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(54) Titre : POLYNUCLEOTIDES ET PROCEDE PERMETTANT DE DETERMINER L'EFFICACITE DE LA TRADUCTION
D'UN CODON
(54) Title: METHOD AND POLYNUCLEOTIDES FOR DETERMINING TRANSLATIONAL EFFICIENCY OF A CODON

(57) **Abrégé/Abstract:**

A method is disclosed for determining the translational efficiency of an individual codon in a cell. The method comprises introducing into the cell a synthetic construct comprising a reporter polynucleotide fused in frame with a tandem repeat of said individual codon, wherein said reporter polynucleotide encodes a reporter protein, and wherein said synthetic construct is operably linked to a regulatory polynucleotide and measuring expression of said reporter protein in said cell to determine the translational efficiency of said codon.

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(54) Title: METHOD AND POLYNUCLEOTIDES FOR DETERMINING TRANSLATIONAL EFFICIENCY OF A CODON (57) Abstract A method is disclosed for determining the translational efficiency of an individual codon in a cell. The method comprises introducing into the cell a synthetic construct comprising a reporter polynucleotide fused in frame with a tandem repeat of said individual codon, wherein said reporter polynucleotide encodes a reporter protein, and wherein said synthetic construct is operably linked to a regulatory polynucleotide and measuring expression of said reporter protein in said cell to determine the translational efficiency of said codon.		

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**METHOD AND POLYNUCLEOTIDES FOR DETERMINING
TRANSLATIONAL EFFICIENCY OF A CODON**

FIELD OF THE INVENTION

THIS INVENTION relates generally to gene expression and
5 in particular, to a method and polynucleotides for
determining codon utilization in particular cells or tissues
of an organism. More particularly, the method and
polynucleotides of the invention are concerned with
ascertaining codon preferences in cells or tissues for the
10 purpose of modifying the translational efficiency of protein-
encoding polynucleotides in those cells or tissues.

BACKGROUND OF THE INVENTION

It is well known that a "triplet" codon of four
possible nucleotide bases can exist in 64 variant forms.
15 These forms provide the message for only 20 different amino
acids (as well as translation initiation and termination) and
this means that some amino acids can be encoded by more than
one codon. Some amino acids have as many as six "redundant",
alternative codons while some others have a single, required
20 codon.

For reasons not completely understood, codon
utilization is highly biased in that alternative codons are
not at all uniformly present in the endogenous DNA of
differing cell types. In this regard, there appears to exist
25 a variable natural hierarchy of "preference" for certain
codons between different cell types or between different
organisms.

Codon usage patterns have been shown to correlate with
relative abundance of isoaccepting transfer RNA (iso-tRNA)
30 species, and with genes encoding proteins of high versus low
abundance. Moreover, the present inventors recently

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discovered that the intracellular abundance of different iso-tRNAs varies in different cells or tissues of a single multicellular organism (see copending International Application No. PCT/AU98/00530).

5 The implications of codon preference phenomena on gene expression are manifest in that these phenomena can affect the translational efficiency of messenger RNA (mRNA). It is widely known in this regard that translation of "rare codons", for which the corresponding iso-tRNA is in
10 relatively low abundance, may cause a ribosome to pause during translation which can lead to a failure to complete a nascent polypeptide chain and an uncoupling of transcription and translation.

 A primary goal in recombinant research is to provide
15 transgenic organisms with expression of a foreign gene in an amount sufficient to confer the desired phenotype to the organism. However, expression of the foreign gene may be severely impeded if a particular host cell of the organism or the organism itself has a low abundance of iso-tRNAs
20 corresponding to one or more codons of the foreign gene. Accordingly, a major aim of investigators in this field is to first ascertain the codon preference for particular cells or tissues in which a foreign gene is to be expressed, and to subsequently alter the codon composition of the foreign gene
25 for optimized expression in those cells or tissues.

 Codon preference may be determined simply by analyzing the frequency at which codons are used by genes expressed in a particular cell or tissue or in a plurality of cells or tissues of a given organism. Codon frequency tables as well
30 as suitable methods for determining frequency of codon usage in an organism are described, for example, in an article by Sharp et al (1988, *Nucleic Acids Res.* **16** 8207-8211). The relative level of gene expression (e.g., detectable protein expression Vs no detectable protein expression) can provide

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an indirect measure of the relative abundance of specific iso-tRNAs expressed in different cells or tissues.

Alternatively, codon preference may be determined by measuring the relative intracellular abundance of different iso-tRNA species. For example, reference may be made to copending International Application No. PCT/AU98/00530 that describes a method that utilizes labeled oligonucleotides specific for different iso-tRNAs to probe an RNA extract prepared from a particular cell or tissue source.

The above methods provide useful indirect evidence for determining codon preference. However, such indirect evidence may not provide an accurate indication of the translational efficiency of a given codon. Accordingly, there is a need to provide a method that more directly ascertains the translational efficiency of a codon in a cell or tissue.

SUMMARY OF THE INVENTION

According to one aspect of the present invention, there is provided a synthetic construct comprising a regulatory polynucleotide that is operable in a eukaryotic cell and that is operably linked to a tandem repeat of a codon fused in frame with a reporter polynucleotide that encodes a reporter protein.

