaaca gagtgttcgc gaagtatcca 240
 gaagacatac cagacttttt caagcaggtg tttcctgaag ggtaccactg ggaaagaagt 300

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attacctttg aagatcaggc cgtttgtacg gcaaccagcc acataaggct ggaccagaaa 360
gagatgtggt ttatctatga cgtccgtttt cacggtgtga actttcccg ccaatggccca 420
atcatgcaga agaagatact gggatgggag ccatccactg agaaaatgta tgcacgtgat 480
ggggtgctga aggggtgatgt taatatgact cttcgtgttg aaggaggtgg ccattaccga 540
gctgacttca gaactactta caaagcaaag aagccagtca acctgccagg ctatcacttc 600
atagaccacc gcattgagat taccaagcac agcaaagatt acaccaatgt tgctttgtat 660
gaggcagcag ttgctcgtca ttctccgctg cctaagggtg ctcatcacca tcaccatcac 720
taataa 726

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<210> 39
<211> 725
<212> DNA
<213> Agaricia fragilis

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```

<400> 39
ttgattgatt gaaggagaaa tatcatgagt gtgattgtaa aggaaatgat gactaagcta 60
cacatggaag gtactgttaa cgggcacgcc tttaacaattg aaggcaaagg aaaaggcgat 120
ccttacaatg gagtgcagtc tatgaacctt gacgtcaaag gcggtgcgcc tttgccgttc 180
tctttcgate tcttgacgcc agcattcatg tacggcaaca gagtgttcac gaagtatcca 240
gaagacatac cagacttttt caagcaggtg tttcctgaag ggtaccactg ggaaagaagt 300
attacctttg aagatcaggc cgtttgtacg gcaaccagcc acataaggct ggaccagaaa 360
gagatgtggt ttatctatga cgtccgtttt cacggtgtga actttcccg ccaatggccca 420
atcatgcaga agaagatact gggatgggag ccatccactg agaaaatgta tgcacgtgat 480
ggggtgctga aggggtgatgt taatatgact cttcgtgttg aaggaggtgg ccattaccga 540
gctgacttca gaactactta caaagcaaag aagccagtca acctgccagg ctatcacttc 600
atagaccacc gcattgagat taccaagcac agcaaagatt acaccaatgt tgctttgtat 660
gaggcagcag ttgctcgtca ttctccgctg cctaagggtg ctcatcacca tcacatcact 720
aataa 725

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<210> 40
<211> 726
<212> DNA
<213> Agaricia fragilis

```