According to another aspect of the present invention, there is provided a plurality of synthetic constructs for determining the translational efficiencies of different codons, each construct comprising a regulatory polynucleotide that is operable in a eukaryotic cell and that is operably linked to a tandem repeat of a codon fused in frame with a reporter polynucleotide that encodes a reporter protein, wherein the tandemly repeated codon of a first

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construct is different to the tandemly repeated codon of a second construct.

According to still another aspect of the present invention, there is provided a vector comprising the
5 synthetic construct as described herein.

According to still another aspect of the present invention, there is provided a cell *in vitro* comprising the synthetic construct as described herein.

According to still another aspect of the present
10 invention, there is provided a cell *in vitro* comprising the vector as described herein.

According to still another aspect of the present invention, there is provided a method for determining the translational efficiency of a codon in a cell, the method
15 comprising: introducing into the cell *in vitro* the synthetic construct as described herein; and measuring expression of the reporter protein in the cell to determine the translational efficiency of the codon.

According to yet another aspect of the present
20 invention, there is provided a method of constructing a synthetic polynucleotide, the method comprising: selecting a first codon of a parent polynucleotide that encodes a polypeptide for replacement with a synonymous codon, wherein the synonymous codon is selected on the basis that it
25 exhibits a higher translational efficiency in a first cell of an organism than in a second cell of the organism; and replacing the first codon with the synonymous codon to construct the synthetic polynucleotide, wherein the first codon and the synonymous codon are selected on the basis of a
30 comparison of translational efficiencies in cells of the same type as the first cell and in cells of the same type as the

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second cell, wherein the translational efficiencies are compared by: separately introducing into cells of a specific type *in vitro* individual synthetic constructs as described herein, each comprising a different tandemly repeated codon
5 than the tandemly repeated codon of other constructs; comparing expression of the reporter protein in the cells to determine the relative translational efficiencies of the codons.

According to a further aspect of the present
10 invention, there is provided a method of constructing a synthetic polynucleotide, the method comprising: selecting a first codon of a parent polynucleotide that encodes a polypeptide for replacement with a synonymous codon, wherein the synonymous codon is selected on the basis that it
15 exhibits a higher translational efficiency in a first cell than the first codon in a comparison of translational efficiencies in cells of the same type as the first cell; and replacing the first codon with the synonymous codon to construct the synthetic polynucleotide, wherein the
20 translational efficiencies in the cells are compared by: separately introducing into the cells *in vitro* individual synthetic constructs as described herein, each comprising a different tandemly repeated codon than the tandemly repeated codon of other constructs; comparing expression of the
25 reporter protein in the cells to determine the relative translational efficiencies of the codons.

According to yet a further aspect of the present invention, there is provided the method as defined above, wherein the synthetic construct is provided by: introducing
30 the synthetic construct into a progenitor of the cell; and producing the cell from the progenitor, wherein the cell contains the synthetic construct.

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According to still a further aspect of the present invention, there is provided the method as defined above, wherein the synthetic construct is provided by: introducing the synthetic construct into a progenitor of the cell; and
5 growing a non-human organism or part thereof from the progenitor, wherein the organism or part thereof comprises the cell containing the synthetic construct.

According to another aspect of the present invention, there is provided the method as defined above,
10 wherein the synthetic construct is provided by: introducing the synthetic construct into an organism or part thereof such that the synthetic construct is introduced into the cell.

In one aspect of the invention, there is provided a
15 method for determining the translational efficiency of an individual codon in a cell, said method comprising:

- introducing into said cell a synthetic construct comprising a reporter polynucleotide fused in frame with a tandem repeat of said individual codon, wherein said reporter
20 polynucleotide encodes a reporter protein, and wherein said synthetic construct is operably linked to a regulatory polynucleotide; and

- measuring expression of said reporter protein in said cell to determine the translational efficiency of said
25 codon.

Preferably, the method further comprises comparing:

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- expression of said reporter protein in a cell to which a synthetic construct comprising a tandem repeat of said individual codon was provided; and

- expression of said reporter protein in a cell to which a synthetic construct comprising a tandem repeat of another individual codon was provided;

to thereby determine the relative translational efficiency of said individual codons in said cell.

Suitably, the method further comprises comparing:

- expression of said reporter protein in a cell to which a synthetic construct comprising a tandem repeat of said individual codon was provided; and

- expression of said reporter protein in another cell to which a synthetic construct comprising a tandem repeat of said individual codon was provided;

to thereby determine the translational efficiency of said individual codon in said cell relative to said other cell.

Preferably, the method further comprises:

- introducing the synthetic construct into a progenitor cell of said cell; and

- producing said cell from said progenitor cell; wherein said cell contains said synthetic construct.

Suitably, the method further comprises:

- introducing the synthetic construct into a progenitor of said cell; and

- growing an organism or part thereof from said progenitor cell;

wherein said organism comprises said cell containing said synthetic construct.

Suitably, the method further comprises:

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- introducing the synthetic construct into an organism or part thereof such that said synthetic construct is introduced into said cell.

5 In another aspect, the invention resides in a synthetic construct comprising a reporter polynucleotide fused in frame with a tandem repeat of individual codons, wherein said reporter polynucleotide encodes a reporter protein, and wherein said synthetic construct is operably linked to a regulatory polynucleotide.

10 In yet another aspect of the invention, there is provided an improved method of constructing a synthetic polynucleotide from which a protein is selectively expressible in a target cell of an organism, relative to another cell of the organism, said method comprising:

15 - selecting a first codon of a parent polynucleotide for replacement with a synonymous codon which has a higher translational efficiency in said target cell than in said other cell; and

20 - replacing said first codon with said synonymous codon to form said synthetic polynucleotide, wherein said first codon and said synonymous codon are selected by:

25 - comparing translational efficiencies of individual codons in said target cell relative to said other cell using the method broadly described above; and

- selecting said first codon and said synonymous codon based on said comparison.

30 Preferably, said synonymous codon corresponds to a reporter construct from which the reporter protein is expressed in said target cell at a level that is at least 110%, preferably at least 200%, more preferably at least 500%, and most preferably at least 1000%, of that expressed from said reporter construct in said other cell.

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In a further aspect, the invention provides an improved method of constructing a synthetic polynucleotide from which a protein is expressible in a target cell of an organism at a higher level than from a parent polynucleotide encoding said protein, said method comprising:

- selecting a first codon of the parent polynucleotide for replacement with a synonymous codon which has a higher translational efficiency in said target cell than said first codon;

- replacing said first codon with said synonymous codon to form said synthetic polynucleotide, wherein said first codon and said synonymous codon are selected by:

- comparing translational efficiencies of different individual codons in said target cell using the method broadly described above; and

- selecting said first codon and said synonymous codon based on said comparison.

Suitably, said synonymous codon corresponds to a reporter construct from which the reporter protein is expressed in said target cell at a level that is at least 110%, preferably at least 200%, more preferably at least 500%, and most preferably at least 1000%, of that expressed from the different reporter construct corresponding to said first codon.

DETAILED DESCRIPTION

1. Definitions

The articles "a" and "an" are used herein to refer to one or to more than one (*i.e.*, to at least one) of the grammatical object of the article. By way of example, "an element" means one element or more than one element.

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Throughout this specification, unless the context requires otherwise, the words "comprise", "comprises" and "comprising" will be understood to imply the inclusion of a stated step or element or group of steps or elements but not the exclusion of any other step or element or group of steps or elements.

By "expressible" is meant expression of a protein to a level sufficient to effect a particular function associated with the protein. By contrast, the terms "not expressible" and "not substantially expressible" as used interchangeably herein refers to (a) no expression of a protein, (b) expression of a protein to a level that is not sufficient to effect a particular function associated with the protein, (c) expression of a protein, which cannot be detected by a monoclonal antibody specific for the protein, or (d) expression of a protein, which is less than 1% of the level expressed in a wild-type cell that normally expresses the protein.

By "expressing said synthetic construct" is meant transcribing the synthetic construct such that mRNA is produced.

By "expression vector" is meant any autonomous genetic element capable of directing the synthesis of a protein encoded by the vector. Such expression vectors are known by practitioners in the art.

As used herein, the term "function" refers to a biological, enzymatic, or therapeutic function.

By "highly expressed genes" is meant genes that express high levels of mRNA, and preferably high level of protein, relative to other genes.

By "isoaccepting transfer RNA" or "iso-tRNA" is meant one or more transfer RNA molecules that differ in their

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anticodon nucleotide sequence but are specific for the same amino acid.

By "*natural gene*" is meant a gene that naturally encodes the protein. However, it is possible that the parent
5 polynucleotide encodes a protein that is not naturally-occurring but has been engineered using recombinant techniques.

The term "*non-cycling cell*" as used herein refers to a cell that has withdrawn from the cell cycle and has entered
10 the G0 state. In this state, it is known that transcription of endogenous genes and protein translation are at substantially reduced levels compared to phases of the cell cycle, namely G1, S, G2 and M. By contrast, the term "*cycling cell*" as used herein refers to a cell, which is in
15 one of the above phases of the cell cycle.

By "*obtained from*" is meant that a sample such as, for example, a polynucleotide extract or polypeptide extract is isolated from, or derived from, a particular source of the host. For example, the extract can be obtained from a tissue
20 or a biological fluid isolated directly from the host.

The term "*oligonucleotide*" as used herein refers to a polymer composed of a multiplicity of nucleotide residues (deoxyribonucleotides or ribonucleotides, or related structural variants or synthetic analogues thereof) linked
25 via phosphodiester bonds (or related structural variants or synthetic analogues thereof). Thus, while the term "*oligonucleotide*" typically refers to a nucleotide polymer in which the nucleotide residues and linkages between them are naturally occurring, it will be understood that the term also
30 includes within its scope various analogues including, but not restricted to, peptide nucleic acids (PNAs), phosphoramidates, phosphorothioates, methyl phosphonates, 2-O-methyl ribonucleic acids, and the like. The exact size of the molecule can vary depending on the particular

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application. An oligonucleotide is typically rather short in length, generally from about 10 to 30 nucleotide residues, but the term can refer to molecules of any length, although the term "polynucleotide" or "nucleic acid" is typically used for large oligonucleotides.