```

<400> 40
ttgattgatt gaaggagaaa tatcatgagt gtgattgtaa aggaaatgat gactaagcta 60

```

cacatggaag gtactgttaa cgggcacgcc tttaacaattg aaggcaaagg aaaaggcgat 120
 ccttacaatg gagtgcagtc tatgaacctt gacgtcaaag gcggtgcgcc ttgcccgttc 180
 tctttcgatc tcttgacgcc agcattcatg tacggcaaca gagtggtcac gaagtatcca 240
 gaagacatac cagacttttt caagcaggtg ttctctgaag ggtaccactg ggaaagaagt 300
 attacctttg aagatcaggc cgtttgtacg gcaaccagcc acataaggct ggaccagaaa 360
 gagatgtggt ttatctatga cgtccgtttt caggtgtga actttccgc caatggccca 420
 atcatgcaga agaagatact gggatgggag ccatccactg agaaaatgta tgcacgtgat 480
 ggggtgctga agggatgatg taatatgact cttcgtgttg aaggaggtgg ccattaccga 540
 gctgacttca gaactactta caaagcaaag aagccagtca acctgccagg ctatcacttc 600
 atagaccacc gcattgagat taccaagcac agcaaagatt acaccaatgt tgctttgtat 660
 ggggcagcag ttgctcgtca ttctccgtg cctaaggttt ctcatcacca tcaccatcac 720
 taataa 726

<210> 41
 <211> 725
 <212> DNA
 <213> *Agaricia fragilis*

<400> 41
 ttgattgatt gaaggaaaat atcatgagtg tgattgtaaa ggaaatgatg actaagctac 60
 acatggaagg tactgttaac gggcacgcct ttacaattga aggcaaagga aaaggcgatc 120
 cttacaatgg agtgcagtct atgaaccttg acgtcaaagg cggtgcgcct ttgccgttct 180
 ctttcgatct cttgacgcca gcattcatgt acggcaacag agtggtcacg aagtatccag 240
 aagacatacc agactttttc aagcaggtgt ttctgaagg gtaccactgg gaaagaagta 300
 ttacctttga agatcaggcc gtttgtacgg caaccagcca cataaggctg gaccagaaag 360
 agatgtgttt tatctatgac gtccgttttc acggtgtgaa ctttcccgcc aatggcccaa 420
 tcatgcagaa gaagatactg ggatgggagc catccactga gaaaatgtat gcacgtgatg 480
 ggggtgctgaa gggatgatgtt aatgtgactc ttcgtgttga aggaggtggc cattaccgag 540
 ctgacttcag aactacttac aaagcaaaga agccagtcaa cctgccaggc tatcacttca 600
 tagaccaccg cattgagatt accaagcaca gcaaagatta caccaatgtt gctttgtatg 660
 aggcagcagt tgctcgtcat tctccgtgct ctaagggttc tcatcaccat caccatcact 720
 aataa 725

<210> 42

<211> 726
 <212> DNA
 <213> *Agaricia fragilis*

<400> 42
 ttgattgatt gaaggagaaa tatcatgagt gtgattgtaa aggaaatgat gactaagcta 60
 cacatggaag gtactgttaa cgggcacgcc tttaaatg aaggcaaagg agagggcgat 120
 ccttacaatg gaggcagtc tatgaacctt gacgtcaaag gcgggtgcgcc tttgccgttc 180
 tctttcgatc tcttgacgcc agcattcatg tacggcaaca gagggttcac gaagtatcca 240
 gaagacatac cagacttttt caagcagggtg tttcctgaag ggtaccactg ggaaagaagt 300
 attacctttg aagatcaggc cgtttgtacg gctaccagcc acataaggct ggaccagaaa 360
 gagatgtggt ttatctatga cgtccgtttt cacgggtgtga actttccgc caatggccca 420
 atcatgcaga agaagatact gggatgggag ccatccactg agaaaatgta tgcacgtgat 480
 ggggtgctga aggggtgatgt taatatgact cttcgtgttg aaggaggtgg ccattaccga 540
 gctgacttca gaactactta caaagcaaag aagccagtca acctgccagg ctatcacttc 600
 atagaccacc gcattgagat taccaagcac agcaaagatt acaccaatgt tgctttgtat 660
 ggggcagcag ttgctcgtca ttctccgtg cctaagggtg ctcacacca tcaccatcac 720
 taataa 726

<210> 43
 <211> 726
 <212> DNA
 <213> *Agaricia fragilis*

<400> 43
 ttgattgatt gaaggagaaa tatcatgagt gtgattgtaa aggaaatgat gactaagcta 60
 cacatggaag gtactgttaa cgggcacgcc tttaaatg aaggcaaagg aaaaggcgat 120
 ccttacaatg gaggcagtc tatgaacctt gacgtcaaag gcgggtgcgcc tttgccgttc 180
 tctttcgatc tcttgacgcc agcattcatg tacggcaaca gagggttcac gaagtatcca 240
 gaagacatac cagacttttt caagcagggtg tttcctgaag ggtaccactg ggaaagaagt 300
 attacctttg aagatcaggc cgtttgtacg gcaaccagcc acataaggct ggaccagaaa 360
 gagatgtggt ttatctatga cgtccgtttt cacgggtgtga actttccgc caatggccca 420
 atcatgcaga agaagatact gggatgggag ccatccactg agaaaatgta tgcacgtgat 480
 ggggtgctga aggggtgatgt taatatgact cttcgtgttg aaggaggtgg ccattaccga 540
 gctgacttca gaactactta caaagcaaag aagccagtca acctgccagg ctatcacttc 600
 atagaccacc gcattgagat taccaagcac agcaaagatt acaccaatgt tgctttgtat 660

gagggcagcag ttgctcgtca ttctccgctg cctaaggttg ctcatcacca tcaccatcac 720
 taataa 726

<210> 44
 <211> 726
 <212> DNA
 <213> *Agaricia fragilis*

<400> 44
 ttgattgatt gaaggagaaa tatcatgagt gtgattgtaa aggaaatgat gactaagcta 60
 cacatggaag gtactgttaa cgggcacgcc tttaacaattg aaggcaaagg aaaaggcgat 120
 ccttacaatg gagtgcagtc tatgaacctt gacgtcaaag gcggtgcgcc ttgcccgttc 180
 tctttcgatc tcttgacgcc agcattcatg tacggcaaca gagtgttcac gaagtatcca 240
 gaagacatac cagacttttt caagcaggtg tttcctgaag ggtaccactg ggaaagaagt 300
 attacctttg aagatcaggc cgtttgtacg gcaaccagcc acataaggct ggaccagaaa 360
 gagatgtggt ttatctatga cgtccgtttt caggtgtga actttcccgc caatggccca 420
 atcatgcaga agaagatact gggatgggag ccatccactg agaaaatgta tgcacgtgat 480
 ggggtgctga agggatgatgt taatacgact cttcgtgttg aaggaggtgg ccattaccga 540
 gctgacttca gaactactta caaagcaaag aagccagtca acctgccagg ctatcacttc 600
 atagaccacc gcattgagat taccaagcac agcaaagatt acaccaatgt tgctttgtat 660
 gagggcagcag ttgctcgtca ttctccgctg cctaaggttg ctcatcacca tcaccatcac 720
 taataa 726

<210> 45
 <211> 237
 <212> PRT
 <213> *Acropora aculeus*

<400> 45

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

Arg Met Glu Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Val
 20 25 30

Gly Thr Gly Tyr Pro Tyr Glu Gly Lys Gln Met Ser Glu Leu Val Ile
 35 40 45

Ile Lys Pro Lys Gly Lys Pro Leu Pro Phe Ser Phe Asp Ile Leu Ser
 50 55 60

Ser Val Phe Gln Tyr Gly Asn Arg Cys Phe Thr Lys Tyr Pro Ala Asp
 65 70 75 80
 Met Pro Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Tyr Glu
 85 90 95
 Arg Ser Phe Leu Phe Glu Asp Gly Ala Val Ala Thr Ala Ser Trp Asn
 100 105 110
 Ile Arg Leu Glu Gly Asn Cys Phe Ile His Asn Ser Ile Phe His Gly
 115 120 125
 Val Asn Phe Pro Asp Asp Gly Pro Val Met Lys Lys Lys Thr Ile Gly
 130 135 140
 Trp Asp Lys Ser Phe Glu Lys Met Thr Val Ser Lys Glu Val Leu Arg
 145 150 155 160
 Gly Asp Val Thr Met Phe Leu Met Leu Glu Gly Gly Gly Tyr His Arg
 165 170 175
 Cys Gln Phe His Ser Thr Tyr Lys Thr Glu Lys Pro Val Glu Leu Pro
 180 185 190
 Pro Asn His Val Val Glu His Gln Ile Val Arg Thr Asp Leu Gly Gln
 195 200 205
 Ser Ala Lys Gly Phe Thr Val Lys Leu Glu Ala His Ala Ala Ala His
 210 215 220
 Val Asn Pro Leu Lys Val Gln Gln His His His His His
 225 230 235

<210> 46
 <211> 237
 <212> PRT
 <213> Acropora aculeus

<400> 46

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

Arg Ser Phe Val Tyr Gln Asp Gly Gly Ile Ala Thr Ala Ser Trp Asn
 100 105 110
 Val Ser Leu Glu Gly Asn Cys Phe Ile His Lys Ser Thr Tyr Leu Gly
 115 120 125
 Val Asn Phe Pro Ala Asp Gly Pro Val Met Thr Lys Lys Thr Ile Gly
 130 135 140
 Trp Asp Lys Ala Phe Glu Lys Met Thr Gly Phe Asn Glu Val Leu Arg
 145 150 155 160
 Gly Asp Val Thr Glu Phe Leu Met Leu Glu Gly Gly Gly Tyr His Ser
 165 170 175
 Cys Gln Phe His Ser Thr Tyr Lys Pro Glu Lys Pro Val Glu Leu Pro
 180 185 190
 Pro Asn His Val Ile Glu His His Ile Val Arg Thr Asp Leu Gly Lys
 195 200 205
 Thr Ala Lys Gly Phe Met Val Lys Leu Val Gln His Ala Ala Ala His
 210 215 220
 Val Asn Thr Leu Lys Val Gln His His His His His His
 225 230 235

<210> 47
 <211> 265
 <212> PRT
 <213> Acropora aculeus

<400> 47

Met Thr Met Ile Thr Pro Ser Tyr Leu Gly Asp Thr Ile Glu Tyr Ser
 1 5 10 15
 Ser Tyr Ala Ser Asn Ala Leu Gly Ala Leu Pro Tyr Gly Arg Pro Ala
 20 25 30
 Gly Gly Arg Thr Ser Asp Leu Ser Tyr Ser Lys Gln Gly Ile Val Gln
 35 40 45
 Glu Met Lys Thr Lys Tyr Arg Met Glu Gly Ser Val Asn Gly His Glu
 50 55 60
 Phe Thr Ile Glu Gly Val Gly Thr Gly Tyr Pro Tyr Glu Gly Lys Gln
 65 70 75 80
 Met Ser Glu Leu Val Ile Val Lys Pro Lys Gly Lys Pro Leu Pro Phe
 85 90 95
 Ser Phe Asp Ile Leu Ser Ser Val Phe Gln Tyr Gly Asn Arg Cys Phe
 100 105 110
 Thr Lys Tyr Pro Ala Asp Met Pro Asp Tyr Phe Lys Gln Ala Phe Pro
 115 120 125

Asp Gly Met Ser Tyr Glu Arg Ser Phe Leu Phe Glu Asp Gly Ala Val
 130 135 140
 Ala Thr Ala Ser Trp Asn Ile Arg Leu Glu Gly Asn Cys Phe Ile His
 145 150 155 160
 Asn Ser Ile Phe His Gly Val Asn Phe Pro Ala Asp Gly Pro Val Met
 165 170 175
 Lys Lys Lys Thr Ile Gly Trp Asp Lys Ser Phe Glu Lys Met Thr Val
 180 185 190
 Ser Lys Glu Val Leu Arg Gly Asp Val Thr Met Phe Leu Met Leu Glu
 195 200 205
 Gly Gly Gly Tyr His Arg Cys Gln Phe His Ser Thr Tyr Lys Thr Val
 210 215 220
 Lys Pro Val Glu Leu Pro Pro Asn His Val Val Glu His Gln Ile Val
 225 230 235 240
 Arg Thr Asp Leu Gly Gln Ser Ala Lys Gly Phe Thr Val Lys Leu Glu
 245 250 255
 Ala His Ala Ala Ala His Val Thr Leu
 260 265

<210> 48
 <211> 237
 <212> PRT
 <213> Acropora aculeus

<400> 48

Met Ser Leu Ser Lys His Gly Ile Thr Gln Glu Met Pro Thr Lys Tyr
 1 5 10 15
 His Met Lys Gly Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Val
 20 25 30
 Gly Thr Gly His Pro Tyr Glu Gly Thr His Met Ala Glu Leu Val Ile
 35 40 45
 Ile Lys Pro Ala Gly Lys Pro Leu Pro Phe Ser Phe Asp Ile Leu Ser
 50 55 60
 Thr Val Ile Gln Tyr Gly Asn Arg Cys Phe Thr Lys Tyr Pro Ala Asp
 65 70 75 80
 Leu Pro Asp Tyr Phe Lys Gln Ala Tyr Pro Gly Gly Met Ser Tyr Glu
 85 90 95
 Arg Ser Phe Val Phe Gln Asp Gly Gly Ile Ala Thr Ala Ser Trp Asn
 100 105 110
 Val Gly Leu Glu Gly Asn Cys Phe Ile His Lys Ser Thr Tyr Leu Gly
 115 120 125

Val Asn Phe Pro Ala Asp Gly Pro Val Met Thr Lys Lys Thr Ile Gly
 130 135 140

Trp Asp Lys Ala Phe Glu Lys Met Thr Gly Phe Asn Glu Val Leu Arg
 145 150 155 160

Gly Asp Val Thr Glu Phe Leu Met Leu Glu Gly Gly Gly Tyr His Ser
 165 170 175

Cys Gln Phe His Ser Thr Tyr Lys Pro Glu Lys Pro Val Lys Leu Pro
 180 185 190

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

Thr Ala Lys Gly Phe Met Val Lys Leu Val Gln His Ala Ala Ala His
 210 215 220

Val Asn Pro Leu Lys Val Gln His His His His His His
 225 230 235

<210> 49
 <211> 237
 <212> PRT
 <213> Acropora aculeus

<400> 49