By "*operably linked*" is meant that transcriptional and translational regulatory polynucleotides are positioned relative to a polypeptide-encoding polynucleotide in such a manner that the polynucleotide is transcribed and the polypeptide is translated.

By "*pharmaceutically-acceptable carrier*" is meant a solid or liquid filler, diluent or encapsulating substance that can be safely used in topical or systemic administration to a mammal.

"*Polypeptide*", "*peptide*" and "*protein*" are used interchangeably herein to refer to a polymer of amino acid residues and to variants and synthetic analogues of the same. Thus, these terms apply to amino acid polymers in which one or more amino acid residues is a synthetic non-naturally occurring amino acid, such as a chemical analogue of a corresponding naturally occurring amino acid, as well as to naturally-occurring amino acid polymers.

The term "*polynucleotide*" or "*nucleic acid*" as used herein designates mRNA, RNA, cRNA, cDNA or DNA. The term typically refers to oligonucleotides greater than 30 nucleotide residues in length.

By "*primer*" is meant an oligonucleotide which, when paired with a strand of DNA, is capable of initiating the synthesis of a primer extension product in the presence of a suitable polymerizing agent. The primer is preferably single-stranded for maximum efficiency in amplification but can alternatively be double-stranded. A primer must be sufficiently long to prime the synthesis of extension products in the presence of the polymerization agent. The

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length of the primer depends on many factors, including application, temperature to be employed, template reaction conditions, other reagents, and source of primers. For example, depending on the complexity of the target sequence, the oligonucleotide primer typically contains 15 to 35 or more nucleotide residues, although it can contain fewer nucleotide residues. Primers can be large polynucleotides, such as from about 200 nucleotide residues to several kilobases or more. Primers can be selected to be "substantially complementary" to the sequence on the template to which it is designed to hybridize and serve as a site for the initiation of synthesis. By "substantially complementary", it is meant that the primer is sufficiently complementary to hybridize with a target polynucleotide. Preferably, the primer contains no mismatches with the template to which it is designed to hybridize but this is not essential. For example, non-complementary nucleotide residues can be attached to the 5' end of the primer, with the remainder of the primer sequence being complementary to the template. Alternatively, non-complementary nucleotide residues or a stretch of non-complementary nucleotide residues can be interspersed into a primer, provided that the primer sequence has sufficient complementarity with the sequence of the template to hybridize therewith and thereby form a template for synthesis of the extension product of the primer.

"Probe" refers to a molecule that binds to a specific sequence or sub-sequence or other moiety of another molecule. Unless otherwise indicated, the term "probe" typically refers to a polynucleotide probe that binds to another polynucleotide, often called the "target polynucleotide", through complementary base pairing. Probes can bind target polynucleotides lacking complete sequence complementarity with the probe, depending on the stringency of the

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hybridization conditions. Probes can be labeled directly or indirectly.

The terms "*precursor cell or tissue*" and "*progenitor cell or tissue*" as used herein refer to a cell or tissue that can give rise to a particular cell or tissue in which protein expression is to be targeted or in which translational efficiency of a codon is to be determined.

By "*recombinant polypeptide*" is meant a polypeptide made using recombinant techniques, i.e., through the expression of a recombinant or synthetic polynucleotide.

"*Stringency*" as used herein, refers to the temperature and ionic strength conditions, and presence or absence of certain organic solvents, during hybridization. The higher the stringency, the higher will be the degree of complementarity between immobilized polynucleotides and the labeled polynucleotide.

"*Stringent conditions*" refers to temperature and ionic conditions under which only polynucleotides having a high frequency of complementary bases will hybridize. The stringency required is nucleotide sequence dependent and depends upon the various components present during hybridization. Generally, stringent conditions are selected to be about 10 to 20°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which 50% of a target sequence hybridizes to a complementary probe.

The term "*synthetic polynucleotide*" as used herein refers to a polynucleotide formed *in vitro* by the manipulation of a polynucleotide into a form not normally found in nature. For example, the synthetic polynucleotide can be in the form of an expression vector. Generally, such expression vectors include transcriptional and translational

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regulatory polynucleotide operably linked to the polynucleotide.

The term "*synonymous codon*" as used herein refers to a codon having a different nucleotide sequence than another codon but encoding the same amino acid as that other codon.

By "*translational efficiency*" is meant the efficiency of a cell's protein synthesis machinery to incorporate the amino acid encoded by a codon into a nascent polypeptide chain. This efficiency can be evidenced, for example, by the rate at which the cell is able to synthesize the polypeptide from an RNA template comprising the codon, or by the amount of the polypeptide synthesized from such a template.

By "*vector*" is meant a polynucleotide molecule, preferably a DNA molecule derived, for example, from a plasmid, bacteriophage, or plant virus, into which a polynucleotide can be inserted or cloned. A vector preferably contains one or more unique restriction sites and can be capable of autonomous replication in a defined host cell including a target cell or tissue or a progenitor cell or tissue thereof, or be integrable with the genome of the defined host such that the cloned sequence is reproducible. Accordingly, the vector can be an autonomously replicating vector, i.e., a vector that exists as an extrachromosomal entity, the replication of which is independent of chromosomal replication, e.g., a linear or closed circular plasmid, an extrachromosomal element, a minichromosome, or an artificial chromosome. The vector can contain any means for assuring self-replication. Alternatively, the vector can be one which, when introduced into the host cell, is integrated into the genome and replicated together with the chromosome(s) into which it has been integrated. A vector system can comprise a single vector or plasmid, two or more vectors or plasmids, which together contain the total DNA to be introduced into the genome of the host cell, or a

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transposon. The choice of the vector will typically depend on the compatibility of the vector with the host cell into which the vector is to be introduced. The vector can also include a selection marker such as an antibiotic resistance gene that can be used for selection of suitable transformants. Examples of such resistance genes are known to those of skill in the art and include the *nptII* gene that confers resistance to the antibiotics kanamycin and G418 (Geneticin®) and the *hph* gene which confers resistance to the antibiotic hygromycin B.

2. Method of the invention

The present invention is based, at least in part, on the discovery that different but synonymous stretches of identical codons fused respectively in frame with a reporter polynucleotide can give rise to different levels of reporter protein expressed within a given cell type. Not wishing to be bound by any particular theory, it is believed that a tandem series of identical codons causes a ribosome to pause during translation if the iso-tRNA corresponding to the identical codons is limiting. In this regard, it is known that ribosomal pausing leads to a failure to complete a nascent polypeptide chain and an uncoupling of transcription and translation. Accordingly, the levels of reporter protein expressed in the different cells or tissues are sensitive to the intracellular abundance of the iso-tRNA species corresponding to the identical codons and, therefore, provide a direct correlation of a cell's or tissue's preference for translating a given codon. This means, for example, that if the levels of the reporter protein obtained in a cell or tissue type to which a synthetic construct having a tandem series of identical first codons is provided are lower than the levels expressed in the same cell or tissue type to which a different synthetic construct having a tandem series of identical second codons is provided (*i.e.*, wherein the first

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codons are different from, but synonymous with, the second codons), then it can be deduced that the cell or tissue has a higher preference for the second codon relative to the first codon with respect to translation. Put another way, the second codon has a higher translational efficiency compared to the first codon in the cell or tissue type.

With regard to differential protein expression between different cell or tissue types, it will be appreciated that if the levels of the reporter protein obtained in a target cell or tissue type to which a synthetic construct having a tandem series of identical codons is provided are lower than the levels expressed in the another cell or tissue type to which the same synthetic construct is provided, then it can be deduced that the target cell or tissue has a higher preference for the codon relative to the other cell or tissue with respect to translation. Put another way, the codon has a higher translational efficiency in the target cell or tissue relative to the other cell or tissue type.

As used herein, expression of a protein in a tissue refers alternatively to expression of the protein within a cell of the tissue or production of the protein within a cell and export of the protein from the cell to, for example, the extracellular matrix of a tissue.

Suitably, the tandem repeat comprises at least three identical codons. Preferably, the tandem repeat comprises four identical codons, more preferably five or seven identical codons and most preferably six identical codons.

The tandem repeat can be fused at a location adjacent to, or within, the reporter polynucleotide. The location is preferably selected such that the tandem repeat interferes with translation of at least a detectable portion of the reporter protein such that expression of the protein can be detected or assessed. Preferably, the tandem repeat is

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located immediately upstream (translationally) from the reporter polynucleotide.

It is of course possible that a tandem repeat of identical amino acid residues (e.g., an oligo-proline repeat) can render the reporter protein unstable. Typically, protein instability is detected when expression of the reporter gene is not detectable with any choice of isoaccepting codon specific for the amino acid corresponding to the tandem repeat. The inventors have found in this regard that protein instability can be alleviated by use of at least one spacer codon within the tandem repeat of identical codons, wherein the spacer codon encodes a neutral amino acid.

The at least one spacer codon can be placed adjacent to, or interposed between, some or all of the identical codons corresponding to the tandem repeat. For example, a suitable interposition for a *penta*-repeat of identical codons can be selected from the group consisting of: (a) I-S-I-S-I-S-I-S-I-S; (b) S-I-S-I-S-I-S-I-S-I; (c) I-S-I-S-I-I-S-I; (d) I-S-I-I-S-I-S-I; (e) I-S-I-S-I-I-I; (f) I-I-S-I-S-I-I; (g) I-I-I-S-I-S-I; (h) I-S-I-I-S-I-I; (i) I-I-S-I-I-S-I; (j) I-S-I-I-I-S-I; (k) I-S-I-I-I-I; (l) I-I-S-I-I-I; (m) I-I-I-S-I-I; and (n) I-I-I-I-S-I, wherein I corresponds to an identical codon of a tandem repeat and S corresponds to a spacer codon.