Met Ser Leu Ser Lys His Gly Ile Thr Gln Glu Met Pro Thr Lys Tyr
 1 5 10 15

His Met Lys Gly Asn Val Asn Gly His Glu Phe Glu Ile Glu Gly Val
 20 25 30

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

Ile Lys Pro Ala Gly Lys Pro Leu Pro Phe Ser Phe Asp Ile Leu Ser
 50 55 60

Thr Val Ile Gln Tyr Gly Asn Arg Cys Phe Thr Lys Tyr Pro Ala Asp
 65 70 75 80

Leu Pro Asp Tyr Phe Lys Gln Ala Tyr Pro Gly Gly Met Ser Tyr Glu
 85 90 95

Arg Ser Phe Val Phe Gln Asp Gly Gly Ile Ala Thr Ala Ser Trp Asn
 100 105 110

Val Gly Leu Glu Gly Asn Cys Phe Ile His Lys Ser Thr Tyr Leu Gly
 115 120 125

Val Asn Phe Pro Ala Asp Gly Pro Val Met Thr Lys Lys Thr Ile Gly
 130 135 140

Trp Asp Lys Ala Phe Glu Lys Met Thr Gly Phe Asn Glu Val Leu Arg
 145 150 155 160

Gly Asp Val Thr Gly Phe Leu Met Leu Glu Gly Gly Gly Tyr His Ser
165 170 175

Cys Gln Phe His Ser Thr Tyr Lys Pro Glu Lys Pro Val Lys Leu Pro
180 185 190

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

Thr Ala Lys Gly Phe Met Val Lys Leu Val Gln His Ala Ala Ala His
210 215 220

Val Asn Pro Leu Lys Val Gln His His His His His His
225 230 235

<210> 50

<211> 227

<212> PRT

<213> Acropora aculeus

<400> 50

Met Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1 5 10 15

Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
20 25 30

Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly
35 40 45

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly
50 55 60

Ser Ile Pro Phe Thr Lys Tyr Pro Asp Asp Ile Pro Asp Tyr Val Lys
65 70 75 80

Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
85 90 95

Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
100 105 110

Cys Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
115 120 125

Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
130 135 140

Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145 150 155 160

Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
165 170 175

Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Val Asp
180 185 190

Arg Lys Leu Asp Val Thr Asn His Asn Arg Asp Tyr Thr Ser Val Glu
 195 200 205

Gln Arg Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala His His His
 210 215 220

His His His
 225

<210> 51
 <211> 227
 <212> PRT
 <213> Acropora aculeus

<400> 51

Met Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
 1 5 10 15

Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
 20 25 30

Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly
 35 40 45

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Ser Gln Tyr Gly
 50 55 60

Ser Ile Pro Phe Thr Lys Tyr Pro Asp Asp Ile Pro Asp Tyr Val Lys
 65 70 75 80

Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe Glu
 85 90 95

Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
 100 105 110

Cys Phe Ile Tyr Asn Val Lys Phe Ser Gly Leu Asn Phe Pro Pro Asn
 115 120 125

Gly Pro Val Met Arg Lys Lys Thr Arg Gly Trp Glu Pro Asn Thr Glu
 130 135 140

Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
 145 150 155 160

Leu Lys Leu Glu Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
 165 170 175

Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Val Asp
 180 185 190

Arg Lys Leu Asp Val Thr Asn His Asn Arg Asp Tyr Thr Ser Val Glu
 195 200 205

Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala His His His
 210 215 220

His His His
225

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<210> 52
<211> 227
<212> PRT
<213> Acropora hyacinthus
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<400> 52

[illegible]

<210>	53
<211>	237

<212> PRT

<213> Acropora millepora

<400> 53

Met Ser Tyr Ser Lys Gln Gly Ile Ala Gln Val Met Lys Thr Lys Tyr
 1 5 10 15

His Met Glu Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Val
 20 25 30

Gly Thr Gly Asn Pro Tyr Glu Gly Thr Gln Met Ser Glu Leu Val Ile
 35 40 45

Thr Glu Pro Ala Gly Lys Pro Leu Pro Phe Ser Phe Asp Ile Leu Ser
 50 55 60

Thr Val Phe Gln Tyr Gly Asn Arg Cys Phe Thr Lys Tyr Pro Glu Gly
 65 70 75 80

Met Thr Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Phe Glu
 85 90 95

Arg Ser Phe Leu Tyr Glu Asp Gly Gly Val Ala Thr Ala Ser Trp Asn
 100 105 110

Ile Arg Leu Glu Arg Asp Cys Phe Ile His Lys Ser Ile Tyr His Gly
 115 120 125

Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Lys Thr Ile Gly
 130 135 140

Trp Asp Lys Ala Phe Glu Lys Met Thr Val Ser Lys Asp Val Leu Arg
 145 150 155 160

Gly Asp Val Thr Glu Phe Leu Met Leu Glu Gly Gly Gly Tyr His Ser
 165 170 175

Cys Gln Phe His Ser Thr Tyr Lys Pro Glu Lys Pro Val Thr Leu Pro
 180 185 190

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

Thr Ala Lys Gly Phe Thr Val Lys Leu Glu Glu His Ala Ala Ala His
 210 215 220

Val Asn Pro Leu Lys Val His His His His His His His
 225 230 235

<210> 54

<211> 311

<212> PRT

<213> Acropora millepora

<400> 54

Met Ser Tyr Ser Lys Gln Gly Ile Val Gln Glu Met Lys Thr Lys Tyr

36

1	5	10	15
His Met Glu Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Val	20	25	30
Gly Thr Gly Tyr Pro Tyr Glu Gly Lys Gln Ile Ser Glu Leu Val Ile	35	40	45
Ile Lys Pro Ala Gly Lys Pro Leu Pro Phe Ser Phe Asp Ile Leu Ser	50	55	60
Ser Val Phe Gln Tyr Gly Asn Arg Cys Phe Thr Lys Tyr Pro Ala Asp	65	70	75
Met Pro Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Tyr Glu	85	90	95
Arg Ser Phe Leu Phe Glu Asp Gly Ala Val Ala Thr Ala Ser Trp Asn	100	105	110
Ile Arg Leu Glu Gly Asn Cys Phe Ile His Lys Ser Ile Phe His Gly	115	120	125
Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Lys Thr Ile Asp	130	135	140
Trp Asp Lys Ser Phe Glu Lys Met Thr Val Ser Lys Glu Val Leu Arg	145	150	155
Gly Asp Val Thr Met Phe Leu Met Leu Glu Gly Gly Gly Ser His Arg	165	170	175
Cys Gln Phe His Ser Thr Tyr Lys Thr Glu Lys Pro Val Thr Leu Pro	180	185	190
Pro Asn His Val Val Glu His Gln Ile Val Arg Thr Asp Leu Gly Gln	195	200	205
Thr Ala Lys Gly Phe Thr Val Lys Leu Glu Glu His Ala Ala Ala His	210	215	220
Val Ser Leu Ile Pro Arg Pro Trp Arg Pro Gly Ala Cys Asp Val Gly	225	230	235
Pro Asn Ser Pro Tyr Ser Glu Ser Tyr Tyr Asn Ser Leu Ala Val Val	245	250	255
Leu Gln Arg Arg Asp Trp Glu Asn Pro Gly Val Thr Gln Leu Asn Arg	260	265	270
Leu Ala Ala His Pro Pro Phe Ala Ser Trp Arg Asn Ser Glu Glu Ala	275	280	285
Arg Thr Asp Arg Pro Ser Gln Gln Leu Arg Ser Leu Asn Gly Glu Trp	290	295	300
Thr Arg Pro Val Ala Ala His	305	310	

<210> 55
 <211> 227
 <212> PRT
 <213> Acropora millepora

<400> 55

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

His Met Glu Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Val
 20 25 30

Gly Thr Gly Tyr Pro Tyr Glu Gly Lys Gln Met Ser Glu Leu Val Ile
 35 40 45

Ile Lys Pro Ala Gly Lys Pro Leu Pro Phe Ser Phe Asp Ile Leu Ser
 50 55 60

Ser Val Phe Gln Tyr Gly Asn Arg Cys Phe Thr Lys Tyr Pro Ala Asp
 65 70 75 80

Met Pro Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Tyr Glu
 85 90 95

Arg Ser Phe Leu Phe Glu Asp Gly Ala Val Ala Thr Ala Ser Trp Asn
 100 105 110

Ile Arg Leu Glu Gly Asn Cys Phe Ile His Lys Ser Ile Phe His Gly
 115 120 125

Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Lys Thr Ile Asp
 130 135 140

Trp Asp Lys Ser Phe Glu Lys Met Thr Val Ser Lys Glu Val Leu Arg
 145 150 155 160

Gly Asp Val Thr Met Phe Leu Met Leu Glu Gly Gly Gly Ser His Arg
 165 170 175

Cys Gln Phe His Ser Thr Tyr Lys Thr Glu Lys Pro Val Thr Leu Pro
 180 185 190

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

Thr Ala Lys Gly Phe Thr Val Lys Leu Glu Glu His Ala Ala Ala His
 210 215 220

Val Thr Leu
 225

<210> 56
 <211> 237
 <212> PRT
 <213> Acropora millepora

<400> 56

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

Arg Met Glu Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Val
          20           25           30

Gly Thr Gly Tyr Pro Tyr Glu Gly Lys Gln Met Ser Glu Leu Val Ile
          35           40           45

Val Lys Pro Lys Gly Lys Pro Leu Pro Phe Ser Phe Asp Ile Leu Ser
          50           55           60

Ser Val Phe Gln Tyr Gly Asn Arg Cys Phe Thr Lys Tyr Pro Ala Asp
65           70           75           80

Met Pro Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Tyr Glu
          85           90           95

Arg Ser Phe Leu Phe Glu Asp Gly Ala Val Ala Thr Ala Ser Trp Asn
          100          105          110

Ile Arg Leu Glu Gly Asn Cys Phe Ile His Asn Ser Ile Phe His Gly
          115          120          125

Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Lys Thr Ile Gly
          130          135          140

Trp Asp Lys Ser Phe Glu Lys Met Thr Val Ser Lys Glu Val Leu Arg
145          150          155          160

Gly Asp Val Thr Met Phe Leu Met Leu Glu Gly Gly Gly Tyr His Arg
          165          170          175

Cys Gln Phe His Ser Thr Tyr Lys Thr Val Lys Pro Val Glu Leu Pro
          180          185          190

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

Ser Ala Lys Gly Phe Thr Val Lys Leu Glu Ala His Ala Ala Ala His
          210          215          220

Val Asn Pro Leu Lys Val Gln His His His His His His
225          230          235

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<210> 57

<211> 237

<212> PRT

<213> Acropora millepora

<400> 57

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Met Ser His Ser Lys Gln Gly Ile Ala Gln Val Met Lys Thr Lys Tyr
1           5           10           15

His Met Glu Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Val