Preferably, a spacer codon is efficiently translated in the cell or tissue type relative to other synonymous codons. This is important so that translation of the spacer codon is not rate limiting. The neutral amino acid includes, but is not restricted to, alanine and glycine.

The reporter polynucleotide can encode any suitable protein for which expression can be detected directly or indirectly such as by suitable assay. Suitable reporter polynucleotides include, but are not restricted to, polynucleotides encoding β -galactosidase, firefly luciferase, alkaline phosphatase, chloramphenicol acetyltransferase

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(CAT), β -glucuronidase (GUS), herbicide resistance genes such as the bialophos resistance (BAR) gene that confers resistance to the herbicide BASTA, and green fluorescent protein (GFP). Assays for the activities associated with such proteins are known by those of skill in the art. Preferably, the reporter polynucleotide encodes GFP.

Persons of skill in the art will appreciate that reporter polynucleotides need not correspond to a full-length gene encoding a particular reporter protein. In this regard, the invention also contemplates reporter polynucleotide sub-sequences encoding desired portions of a parent reporter protein, wherein an activity or function of the parent protein is retained in said portions. A polynucleotide sub-sequence encodes a domain of the reporter protein having an activity associated therewith and preferably encodes at least 10, 20, 50, 100, 150, or 500 contiguous amino acid residues of the reporter protein.

The instant method is applicable to any suitable cell or tissue type and, hence, is not restricted to application to mammalian cells/tissues. Accordingly, the cell or tissue type can be of any animal or plant origin. The cell or tissue type can be of any suitable lineage. For example, a suitable cell can include a eukaryotic cell, and preferably a cell or cell line capable of being grown *in vitro*. Suitable cell lines can include, for example, CV-1 cells, COS cells, yeast or spodoptera cells. The invention also contemplates cells that can be prokaryotic in origin.

Suitable methods for isolating particular cells or tissues are known to those of skill in the art. For example, one can take advantage of one or more particular characteristics of a cell or tissue to specifically isolate the cell or tissue from a heterogeneous population. Such characteristics include, but are not limited to, anatomical location of a tissue, cell density, cell size, cell

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morphology, cellular metabolic activity, cell uptake of ions such as Ca^{2+} , K^+ , and H^+ ions, cell uptake of compounds such as stains, markers expressed on the cell surface, protein fluorescence, and membrane potential. Suitable methods that can be used in this regard include surgical removal of tissue, flow cytometry techniques such as fluorescence-activated cell sorting (FACS), immunoaffinity separation (e.g., magnetic bead separation such as Dynabead™ separation), density separation (e.g., metrizamide, Percoll™, or Ficoll™ gradient centrifugation), and cell-type specific density separation.

In an alternate embodiment, progenitor cells or tissues can be used for initially introducing the synthetic construct. Any suitable progenitor cell or tissue can be used which gives rise to a particular cell or tissue of interest for which codon preference is to be ascertained. For example, a suitable progenitor cell can comprise an undifferentiated cell. In the case of a plant, a suitable progenitor cell and tissue can include a meristematic cell and a callus tissue, respectively.

In another embodiment, the synthetic construct can be introduced first into an organism or part thereof before subsequent expression of the construct in a particular cell or tissue type. Any suitable organism is contemplated by the invention including unicellular and as multi-cellular organisms. Exemplary multi-cellular organisms include plants and animals such as mammals (e.g., humans).

The invention further provides a synthetic construct comprising a reporter polynucleotide fused in frame with a tandem repeat of (e.g., 2, 3, 4, 5, 6, or 7 or more) identical codons, wherein said reporter polynucleotide encodes a reporter protein, and wherein said synthetic construct is operably linked to one or more regulatory polynucleotides.

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The construction of the synthetic construct can be effected by any suitable technique. For example, *in vitro* mutagenesis methods can be employed, which are known to those of skill in the art. Suitable mutagenesis methods are described for example in the relevant sections of Ausubel, *et al.* (*supra*) and of Sambrook, *et al.*, (*supra*). Alternatively, suitable methods for altering DNA are set forth, for example, in U.S. Patent Nos. 4,184,917, 4,321,365 and 4,351,901. Instead of *in vitro* mutagenesis, the synthetic construct can be synthesized *de novo* using readily available machinery. Sequential synthesis of DNA is described, for example, in U.S. Patent No. 4,293,652. However, it should be noted that the present invention is not dependent on, and not directed to, any one particular technique for constructing the synthetic construct.

Regulatory polynucleotides which can be utilized to regulate expression of the synthetic construct include, but are not limited to, a promoter, an enhancer, and a transcriptional terminator. Such regulatory polynucleotides are known to those of skill in the art. The construct preferably comprises at least one promoter. Suitable promoters that can be utilized to induce expression of the polynucleotides of the invention include constitutive promoters and inducible promoters.

The step of introducing the synthetic construct into a particular cell or tissue type, or into a progenitor cell or tissue thereof, or into an organism or part thereof for subsequent introduction into a particular cell or tissue will differ depending on the intended use and or species, and may involve lipofection, electroporation, micro-projectile bombardment infection by *Agrobacterium tumefaciens* or *A. rhizogenes*, or protoplast fusion. Such methods are known to those skilled in the art.

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Alternatively, the step of introduction may involve non-viral and viral vectors, cationic liposomes, retroviruses and adenoviruses such as, for example, described in Mulligan, R. C., (1993 *Science* **260** 926-932). Such methods may include:

5 A. Local application of the synthetic nucleic acid sequence by injection (Wolff et al., 1990, *Science* **247** 1465-1468), surgical implantation, instillation or any other means. This method may also be used in combination with local application by injection, surgical implantation,
10 instillation or any other means, of cells responsive to the reporter protein encoded by the synthetic construct. This method may also be used in combination with local application by injection, surgical implantation, instillation or any other means, of another factor or factors required for the
15 activity of said reporter protein.

B. General systemic delivery by injection of DNA, (Calabretta et al., 1993, *Cancer Treat. Rev.* **19** 169-179), or RNA, alone or in combination with liposomes (Zhu et al., 1993, *Science* **261** 209-212), viral capsids or nanoparticles
20 (Bertling et al., 1991, *Biotech. Appl. Biochem.* **13** 390-405), or any other mediator of delivery. Improved targeting might be achieved by linking the synthetic construct to a targeting molecule (the so-called "magic bullet" approach employing for example, an antibody), or by local application by injection,
25 surgical implantation or any other means, of another factor or factors required for the activity of the protein produced from said synthetic construct, or of cells responsive to said reporter protein.

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C. Injection or implantation or delivery by any means, of cells that have been modified *ex vivo* by transfection (for example, in the presence of calcium phosphate: Chen *et al.*, 1987, *Mole. Cell Biochem.* **7** 2745-2752, or of cationic lipids and polyamines: Rose *et al.*, 1991, *BioTech.* **10** 520-525), infection, injection, electroporation (Shigekawa *et al.*, 1988, *BioTech.* **6** 742-751) or any other way so as to increase the expression of said synthetic construct in those cells. The modification may be mediated by plasmid, bacteriophage, cosmid, viral (such as adenoviral or retroviral; Mulligan, 1993, *Science* **260** 926-932; Miller, 1992, *Nature* **357** 455-460; Salmons *et al.*, 1993, *Hum. Gen. Ther.* **4** 129-141) or other vectors, or other agents of modification such as liposomes (Zhu *et al.*, 1993, *Science* **261** 209-212), viral capsids or nanoparticles (Bertling *et al.*, 1991, *Biotech. Appl. Biochem.* **13** 390-405), or any other mediator of modification. The use of cells as a delivery vehicle for genes or gene products has been described by Barr *et al.*, 1991, *Science* **254** 1507-1512 and by Dhawan *et al.*, 1991, *Science* **254** 1509-1512. Treated cells may be delivered in combination with any nutrient, growth factor, matrix or other agent that will promote their survival in the treated subject.

Advantageously, the translational efficiencies of different codons may be determined by comparing expression of the reporter protein in a given cell or tissue type or between different cell or tissue types. One of ordinary skill in the art will thereby be able to determine a "codon

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preference table" for one or more cells or tissues. Comparison of codon preference tables relating to different cell or tissue types may be used to identify codons for tailoring a synthetic polynucleotide to target expression of a protein to a particular cell or tissue, as described hereinafter. Comparison of codons within a codon preference table for a particular cell or tissue type can be used to identify codons for tailoring a synthetic polynucleotide to express a protein at higher or lower levels in that cell or tissue type than a parent polynucleotide, as described hereinafter.

The invention further contemplates cells or tissues containing therein the synthetic construct of the invention, or alternatively, cells or tissues produced from the method of the invention.

3. Synthetic polynucleotides for targeting protein expression to a particular cell or tissue

The invention also provides an improved method of constructing a synthetic polynucleotide from which a protein is selectively expressible in a target cell of an organism, relative to another cell of the organism. This method is based in part on the method disclosed in International application PCT/AU98/00530 (WO99/002694) in which a first codon of a parent polynucleotide is replaced with a synonymous codon which has a higher translational efficiency in said target cell than in said other cell. The improved method of the invention is characterized by selecting the first and synonymous codons by comparing translational efficiencies of individual codons in said target cell relative to said other cell using the method broadly described in Section 2.

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3.1. Selection of synonymous and first codons

The present method preferably includes the step of selecting the codons such that the synonymous codon has a higher translational efficiency in said target cell or tissue ("cell or tissue" is sometimes referred to herein as "cell/tissue") relative to said one or more other cells or tissues.