```

20 25 30
 Gly Thr Gly Asn Pro Tyr Glu Gly Ser Gln Met Ser Glu Leu Val Ile
 35 40 45
 Thr Lys Pro Ala Gly Lys Pro Leu Pro Phe Ser Phe Asp Ile Leu Ser
 50 55 60
 Thr Val Phe Gln Tyr Gly Asn Arg Cys Phe Thr Lys Tyr Pro Glu Gly
 65 70 75 80
 Met Thr Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Tyr Glu
 85 90 95
 Arg Ser Phe Leu Tyr Glu Asp Gly Gly Val Ala Thr Ala Ser Trp Asn
 100 105 110
 Ile Arg Leu Glu Arg Gly Cys Phe Ile His Lys Ser Ile Tyr His Gly
 115 120 125
 Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Lys Thr Ile Gly
 130 135 140
 Trp Asp Lys Ala Phe Glu Lys Met Thr Val Ser Lys Asp Val Leu Arg
 145 150 155 160
 Gly Asp Val Thr Gly Phe Leu Met Leu Glu Gly Gly Gly Tyr His Asn
 165 170 175
 Cys Gln Phe His Ser Thr Tyr Lys Pro Glu Lys Pro Val Thr Leu Pro
 180 185 190
 Pro Asn His Val Val Glu His His Ile Val Arg Thr Asp Leu Gly Gln
 195 200 205
 Thr Ala Lys Gly Phe Thr Ala Lys Leu Glu Glu His Ala Ala Ala His
 210 215 220
 Val Asn Pro Leu Lys Val Gln His His His His His His
 225 230 235

<210> 58

<211> 237

<212> PRT

<213> Acropora millepora

<400> 58

Met Ser Tyr Ser Lys Gln Gly Ile Val Gln Glu Met Lys Thr Lys Tyr
 1 5 10 15
 His Met Glu Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Val
 20 25 30
 Gly Thr Gly Tyr Pro Tyr Glu Gly Lys Gln Met Ser Glu Leu Val Ile
 35 40 45
 Ile Lys Pro Ala Gly Lys Pro Leu Pro Phe Ser Phe Asp Ile Leu Ser

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<210> 59
<211> 238
<212> PRT
<213> Acropora millepora
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<400> 59

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

41

85 90 95
 Leu Leu Phe Glu Asp Gly Ala Val Cys Thr Thr Ser Ala Asp Ile Thr
 100 105 110
 Val Ser Val Glu Glu Asn Cys Phe Tyr His Asn Ser Lys Phe His Gly
 115 120 125
 Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Met Thr Thr Asn
 130 135 140
 Trp Glu Pro Ser Cys Glu Lys Ile Ile Pro Val Pro Arg Gln Gly Ile
 145 150 155 160
 Leu Lys Gly Asp Ile Ala Met Tyr Leu Leu Leu Lys Asp Gly Gly Arg
 165 170 175
 Tyr Arg Cys Gln Phe Asp Thr Ile Tyr Lys Ala Lys Ser Asp Pro Lys
 180 185 190
 Glu Met Pro Glu Trp His Phe Ile Gln His Lys Leu Thr Arg Glu Asp
 195 200 205
 Arg Ser Asp Ala Lys Asn Gln Lys Trp Gln Leu Val Glu His Ala Val
 210 215 220
 Ala Ser Arg Ser Ala Leu Pro Gly His His His His His His
 225 230 235

<210> 60
 <211> 227
 <212> PRT
 <213> Acropora millepora

<400> 60

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

115 120 125
 Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
 130 135 140
 Arg Leu Phe Ala Arg Asp Gly Met Leu Leu Gly Asn Asn Phe Met Ala
 145 150 155 160
 Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Thr Thr
 165 170 175
 Tyr Lys Ala Lys Lys Pro Val Lys Met Pro Gly Tyr His Tyr Val Asp
 180 185 190
 Arg Lys Leu Asp Val Thr Asn His Asn Lys Asp Tyr Thr Ser Val Glu
 195 200 205
 Gln Cys Glu Ile Ser Ile Ala Arg Lys Pro Val Val Ala His His His
 210 215 220

His His His
225

<210> 61
 <211> 237
 <212> PRT
 <213> Acropora nobilis

<400> 61

Met Ser Tyr Ser Lys Gln Gly Ile Ala Gln Val Met Lys Thr Lys Tyr
 1 5 10 15
 His Met Glu Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Val
 20 25 30
 Gly Thr Gly Asn Pro Tyr Glu Gly Thr Gln Met Ser Glu Leu Val Ile
 35 40 45
 Thr Lys Pro Ala Gly Lys Pro Leu Pro Phe Ser Phe Asp Ile Leu Ser
 50 55 60
 Thr Val Phe Gln Tyr Gly Asn Arg Cys Phe Thr Lys Tyr Pro Glu Gly
 65 70 75 80
 Met Thr Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Cys Glu
 85 90 95
 Arg Ser Phe Leu Tyr Glu Asp Gly Gly Val Ala Thr Ala Ser Trp Asn
 100 105 110
 Ile Arg Leu Glu Arg Asp Cys Phe Ile His Lys Ser Ile Tyr His Gly
 115 120 125
 Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Lys Thr Ile Gly
 130 135 140
 Trp Asp Lys Ala Phe Glu Lys Met Thr Val Ser Lys Asp Val Leu Arg

<400> 62

Met 1	Ser	Tyr	Ser	Lys 5	Gln	Gly	Ile	Ala	Gln 10	Val	Met	Lys	Thr	Lys 15	Tyr
His	Met	Glu	Gly 20	Ser	Val	Asn	Gly	His 25	Glu	Phe 30	Thr	Ile	Glu	Gly	Val
Gly	Thr	Gly 35	Asn	Pro	Tyr	Glu	Gly 40	Thr	Gln	Met	Ser	Glu	Leu	Val	Ile
Thr	Lys 50	Pro	Ala	Gly	Lys	Pro	Leu 55	Pro	Phe	Ser	Phe 60	Asp	Ile	Leu	Ser
Thr 65	Val	Phe	Gln	Tyr	Gly 70	Asn	Arg	Cys	Phe	Thr 75	Lys	Tyr	Pro	Glu	Gly 80
Met	Thr	Asp	Tyr	Phe 85	Lys	Gln	Ala	Phe	Pro 90	Asp	Gly	Met	Ser	Tyr 95	Glu
Arg	Ser	Phe	Leu 100	Tyr	Glu	Asp	Gly	Gly 105	Val	Ala	Thr	Ala	Gly	Trp	Asn
Ile	Arg	Leu	Glu	Arg	Asp	Cys	Phe 120	Ile	His	Lys	Ser	Ile	Tyr	His	Gly
Val	Asn 130	Phe	Pro	Ala	Asp	Gly 135	Pro	Val	Met	Lys	Lys 140	Lys	Thr	Ile	Gly
Trp 145	Asp	Lys	Ala	Phe	Glu 150	Lys	Met	Thr	Val	Ser 155	Lys	Asp	Val	Leu	Arg 160
Gly	Asp	Val	Thr	Gly 165	Phe	Leu	Met	Leu	Glu 170	Gly	Gly	Gly	Tyr	His 175	Ser
Cys	Gln	Phe	His	Ser	Thr	Tyr	Lys	Pro	Glu	Lys	Pro	Ala	Ala	Leu	Pro

180 185 190
 Pro Asn His Val Val Glu His His Ile Val Arg Thr Asp Leu Gly Gln
 195 200 205
 Ser Ala Lys Gly Phe Thr Val Lys Leu Glu Glu His Ala Ala Ala His
 210 215 220
 Val Asn Pro Leu Lys Val Gln His His His His His His
 225 230 235

 <210> 63
 <211> 237
 <212> PRT
 <213> *Acropora nobilis*

 <400> 63

 Met Ser Tyr Ser Lys Gln Gly Ile Ala Gln Glu Met Lys Thr Lys Tyr
 1 5 10 15
 His Met Glu Gly Ser Val Asn Gly His Glu Phe Thr Val Glu Gly Val
 20 25 30
 Gly Thr Gly Tyr Pro Tyr Glu Gly Glu Gln Met Ser Glu Leu Val Ile
 35 40 45
 Ile Glu Pro Ala Gly Lys Pro Leu Pro Phe Ser Phe Asp Ile Leu Ser
 50 55 60
 Ser Val Phe Gln Tyr Gly Asn Arg Cys Phe Thr Lys Tyr Pro Ala Asp
 65 70 75 80
 Met Pro Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Tyr Glu
 85 90 95
 Arg Ser Phe Leu Phe Glu Asp Gly Ala Val Ala Thr Ala Ser Trp Lys
 100 105 110
 Ile Arg Leu Glu Gly Asn Cys Phe Ile His Asn Ser Ile Phe Asn Gly
 115 120 125
 Val Asn Phe Pro Ala Asp Gly Pro Val Met Glu Lys Lys Thr Ile Gly
 130 135 140
 Trp Asp Lys Ser Phe Glu Lys Met Thr Val Ser Lys Glu Val Leu Arg
 145 150 155 160
 Gly Asp Val Thr Met Phe Leu Met Leu Glu Gly Gly Gly Ser His Arg
 165 170 175
 Cys Gln Phe His Ser Thr Tyr Lys Thr Glu Lys Pro Val Thr Leu Pro
 180 185 190
 Pro Asn His Val Val Glu His Gln Ile Val Arg Thr Asp Leu Gly Gln
 195 200 205
 Ser Ala Lys Gly Phe Thr Val Lys Leu Glu Ala His Ala Ala Ala His

210 215 220
 Val Asn Pro Leu Lys Val Lys His His His His His His
 225 230 235

 <210> 64
 <211> 232
 <212> PRT
 <213> Agaricia fragilis

 <400> 64

 Met Ser Val Ile Val Lys Glu Met Met Thr Lys Leu His Met Glu Gly
 1 5 10 15

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

 Pro Tyr Asn Gly Val Gln Ser Met Asn Leu Asp Val Lys Gly Gly Ala
 35 40 45

 Pro Leu Pro Phe Ser Phe Asp Leu Leu Thr Pro Ala Phe Met Tyr Gly
 50 55 60

 Asn Arg Val Phe Ala Lys Tyr Pro Glu Asp Ile Pro Asp Phe Phe Lys
 65 70 75 80

 Gln Val Phe Pro Glu Gly Tyr His Trp Glu Arg Ser Ile Thr Phe Glu
 85 90 95

 Asp Gln Ala Val Cys Thr Ala Thr Ser His Ile Arg Leu Asp Gln Lys
 100 105 110

 Glu Met Cys Phe Ile Tyr Asp Val Arg Phe His Gly Val Asn Phe Pro
 115 120 125

 Ala Asn Gly Pro Ile Met Gln Lys Lys Ile Leu Gly Trp Glu Pro Ser
 130 135 140

 Thr Glu Lys Met Tyr Ala Arg Asp Gly Val Leu Lys Gly Asp Val Asn
 145 150 155 160

 Met Thr Leu Arg Val Glu Gly Gly Gly His Tyr Arg Ala Asp Phe Arg
 165 170 175

 Thr Thr Tyr Lys Ala Lys Lys Pro Val Asn Leu Pro Gly Tyr His Phe
 180 185 190

 Ile Asp His Arg Ile Glu Ile Thr Lys His Ser Lys Asp Tyr Thr Asn
 195 200 205

 Val Ala Leu Tyr Glu Ala Ala Val Ala Arg His Ser Pro Leu Pro Lys
 210 215 220

 Val Ala His His His His His His
 225 230

<210> 65
 <211> 306
 <212> PRT

<213> Agaricia fragilis

<400> 65

Met	Ser	Val	Ile	Val	Lys	Glu	Met	Met	Thr	Lys	Leu	His	Met	Glu	Gly	1	5	10	15
Thr	Val	Asn	Gly	His	Ala	Phe	Thr	Ile	Glu	Gly	Lys	Gly	Lys	Gly	Asp	20	25	30	
Pro	Tyr	Asn	Gly	Val	Gln	Ser	Met	Asn	Leu	Asp	Val	Lys	Gly	Gly	Ala	35	40	45	
Pro	Leu	Pro	Phe	Ser	Phe	Asp	Leu	Leu	Thr	Pro	Ala	Phe	Met	Tyr	Gly	50	55	60	
Asn	Arg	Val	Phe	Thr	Lys	Tyr	Pro	Glu	Asp	Ile	Pro	Asp	Phe	Phe	Lys	65	70	75	80
Gln	Val	Phe	Pro	Glu	Gly	Tyr	His	Trp	Glu	Arg	Ser	Ile	Thr	Phe	Glu	85	90	95	
Asp	Gln	Ala	Val	Cys	Thr	Ala	Thr	Ser	His	Ile	Arg	Leu	Asp	Gln	Lys	100	105	110	
Glu	Met	Cys	Phe	Ile	Tyr	Asp	Val	Arg	Phe	His	Gly	Val	Asn	Phe	Pro	115	120	125	
Ala	Asn	Gly	Pro	Ile	Met	Gln	Lys	Lys	Ile	Leu	Gly	Trp	Glu	Pro	Ser	130	135	140	
Thr	Glu	Lys	Met	Tyr	Ala	Arg	Asp	Gly	Val	Leu	Lys	Gly	Asp	Val	Asn	145	150	155	160
Met	Thr	Leu	Arg	Val	Glu	Gly	Gly	Gly	His	Tyr	Arg	Ala	Asp	Phe	Arg	165	170	175	
Thr	Thr	Tyr	Lys	Ala	Lys	Lys	Pro	Val	Asn	Leu	Pro	Gly	Tyr	His	Phe	180	185	190	
Ile	Asp	His	Arg	Ile	Glu	Ile	Thr	Lys	His	Ser	Lys	Asp	Tyr	Thr	Asn	195	200	205	
Val	Ala	Leu	Tyr	Glu	Ala	Ala	Val	Ala	Arg	His	Ser	Pro	Leu	Pro	Lys	210	215	220	
Val	Ala	His	His	His	His	Ile	Thr	Asn	Lys	Ser	Arg	Gly	His	Gly	Gly	225	230	235	240
Arg	Glu	His	Ala	Thr	Ser	Gly	Pro	Ile	Arg	Pro	Ile	Val	Ser	Arg	Ile	245	250	255	
Thr	Ile	His	Trp	Pro	Ser	Phe	Tyr	Asn	Val	Val	Thr	Gly	Lys	Thr	Leu	260	265	270	

Ala Leu Pro Asn Leu Ile Ala Leu Gln His Ile Pro Leu Ser Pro Ala
 275 280 285

Gly Val Ile Ala Lys Arg Pro Ala Pro Ile Ala Leu Pro Asn Ser Cys
 290 295 300

Ala Ala
 305

<210> 66
 <211> 232
 <212> PRT
 <213> Agaricia fragilis

<400> 66

Met Ser Val Ile Val Lys Glu Met Met Thr Lys Leu His Met Glu Gly
 1 5 10 15

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

Pro Tyr Asn Gly Val Gln Ser Met Asn Leu Asp Val Lys Gly Gly Ala
 35 40 45

Pro Leu Pro Phe Ser Phe Asp Leu Leu Thr Pro Ala Phe Met Tyr Gly
 50 55 60

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

Gln Val Phe Pro Glu Gly Tyr His Trp Glu Arg Ser Ile Thr Phe Glu
 85 90 95

Asp Gln Ala Val Cys Thr Ala Thr Ser His Ile Arg Leu Asp Gln Lys
 100 105 110

Glu Met Cys Phe Ile Tyr Asp Val Arg Phe His Gly Val Asn Phe Pro
 115 120 125

Ala Asn Gly Pro Ile Met Gln Lys Lys Ile Leu Gly Trp Glu Pro Ser
 130 135 140

Thr Glu Lys Met Tyr Ala Arg Asp Gly Val Leu Lys Gly Asp Val Asn
 145 150 155 160

Met Thr Leu Arg Val Glu Gly Gly Gly His Tyr Arg Ala Asp Phe Arg
 165 170 175

Thr Thr Tyr Lys Ala Lys Lys Pro Val Asn Leu Pro Gly Tyr His Phe
 180 185 190

Ile Asp His Arg Ile Glu Ile Thr Lys His Ser Lys Asp Tyr Thr Asn
 195 200 205

Val Ala Leu Tyr Gly Ala Ala Val Ala Arg His Ser Pro Leu Pro Lys
 210 215 220

Val Ser His His His His His His
225 230

<210> 67
<211> 232
<212> PRT
<213> Agaricia fragilis

<400> 67

Met Ser Val Ile Val Lys Glu Met Met Thr Lys Leu His Met Glu Gly
1 5 10 15
Thr Val Asn Gly His Ala Phe Thr Ile Glu Gly Lys Gly Lys Gly Asp
20 25 30
Pro Tyr Asn Gly Val Gln Ser Met Asn Leu Asp Val Lys Gly Gly Ala
35 40 45
Pro Leu Pro Phe Ser Phe Asp Leu Leu Thr Pro Ala Phe Met Tyr Gly
50 55 60
Asn Arg Val Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Phe Phe Lys
65 70 75 80
Gln Val Phe Pro Glu Gly Tyr His Trp Glu Arg Ser Ile Thr Phe Glu
85 90 95
Asp Gln Ala Val Cys Thr Ala Thr Ser His Ile Arg Leu Asp Gln Lys
100 105 110
Glu Met Cys Phe Ile Tyr Asp Val Arg Phe His Gly Val Asn Phe Pro
115 120 125
Ala Asn Gly Pro Ile Met Gln Lys Lys Ile Leu Gly Trp Glu Pro Ser
130 135 140
Thr Glu Lys Met Tyr Ala Arg Asp Gly Val Leu Lys Gly Asp Val Asn
145 150 155 160
Val Thr Leu Arg Val Glu Gly Gly Gly His Tyr Arg Ala Asp Phe Arg
165 170 175
Thr Thr Tyr Lys Ala Lys Lys Pro Val Asn Leu Pro Gly Tyr His Phe
180 185 190
Ile Asp His Arg Ile Glu Ile Thr Lys His Ser Lys Asp Tyr Thr Asn
195 200 205
Val Ala Leu Tyr Glu Ala Ala Val Ala Arg His Ser Pro Leu Pro Lys
210 215 220
Val Ala His His His His His His
225 230

<210> 68
<211> 232

<212> PRT

<213> *Agaricia fragilis*

<400> 68

Met Ser Val Ile Val Lys Glu Met Met Thr Lys Leu His Met Glu Gly
1 5 10 15

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

Pro Tyr Asn Gly Val Gln Ser Met Asn Leu Asp Val Lys Gly Gly Ala
35 40 45

Pro Leu Pro Phe Ser Phe Asp Leu Leu Thr Pro Ala Phe Met Tyr Gly
50 55 60

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

Gln Val Phe Pro Glu Gly Tyr His Trp Glu Arg Ser Ile Thr Phe Glu
85 90 95

Asp Gln Ala Val Cys Thr Ala Thr Ser His Ile Arg Leu Asp Gln Lys
100 105 110

Glu Met Cys Phe Ile Tyr Asp Val Arg Phe His Gly Val Asn Phe Pro
115 120 125

Ala Asn Gly Pro Ile Met Gln Lys Lys Ile Leu Gly Trp Glu Pro Ser
130 135 140

Thr Glu Lys Met Tyr Ala Arg Asp Gly Val Leu Lys Gly Asp Val Asn
145 150 155 160

Met Thr Leu Arg Val Glu Gly Gly Gly His Tyr Arg Ala Asp Phe Arg
165 170 175

Thr Thr Tyr Lys Ala Lys Lys Pro Val Asn Leu Pro Gly Tyr His Phe
180 185 190

Ile Asp His Arg Ile Glu Ile Thr Lys His Ser Lys Asp Tyr Thr Asn
195 200 205

Val Ala Leu Tyr Gly Ala Ala Val Ala Arg His Ser Pro Leu Pro Lys
210 215 220

Val Ala His His His His His His
225 230

<210> 69

<211> 232

<212> PRT

<213> *Agaricia fragilis*

<400> 69

Met Ser Val Ile Val Lys Glu Met Met Thr Lys Leu His Met Glu Gly

50

<400> 70

Met	Ser	Val	Ile	Val	Lys	Glu	Met	Met	Thr	Lys	Leu	His	Met	Glu	Gly
1				5					10					15	
Thr	Val	Asn	Gly	His	Ala	Phe	Thr	Ile	Glu	Gly	Lys	Gly	Lys	Gly	Asp
			20					25					30		
Pro	Tyr	Asn	Gly	Val	Gln	Ser	Met	Asn	Leu	Asp	Val	Lys	Gly	Gly	Ala

35										40					45				
Pro	Leu	Pro	Phe	Ser	Phe	Asp	Leu	Leu	Thr	Pro	Ala	Phe	Met	Tyr	Gly				
50						55					60								
Asn	Arg	Val	Phe	Thr	Lys	Tyr	Pro	Glu	Asp	Ile	Pro	Asp	Phe	Phe	Lys				
65					70					75					80				
Gln	Val	Phe	Pro	Glu	Gly	Tyr	His	Trp	Glu	Arg	Ser	Ile	Thr	Phe	Glu				
				85					90					95					
Asp	Gln	Ala	Val	Cys	Thr	Ala	Thr	Ser	His	Ile	Arg	Leu	Asp	Gln	Lys				
			100					105					110						
Glu	Met	Cys	Phe	Ile	Tyr	Asp	Val	Arg	Phe	His	Gly	Val	Asn	Phe	Pro				
	115						120					125							
Ala	Asn	Gly	Pro	Ile	Met	Gln	Lys	Lys	Ile	Leu	Gly	Trp	Glu	Pro	Ser				
	130					135					140								
Thr	Glu	Lys	Met	Tyr	Ala	Arg	Asp	Gly	Val	Leu	Lys	Gly	Asp	Val	Asn				
145					150					155					160				
Thr	Thr	Leu	Arg	Val	Glu	Gly	Gly	Gly	His	Tyr	Arg	Ala	Asp	Phe	Arg				
				165					170					175					
Thr	Thr	Tyr	Lys	Ala	Lys	Lys	Pro	Val	Asn	Leu	Pro	Gly	Tyr	His	Phe				
			180					185					190						
Ile	Asp	His	Arg	Ile	Glu	Ile	Thr	Lys	His	Ser	Lys	Asp	Tyr	Thr	Asn				
	195						200					205							
Val	Ala	Leu	Tyr	Glu	Ala	Ala	Val	Ala	Arg	His	Ser	Pro	Leu	Pro	Lys				
	210				215						220								
Val	Ala	His	His	His	His	His	His												
225					230														

<210> 71

<211> 717

<212> DNA

<213> Acropora aculeus

<400> 71

atgtcttatt caaagcaggg catcgtacaa gaaatgaaga cgaaataccg tatggaaggc	60
agtgtcaatg gccatgaatt cacgatcgaa ggtgtaggaa ctgggtaccc ttacgaaggg	120
aaacagatgt ccgaattagt gatcatcaag cctaagggaag agccccttcc attctccttt	180
gacatactgt catcagtctt tcaatatgga aacagggtgct tcacaaagta ccctgcagac	240
atgcctgact atttcaagca agcattccca gatggaatgt catatgaaag gtcatttcta	300
tttgaggatg gagcagttgc tacagccagc tggaacattc gtctcgaagg aaattgcttc	360
atccacaatt ccatctttca tggcgtaaac tttcccgatg atggaccctg aatgaaaaag	420

aagacaattg gctgggataa gtccttcgaa aaaatgactg tgtctaaaga ggtgttaaga 480
 ggtgatgtga ctatgtttct tatgctcgaa ggaggtgggt accacagatg ccagtttcac 540
 tccacttaca aaacagagaa gccggtcgaa ctgccccga atcatgtcgt agaacatcaa 600
 attgtgagga ccgaccttgg ccaaagtgc aaaggcttca cgggtcaagct ggaagcacat 660
 gctgcggctc atgttaaccc tttgaagggt caacagcacc atcaccatca ctaataa 717

<210> 72
 <211> 717
 <212> DNA
 <213> Acropora aculeus

<400> 72
 atgtctcttt caaagcatgg catcacacaa gaaatgccga cgaaatacca tatgaaaggc 60
 agtgtcaatg gccatgaatt cgagatcgaa ggtgtaggaa ctggacaccc ttacgaaggg 120
 acacacatgg ccgaattagt gatcataaag cctgcgggaa aacccttcc attctccttt 180
 gacatactgt caacagtcac tcaatacggg aacagatgct tctaagta ccctgcagac 240
 ctgcctgact atttcaagca agcataccca ggtggaatgt catatgaaag gtcatttgtg 300
 tatcaggatg gaggaattgc tacagcgagc tggaaacgtta gtctcgaggg aaattgcttc 360
 atccacaaat ccacctatct tgggtgaaac tttcctgctg atggaccctg aatgacaaag 420
 aagacaattg gctgggataa agcctttgaa aaaatgactg ggttcaatga ggtgttaaga 480
 ggtgatgtga ctgagtttct tatgctcgaa ggaggtgggt accatcatg ccagtttcac 540
 tccacttaca aaccagagaa gccggtcgaa ctgccccga atcatgtcat agaacatcac 600
 attgtgagga ccgaccttgg caagactgca aaaggcttca tgggtcaagct ggtacaacat 660
 gctgcggctc atgttaacac tttgaagggt caacatcacc atcaccatca ctaataa 717

<210> 73
 <211> 665
 <212> DNA
 <213> Acropora aculeus

<400> 73
 atggaaggca gtgtcaatgg ccatgaattc acgatcgaag gtgtaggaaac tgggtaccct 60
 tacgaaggga agcagatgtc cgaattagt atcgtcaagc ctaagggaaa gcccttcca 120
 ttctcctttg acatactgtc atcagtcttt caatatggaa acagggtgctt cacaagtac 180
 cctgcagaca tgctgacta tttcaagcaa gcattcccag atggaatgtc atatgaaagg 240
 tcatttctat ttgaggatgg agcagttgct acagccagct ggaacattcg tctcgaagga 300
 aattgcttca tccacaattc catctttcat ggcgtaaact ttcccgtga tggaccctga 360

atgaaaaaga agacaattgg ctgggataag tccttcgaaa aaatgactgt gtctaaagag	420
gtgttaagag gtgatgtgac tatgttttctt atgctcgaag gaggtgggta ccacagatgc	480
cagtttctact ccacttataa aacagtgaag ccgggtcgaac tgcccccgaa tcatgtcgta	540
gaacatcaaa ttgtgaggac cgaccttggc caaagtgcaa aaggcttcac agtcaagctg	600
gaagcacatg ctgcggtca tgaaccctt tgaagggtca acatcacat caccatcact	660
aataa	665

<210> 74
 <211> 717
 <212> DNA
 <213> Acropora aculeus

<400> 74	
atgtctctttt caaagcatgg catcacacaa gaaatgccga cgaaatacca tatgaaaggc	60
agtgtcaatg gccatgaatt cgagatcgaa ggtgtaggaa ctggacaccc ttacgaaggg	120
acacacatgg ccgaattagt gatcataaag cctgcgggaa aacccttcc attctccttt	180
gacatactgt caacagtcac tcaatacggg aacagatgct tcactaagta ccctgcagac	240
ctgcctgact atttcaagca agcataccca ggtggaatgt catatgaaag gtcatttgta	300
tttcaggatg gaggaattgc tacagcgagc tggaaactgc gtctcgaggg aaattgcttc	360
atccacaaat ccacctatct tgggtgtaaac tttcctgctg atggaccctg aatgacaaag	420
aagacaattg gctgggataa agcctttgaa aaaatgactg ggttcaatga ggtgttaaga	480
ggtgatgtga ctgagtttct tatgctcgaa ggaggtggtt accattcatg ccagtttcac	540
tccacttaca aaccagagaa gccggtcaaa ctgccccga atcatgtcat agaacatcac	600
attgtgagga ccgaccttgg caagactgca aaaggcttca tgggtcaagct ggtacaacat	660
gctgcggctc atgttaaccc tttgaagggt caacatcacc atcaccatca ctaataa	717

<210> 75
 <211> 717
 <212> DNA
 <213> Acropora aculeus

<400> 75	
atgtctctttt caaagcatgg catcacacaa gaaatgccga cgaaatacca tatgaaaggc	60
aatgtcaatg gccatgaatt cgagatcgaa ggtgtaggaa ctggacaccc ttacgaaggg	120
acacacatgg ccgaattagt gatcataaag cctgcgggaa aacccttcc attctccttt	180
gacatactgt caacagtcac tcaatacggg aacagatgct tcactaagta ccctgcagac	240

ctgcctgact atttcaagca agcgtaccca ggtggaatgt catatgaaag gtcattttgta 300
 tttcaggatg gaggaattgc tacagcgagc tggaacgttg gtctcgaggg aaattgcttc 360
 atccacaaat ccacctatct tgggtgtaaac tttcctgctg atggacccgt aatgacaaag 420
 aagacaattg gctgggataa agcctttgaa aaaatgactg ggttcaatga ggtgttaaga 480
 ggcgatgtga ctgggtttct tatgctcgaa ggaggtggtt accattcatg ccagtttcac 540
 tccacttaca aaccagagaa gccgggtcaaa ctgccccga atcatgtcat agaacatcac 600
 attgtgagga ccgaccttgg caagactgca aaaggcttca tggccaagct ggtacaacat 660
 gctgcggctc atgtgaaccc tttgaagggt caacatcacc atcaccatca ctaataa 717

<210> 76
 <211> 666
 <212> DNA
 <213> Acropora aculeus

<400> 76
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 gatggaaaag gaaagcctta cgagggggag cagacggtga agctcactgt caccaaggga 120
 ggacctctgc catttgcttg ggatatttta tcaccacagt cacagtacgg aagcatacca 180
 ttcaccaa at accctgacga catccctgac tatgtaaagc agtcattccc ggagggatat 240
 acatgggaga ggatcatgaa ctttgaagat ggtgcagtgt gtactgtcag caatgattcc 300
 agcatccaag gcaactgttt catctacaat gtcaagttct ctggtttgaa ctttcctccc 360
 aatggaccgg ttatgcagaa gaagacacag ggctgggaac ccaacactga gcgtctcttt 420
 gcacgagatg gaatgctgat aggaacaac tttatggctc tgaagttaga aggaggtggt 480
 cactatttgt gtgaattcaa atctacttac aaggcaaaga agcctgtgag gatgccaggg 540
 tatcactatg ttgaccgcaa actggatgta accaatcaca acagggatta cacttccggt 600
 gagcagcgtg aaatttccat tgcacgcaaa cctgtggtcg cccatcacca tcaccatcac 660
 taataa 666

<210> 77
 <211> 687
 <212> DNA
 <213> Acropora aculeus

<400> 77
 atgagtgtga tcgctaaaca aatgacctac aaggtttata tgtcaggcac ggtcaatgga 60
 cattactttg aggtcgaagg cgatggaaaa ggaaagcctt acgaggggga gcagacggtg 120
 aagctcactg tcaccaaggg aggacctctg ccatttgctt gggatatttt atcaccgcag 180

tcacagtacg gaagcatacc attcaccaaa taccctgacg acatccctga ctatgtaaag 240
 cagtcattcc cggagggata tacatgggag aggatcatga actttgagga tggcgagtg 300
 tgtactgtca gcaatgattc cagcatccaa ggcaactggt tcactctaaa tgtcaagttc 360
 tctgggttga actttcctcc caatggaccg gttatgcgga agaagacacg gggctgggaa 420
 cccaacactg agcgtctctt tgcacgggat ggaatgctga taggaaacaa ctttatggct 480
 ctgaagttag aaggaggtgg tcactatttg tgtgaattca aatctactta caaggcaaag 540
 aagcctgtga ggatgccagg gtatcactat gttgaccgca aactggatgt aaccaatcac 600
 aacagggatt acacttccgt tgagcagtgt gaaatttcca ttgcacgcaa acctgtggtc 660
 gcccatcacc atcaccatca ctaataa 687

<210> 78
 <211> 666
 <212> DNA
 <213> *Acropora hyacinthus*

<400> 78
 atgacctaca aggtttatat gtcaggcacg gtcaatggac actactttga ggtcgaaggc 60

 gatggaaaag gaaagcctta cgagggggag caaacggtaa ggctgactgt caccaagggc 120
 ggacctctgc cgtttgcttg ggatatttta tcaccacagt cacagtacgg aagcatacca 180
 ttcaccaagt accctgaaga catccctgac tatgtgaagc agtcattccc ggagggatat 240
 acatgggaga ggatcatgaa ctttgaagat ggtgcagtgt gtactgtcag caatgattcc 300
 agcatccaag gcaactgttt catctaccat gtcaagttct ctggtttgaa ctttcctccc 360
 aatggacctg ttatgcagaa gaagacacag ggctgggaac ccaacactga gcgtctcttt 420
 gcacgagatg gagttctgat aggaaacaac tttatggccc tgaagttaga aggaggtggg 480
 cactatttgt gtgaattcaa atctacttac aaggcaaaga agcctgtgaa gatgcctggg 540
 tatcactttg ttgaccgcaa actggatgta accaatcaca acaaggatta cacttctggt 600
 gagcagcgtg aaatttccat tgcacgcaaa cctgtgggtcg ccaccacca tcaccatcac 660
 taataa 666

<210> 79
 <211> 684
 <212> DNA
 <213> *Acropora millepora*

<400> 79
 atgaagacga aataccatat ggaaggcagt gtcaatggcc atgaattcac gatcgaaggc 60

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gtaggaactg gaaaccctta cgaaggcaca cagatgtccg aattagtgat caccgagcct    120
gcaggaaaac cccttccatt ctcctttgac attctgtcaa cagtctttca gtatggaaac    180
agggtgcttca caaagtaccc tgaaggaatg actgactatt tcaagcaagc attcccagat    240
ggaatgtcat ttgaaaggtc atttctatat gaggatggag gagttgctac agccagctgg    300
aacattcgtc ttgagagaga ttgcttcata cacaaatcca tctatcatgg cgtaaacttt    360
cccgtgatg gacccgtaat gaaaaagaag accattggct gggataaagc cttcgaaaaa    420
atgactgtgt ccaaagacgt ttaagaggt gatgtgactg agtttcttat gctcgaagga    480
ggtggttacc acagctgcc a gtttactcc acttacaac cagagaagcc ggttacactg    540
ccccctaata atgtcgtgga acatcacatt gtgaggactg accttgcca aactgcaaaa    600
ggcttcacag tcaagctgga agaacatgct gcggctcatg ttaacccttt gaagggtcac    660
catcaccata accatcacta ataa                                           684

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<210> 80
<211> 681
<212> DNA
<213> Acropora millepora

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<400> 80
atgtcttatt caaagcaagg catcgtacaa gaaatgaaga cgaaatacca tatggaaggc    60
agtgtcaatg gccatgaatt cacgatcgaa ggtgtaggaa ctgggtaccc ttacgaaggg    120
aaacagatat ccgaattagt gatcatcaag cctgcgggaa aaccccttcc attctccttt    180
gacatactgt catcagtctt tcaatatgga aacagggtgt tcacaaagta ccctgcagac    240
atgcctgact atttcaagca agcattccca gatggaatgt catatgaaag gtcatttcta    300
tttgaggatg gagcagttgc cacagccagc tggaacattc gtctcgaagg aaattgcttc    360
atccacaaat ccatctttca tggcgtaaac tttcccgctg atggacccgt aatgaaaaag    420
aagacaattg actgggataa gtccttcgaa aaaatgactg tgtctaaaga ggtgctaaga    480
ggtgacgtga ctatgtttct tatgctcgaa ggaggtggtt ctcacagatg ccaatttcac    540
tccacttaca aaacagagaa gccggtcaca ctgccccga atcatgtcgt agaacatcaa    600
attgtgagga ccgaccttgg ccaaactgca aaaggcttca cagtcaagct ggaagaacat    660
gctgcggctc atgttagcct a                                           681

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<210> 81
<211> 684
<212> DNA

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<213> Acropora millepora

<400> 81

```

atgtcttatt caaagcaagg catcgtacaa gaaatgaaga cgaaatacca tatggaaggg      60
agtgtcaatg gccatgaatt cacgatcgaa ggtgtaggaa ctgggtaccc ttacgaaggg      120
aacagatgt ccgaattagt gatcatcaag cctgcgggaa aaccccttcc attctccttt      180
gacatactgt catcagtctt tcaatatgga aacaggtgct tcacaaagta ccctgcagac      240
atgcctgact atttcaagca agcattccca gatggaatgt catatgaaag gtcatttcta      300
tttgaggatg gagcagttgc cacagccagc tggaacattc gtctcgaagg aaattgcttc      360
atccacaaat ccatctttca tggcgtaaac tttcccgctg atggaccctg aatgaaaaag      420
aagacaattg actgggataa gtccttcgaa aaaatgactg tgtctaaaga ggtgctaaga      480
ggtgacgtga ctatgtttct tatgctcgaa ggaggtgggt ctcacagatg ccaatttcac      540
tccacttaca aaacagagaa gccggtcaca ctgccccga atcatgtcgt agaacatcaa      600
attgtgagga ccgaccttgg ccaaactgca aaaggcttca cagtcaagct ggaagaacat      660
gctgcggctc atgtaaccct ttga                                             684

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<210> 82

<211> 717

<212> DNA

<213> Acropora millepora

<400> 82

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atgtcttatt caaagcaggg catcgtacaa gaaatgaaga cgaaataccg tatggaaggg      60
agtgtcaatg gccatgaatt cacgatcgaa ggtgtaggaa ctgggtaccc ttacgaaggg      120
aagcagatgt ccgaattagt gatcgtcaag cctaaggga agccccttcc attctccttt      180
gacatactgt catcagtctt tcaatatgga aacaggtgct tcacaaagta ccctgcagac      240
atgcctgact atttcaagca agcattccca gatggaatgt catatgaaag gtcatttcta      300
tttgaggatg gagcagttgc tacagccagc tggaacattc gtctcgaagg aaattgcttc      360
atccacaatt ccatctttca tggcgtaaac tttcccgctg atggaccctg aatgaaaaag      420
aagacaattg gctgggataa gtccttcgaa aaaatgactg tgtctaaaga ggtgttaaga      480
ggtgatgtga ctatgtttct tatgctcgaa ggaggtgggt accacagatg ccagtttcac      540
tccacttaca aaacagtga gccggtcgaa ctgccccga atcatgtcgt agaacatcaa      600
attgtgagga ccgaccttgg ccaaagtga aaaggcttca cagtcaagct ggaagcacat      660
gctgcggctc atgttaaccc tttgaagggt caacatcacc atcaccatca ctaataa       717

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<210> 83
 <211> 717
 <212> DNA
 <213> *Acropora millepora*

<400> 83
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 agtgtcaatg gccatgaatt cacgatcgaa ggtgtaggaa ctggaaaccc ttacgaaggc 120
 tcacagatgt ccgagttagt gatcaccaag cctgcaggaa aacccttcc attctccttt 180
 gacattctct caacagtctt tcaatatgga aacagggtgt tcacaaagta ccctgaagga 240
 atgactgact atttcaagca agcattccca gatggaatgt catatgaaag gtcatttcta 300
 tatgaggatg gaggagtgtc tacagccagc tggaacattc gtcttgagag aggttgcttc 360
 atccacaaat ccatctatca tggcgtaaac tttcccgctg atggaccctg aatgaaaaag 420
 aagaccattg gctgggataa ggccttcgaa aaaatgactg tgtccaaaga cgtgttaaga 480
 ggtgatgtga ctgggtttct tatgctcgaa ggagggtggt accacaactg ccagtttcac 540
 tccacttaca aaccagaaaa gccggttaca ctgccccga atcatgtcgt ggaacatcac 600
 attgtgagga ctgaccttgg ccaaactgca aaaggcttca cagccaagct ggaagaacat 660
 gctgcggctc atgtaaacc tttgaagggt caacatcacc atcaccatca ctaataa 717

<210> 84
 <211> 684
 <212> DNA
 <213> *Acropora millepora*

<400> 84
 atgaagacga aataccatat ggaaggcagt gtcaatggcc atgaattcac gatcgaaggc 60
 gtaggaactg ggtaccctta cgaagggaaa cagatgtccg aattagtgat catcaagcct 120
 gcgggaaaac cccttccatt ctcttttgac atactgtcat cagtctttca atatggaaac 180
 aggtgcttca caaagtaccc tgcagacatg cctgactatt tcaagcaagc attcccagat 240
 ggaatgtcat atgaaaggct atttctattt gaggatggag cagttgctac agccagctgg 300
 aacattcgct tcgaaggaaa ttgcttcac cacaaatcca tctttcatgg cgtaaacctt 360
 cccgctgatg gaccgtaat gaaaaagaag acaattgact gggataagtc cttcgaaaaa 420
 atgactgtgt ctaaagagggt gctaagagggt gacgtgacta tgtttcttat gctcgaagga 480
 ggtggttctc acagatgcc aattcactcc acttacaaaa cagagaagcc ggtcacactg 540
 ccccggaatc atgtcgtaga acatcaaatt gtgaggaccg accttgacca aagtgcaaaa 600
 ggctttacag tcaagctgga agcacatgct gcggctcatg ttaacccttt gaagggttaa 660

catcaccatc accatcacta ataa

684

<210> 85

<211> 687

<212> DNA

<213> Acropora millepora

<400> 85

atgacgatga aataccacat ggaaggggtct gtcgatgggc ataaatttgt gatcacgggc 60
cacggcaatg gaaatccttt cgaagggaaa cagactatga atctgtgtgt ggttgaaggg 120
ggacccctgc cattctccga agacattttg tctgctacgt ttgactacgg aaacagggtc 180
ttcactgaat atcctcaagg catggttgac tttttcaaga attcatgtcc agctggatac 240
acatggcaca ggtctttact ctttgaagat ggagcagttt gcacaactag tgcagatata 300
acagtgagtg ttgaggagaa ctgcttttat cacaattcca agtttcatgg agtgaacttt 360
cctgctgatg gacctgtgat gaaaaagatg acaactaatt gggagccatc ctgcgagaaa 420
atcataccag tacctagaca ggggatattg aaaggggata ttgccatgta cctccttctg 480
aaggatggtg ggcgttatcg gtgccagttc gacacaattt acaaagcaaa gtctgaccgg 540
aaagagatgc cggagtggca cttcatccaa cataagctca cccgggaaga ccgcagcgat 600
gctaagaacc agaaatggca actggtagaa catgctgttg cttcccgatc cgcattgccc 660
ggacatcacc atcaccatca ctaataa 687

<210> 86

<211> 666

<212> DNA

<213> Acropora millepora

<400> 86

atgacctaca aggtttatat gtcaggcacg gtcaatggac actactttga ggtcgaaggg 60
gatggaaaag gtaagcccta cgagggggag cagacggtaa agctcactgt caccaagggc 120
ggacctctgc catttgcttg ggatatttta tcaccacagt gtcagtacgg aagcatacca 180
ttcaccaagt accctgaaga catccctgac tatgtaaagc agtcattccc ggagggctat 240
acatgggaga ggatcatgaa ctttgaagat ggtgcagtgt gtactgtcag caatgattcc 300
agcatccaag gcaactgttt catctaccat gtcaagttct ctggtttgaa ctttcctccc 360
aatggacctg tcatgcagaa gaagacacag ggctgggaac ccaacactga gcgtctcttt 420
gcacgagatg gaatgctgct aggaaacaac tttatggctc tgaagttaga aggagggcgt 480
cactatttgt gtgaattcaa aactacttac aaggcaaaga agcctgtgaa gatgccaggg 540
tatcactatg ttgaccgcaa actggatgta accaatcaca acaaggatta cacttcgggt 600

gagcagtgtg aaatttccat tgcacgcaaa cctgtggtcg cccatcacca tcaccatcac 660
taataa 666

<210> 87
<211> 717
<212> DNA
<213> *Acropora nobilis*

<400> 87
atgtcttatt caaagcaagg catcgcacaa gtaatgaaga cgaaatacca tatggaaggc 60
agtgtcaatg gccatgaatt cacgatcgaa ggtgtaggaa ctggaaaccc ttacgaaggc 120
acacagatgt ccgaattagt gatcaccaag cctgcaggaa aaccccttcc attctccttt 180
gacattctgt caacagtctt tcaatatgga aacaggtgct tcacaaagta ccctgaagga 240
atgactgact atttcaagca agcattccca gatggaatgt catgtgaaag gtcatttcta 300
tatgaggatg gaggagttgc tacagccagc tggaacattc gtcttgagag agattgcttc 360
atccacaaat ccatctatca tggcgtaaac tttcccgctg atggaccctg aatgaaaaag 420
aagaccattg gctgggataa agccttcgaa aaaatgactg tgtccaaaga cgtgttaaga 480
ggtgatgtga ctgagtttct tatgctcgaa ggaggtggtt accacagctg ccagtttcac 540
tccacttaca aaccagaaaa gccggctgca ctgccccga atcatgtcgt agaacatcac 600
attgtgagga ctgaccttgg ccaaagtgca aaaggcttca cagtcaagct ggaagaacat 660
gctgcggctc atgttaaccc tttgaagggt caacatcacc atcaccatca ctaataa 717

<210> 88
<211> 684
<212> DNA
<213> *Acropora nobilis*

<400> 88
atgaagacga aataccatat ggaaggcagt gtcaatggcc atgaattcac gatcgaaggc 60
gtaggaactg gaaaccctta cgaaggcaca cagatgtccg aattggtgat caccaagcct 120
gcaggaaaac cccttcatt ctcttttgac attctgtcaa cagtctttca atatggaaac 180
aggtgcttca caaagtaccc tgaaggaatg actgactatt tcaagcaagc attcccagat 240
ggaatgtcat atgaaaggtc atttctatat gaggatggag gagttgctac agccggctgg 300
aacattcgtc ttgagagaga ttgcttcac cacaatcca tctatcatgg cgttaacttt 360
cccgtgatg gaccgtaat gaagaagaag accattggct gggataaagc cttcgaaaaa 420
atgactgtgt ccaaagacgt gttaagaggc gatgtgactg gggtttcttat gctcgaagga 480

ggtaggttacc acagctgcc a gtttcaactcc acttacaac cagaaaagcc ggctgcactg 540
 cccccaatc atgtcgtaga acatcacatt gtgaggactg accttggcca aagtgcacaaa 600
 ggcttcacag tcaagctgga agaacatgct gcggctcatg ttaacccttt gaagggtcaa 660
 catcaccatc accatcacta ataa 684

<210> 89
 <211> 684
 <212> DNA
 <213> *Acropora nobilis*

<400> 89
 atgaagacga aataccatat ggaaggcagt gtcaatggcc atgaattcac ggtcgaaggt 60
 gtagggactg ggtaccctta cgaaggggaa cagatgtccg aattagtgat catcgagcct 120
 gcgggaaaac cccttcatt ctcctttgac atactgtcat cagtctttca gtatggaaaac 180
 aggtgcttca caaaataccc tgcagacatg cctgactatt tcaagcaagc atttccagat 240
 ggaatgtcat atgaaaggtc atttctatctt gaggatggag cagttgctac agccagctgg 300
 aaaattcgtc tcgaaggaaa ttgcttcac cacaactcca tctttaatgg cgtaaaacttt 360
 cccgctgatg gaccgtaat ggaaaagaag acaattggct gggataagtc cttcgaaaaa 420
 atgactgtgt ctaaagaggt gctaagaggt gatgtgacta tgtttcttat gctcgaagga 480
 ggtggttctc acagatgcc a gtttcaactcc acttacaac cagagaagcc ggtcacactg 540
 cccccaatc atgtcgtaga acatcaaatt gtgaggaccg accttggcca aagtgcacaaa 600
 ggctttacag tcaagctgga agcacatgct gcggctcatg ttaacccttt gaagggttaa 660
 catcaccatc accatcacta ataa 684

<210> 90
 <211> 681
 <212> DNA
 <213> *Agaricia fragilis*

<400> 90
 atgatgacta agctacacat ggaaggctact gttaacgggc acgcccttac aattgaaggc 60
 aaaggaaaag gcgatcctta caatggagtg cagtctatga accttgacgt caaaggcgggt 120
 gcgcctttgc cgttctcttt cgatctcttg acgccagcat tcatgtacgg caacagagtg 180
 ttgcggaagt atccagaaga cataccagac tttttcaagc aggtgtttcc tgaagggtac 240
 cactgggaaa gaagtattac ctttgaagat caggccgttt gtacggcaac cagccacata 300
 aggctggacc agaaagagat gtgttttatc tatgacgtcc gttttcacgg tgtgaacttt 360

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ccccccaatg gcccaatcat gcagaagaag atactgggat gggagccatc cactgagaaa    420
atgtatgcac gtgatggggg gctgaagggt gatgttaata tgactcttcg tgttgaagga    480
gggtggccatt accgagctga cttcagaact acttaciaaag caaagaagcc agtcaacctg    540
ccaggctatc acttcataga ccaccgcatt gagattacca agcacagcaa agattacacc    600
aatgttgctt tgtatgaggc agcagttgct cgtcattctc cgctgcctaa ggttgctcat    660
caccatcacc atcactaata a                                           681

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<210> 91
<211> 680
<212> DNA
<213> Agaricia fragilis

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<400> 91
atgatgacta agctacacat ggaaggtact gttaacgggc acgcctttac aattgaaggc    60
aaaggaaaag gcgatcctta caatggagtg cagtctatga accttgacgt caaaggcggt    120
gcgcctttgc cgttctcttt cgatctcttg acgccagcat tcatgtacgg caacagagtg    180
ttcacgaagt atccagaaga cataccagac tttttcaagc aggtggtttcc tgaagggtac    240
cactgggaaa gaagtattac ctttgaagat caggccggtt gtacggcaac cagccacata    300
aggctggacc agaaagagat gtgttttacc tatgacgtcc gttttcacgg tgtgaacttt    360
ccccccaatg gcccaatcat gcagaagaag atactgggat gggagccatc cactgagaaa    420
atgtatgcac gtgatggggg gctgaagggt gatgttaata tgactcttcg tgttgaagga    480
gggtggccatt accgagctga cttcagaact acttaciaaag caaagaagcc agtcaacctg    540
ccaggctatc acttcataga ccaccgcatt gagattacca agcacagcaa agattacacc    600
aatgttgctt tgtatgaggc agcagttgct cgtcattctc cgctgcctaa ggttgctcat    660
caccatcaca tcactaataa                                           680

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<210> 92
<211> 681
<212> DNA
<213> Agaricia fragilis

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<400> 92
atgatgacta agctacacat ggaaggtact gttaacgggc acgcctttac aattgaaggc    60
aaaggaaaag gcgatcctta caatggagtg cagtctatga accttgacgt caaaggcggt    120
gcgcctttgc cgttctcttt cgatctcttg acgccagcat tcatgtacgg caacagagtg    180
ttcacgaagt atccagaaga cataccagac tttttcaagc aggtggtttcc tgaagggtac    240

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cactgggaaa gaagtattac ctttgaagat caggccgttt gtacggcaac cagccacata 300
 aggctggacc agaaagagat gtgttttata tatgacgtcc gttttcacgg tgtgaacttt 360
 cccgccaatg gcccaatcat gcagaagaag atactgggat gggagccatc cactgagaaa 420
 atgtatgcac gtgatggggg gctgaagggt gatgttaata tgactcttcg tgttgaagga 480
 ggtggccatt accgagctga cttcagaact acttacaag caaagaagcc agtcaacctg 540
 ccaggctatc acttcataga ccaccgcatt gagattacca agcacagcaa agattacacc 600
 aatgttgctt tgtatggggc agcagttgct cgtcattctc cgctgcctaa ggtttctcat 660
 caccatcacc atcactaata a 681

<210> 93
 <211> 678
 <212> DNA
 <213> *Agaricia fragilis*

<400> 93
 atgactaagc tacacatgga aggtactgtt aacgggcacg cctttacaat tgaaggcaaa 60
 ggaaaaggcg atccttaciaa tggagtgcag tctatgaacc ttgacgtcaa aggcgggtgcg 120
 cctttgccgt tctcttttga tctcttgacg ccagcattca tgtacggcaa cagagtgttc 180
 acgaagtatc cagaagacat accagacttt ttcaagcagg tgtttcctga aggggtaccac 240
 tgggaaagaa gtattacctt tgaagatcag gccgtttgta cggcaaccag ccacataagg 300
 ctggaccaga aagagatgtg ttttatctat gacgtccgtt ttcacgggtg gaactttccc 360
 gccaatggcc caatcatgca gaagaagata ctgggatggg agccatccac tgagaaaatg 420
 tatgcacgtg atgggggtgt gaagggtgat gttaatgtga ctcttcgtgt tgaaggaggt 480
 ggccattacc gagctgactt cagaactact taaaaagcaa agaagccagt caacctgcca 540
 ggctatcact tcatagacca ccgcattgag attaccaagc acagcaaaga ttacaccaat 600
 gttgctttgt atgaggcagc agttgctcgt cattctccgc tgcctaaggt tgctcatcac 660
 catcaccatc actaataa 678

<210> 94
 <211> 681
 <212> DNA
 <213> *Agaricia fragilis*

<400> 94
 atgatgacta agctacacat ggaagggtact gttaacgggc acgcctttac aattgaaggc 60
 aaaggagagg gcgatcctta caatggagtg cagtctatga accttgacgt caaaggcggg 120
 gcgcctttgc cgttctcttt cgatctcttg acgccagcat tcatgtacgg caacagagtg 180

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ttcacgaagt atccagaaga cataccagac tttttcaagc aggtgtttcc tgaagggtag 240
cactgggaaa gaagtattac ctttgaagat caggccggtt gtacggctac cagccacata 300
aggctggacc agaaagagat gtgttttata tatgacgtcc gttttcacgg tgtgaacttt 360
cccgccaatg gcccaatcat gcagaagaag atactgggat gggagccatc cactgagaaa 420
atgtatgcac gtgatggggt gctgaagggt gatgttaata tgactcttcg tgttgaagga 480
ggtggccatt accgagctga cttcagaact acttaciaaag caaagaagcc agtcaacctg 540
ccaggctatc acttcataga ccaccgcatt gagattacca agcacagcaa agattacacc 600
aatgttgctt tgtatggggc agcagttgct cgtcattctc cgctgcctaa ggttgctcat 660
caccatcacc atcactaata a 681

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<210> 95
<211> 681
<212> DNA
<213> Agaricia fragilis

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<400> 95
atgatgacta agctacacat ggaagggtact gttaacgggc acgcctttac aattgaaggc 60
aaaggaaaag gcgatcctta caatggagtg cagtctatga accttgacgt caaaggcggt 120
gcgcctttgc cgttctcttt cgatctcttg acgccagcat tcatgtacgg caacagagtg 180
ttcacgaagt atccagaaga cataccagac tttttcaagc aggtgtttcc tgaagggtag 240
cactgggaaa gaagtattac ctttgaagat caggccggtt gtacggcaac cagccacata 300
aggctggacc agaaagagat gtgttttata tatgacgtcc gttttcacgg tgtgaacttt 360
cccgccaatg gcccaatcat gcagaagaag atactgggat gggagccatc cactgagaaa 420
atgtatgcac gtgatggggt gctgaagggt gatgttaata tgactcttcg tgttgaagga 480
ggtggccatt accgagctga cttcagaact acttaciaaag caaagaagcc agtcaacctg 540
ccaggctatc acttcataga ccaccgcatt gagattacca agcacagcaa agattacacc 600
aatgttgctt tgtatgagggc agcagttgct cgtcattctc cgctgcctaa ggttgctcat 660
caccatcacc atcactaata a 681

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<210> 96
<211> 681
<212> DNA
<213> Agaricia fragilis

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<400> 96
atgatgacta agctacacat ggaagggtact gttaacgggc acgcctttac aattgaaggc 60
aaaggaaaag gcgatcctta caatggagtg cagtctatga accttgacgt caaaggcggt 120

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gcgcctttgc cgttctcttt cgatctcttg acgccagcat tcatgtacgg caacagagtg	180
ttcacgaagt atccagaaga cataccagac tttttcaagc aggtgtttcc tgaagggtag	240
cactgggaaa gaagtattac ctttgaagat caggccgttt gtacggcaac cagccacata	300
aggctggacc agaaagagat gtgttttatc tatgacgtcc gttttcacgg tgtgaacttt	360
cccgccaatg gcccaatcat gcagaagaag atactgggat gggagccatc cactgagaaa	420
atgtatgcac gtgatggggt gctgaagggt gatgttaata cgactcttcg tggtgaagga	480
ggtggccatt accgagctga cttcagaact acttaciaag caaagaagcc agtcaacctg	540
ccaggctatc acttcataga ccaccgcatt gagattacca agcacagcaa agattacacc	600
aatgttgctt tgtatgaggc agcagttgct cgtcattctc cgctgcctaa ggttgctcat	660
caccatcacc atcactaata a	681