A method for determining translational efficiencies of different codons in and between different cells or tissues is described in detail in Section 2. The translational efficiencies so determined can be used to identify which isocoding triplets are differentially translated between the different cells or tissues. In a typical scenario, there will be: (A) codons with higher translational efficiencies in a target cell/tissue relative to one or more other cells/tissues; (B) codons with higher translational efficiencies in the one or more other cells/tissues relative to the target cell/tissue; and (C) codons with about the same translational efficiencies in the target cell/tissue relative to the one or more other cells/tissues. Synonymous codons are selected such that they correspond to (A) codons. Preferably, a synonymous codon is selected such that it has the largest difference in translational efficiency in the target cell or tissue relative to the existing codon (sometimes referred to as a "first codon") that it replaces. Existing codons in a parent polynucleotide are preferably selected such that they do not have the same translational bias as the synonymous codons with respect to the target cell/tissue and the one or more other cell/tissue (i.e., existing codons should preferably not correspond to (A) codons). However, existing codons can have similar translational efficiencies in each of the target cell/tissue and the one or more other cells/tissues (i.e., existing codons can correspond to (C) codons. They can also have a translational bias opposite to that of the synonymous codons

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(i.e., existing codons can, and preferably do, correspond to (B) codons).

Suitably, a synonymous codon has a translational efficiency in the target cell/tissue that is at least 110%, preferably at least 200%, more preferably at least 500%, and still more preferably at least 1000%, of that in the other cell(s)/tissue(s). In the case of two or more synonymous codons having similar translational efficiencies in the target cell/tissue relative to the other cell(s)/tissue(s), it will be appreciated that any one of these codons can be used to replace the existing codon.

It is preferable but not necessary to replace all the existing codons of the parent polynucleotide with synonymous codons having higher translational efficiencies in the target cell/tissue compared to the other cells/tissues. Increased expression can be accomplished even with partial replacement. Suitably, the replacement step affects 5%, 10%, 15%, 20%, 25%, 30%, more preferably 35%, 40%, 50%, 60%, 70% or more of the existing codons of the parent polynucleotide.

The difference in level of protein expressed in the target cell/tissue from a synthetic polynucleotide relative to that expressed in the other cell(s)/tissue(s) depends on the percentage of existing codons replaced by synonymous codons, and the difference in translational efficiencies of the synonymous codons in the target cell/tissue relative to the other cell(s)/tissue(s). Put another way, the fewer such replacements, and/or the smaller the difference in translational efficiencies of the synonymous between the different cells/tissues, the smaller the difference in protein expression between the target cell/tissue and the other cell(s)/tissue(s) will be. Conversely, the more such replacements, and/or the greater the difference in translational efficiencies of the synonymous codons between the different cells/tissues, the greater the difference in

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protein expression between the target cell/tissue and the other cell(s)/tissue(s) will be. The inventors have found in this respect that a protein can be expressed from a synthetic polynucleotide in a target cell/tissue at levels greater than
5 10,000-fold over those expressed in another cell/tissue.

In a preferred embodiment, the synonymous codon is a codon which has a higher translational efficiency in the target cell or tissue relative to a precursor cell or tissue of the target cell or tissue.

10 In an alternate embodiment, the synonymous codon is a codon which has a higher translational efficiency in the target cell or tissue relative to a cell or tissue derived from said target cell or tissue.

The two codons can be selected by measuring
15 translational efficiencies of different codons in the target cell or tissue relative to the one or more other cells or tissues and identifying the at least one existing codon and the synonymous codon based on this measurement.

Suitably, the synonymous codon corresponds to a
20 reporter construct from which the reporter protein is expressed in said target cell at a level that is at least 110%, preferably at least 200%, more preferably at least 500%, and most preferably at least 1000%, of that expressed from the said reporter construct in said other cell.

25 3.2. Construction of synthetic polynucleotides

The step of replacing a synonymous codon for said first codon in a parent polynucleotide may be effected by any suitable technique. For example, *in vitro* mutagenesis methods may be employed as for example discussed in Section
30 2.

It is not necessary to replace all the first codons of the parent polynucleotide with synonymous codons each corresponding to a codon that has a higher translational

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efficiency in the target cell relative to said other cell. Increased expression may be accomplished even with partial replacement. Preferably, the replacing step affects 5%, 10%, 15%, 20%, 25%, 30%, more preferably 35%, 40%, 50%, 60%, 70% or more of the existing codons of the parent nucleic acid sequence.

The parent polynucleotide is preferably a natural gene.

The parent polynucleotide may be obtained from a plant or an animal. Alternatively, the parent polynucleotide may be obtained from any other eukaryotic organism or a prokaryotic organism. In a preferred embodiment, the parent polynucleotide is obtained from a pathogenic organism. In such a case, a natural host of the pathogenic organism is preferably a plant or animal. For example, the pathogenic organism may be a yeast, bacterium or virus. However, it will be understood that the parent polynucleotide need not be obtained from the organism in which a protein is to be expressed but may be obtained from any suitable source such as from another eukaryotic or prokaryotic organism.

Suitable proteins which may be used for selective expression in accordance with the invention include, but are not limited to the cystic fibrosis transmembrane conductance regulator (CFTR) protein, and adenosine deaminase (ADA). In the case of CFTR, a parent nucleic acid sequence encoding the CFTR protein which may be utilized to produce the synthetic nucleic acid sequence is described, for example, in Riordan et al (1989, *Science* **245** 1066-1073), and in the GenBank database under Accession No. HUMCFTRM.

Regulatory polynucleotides which may be utilized to regulate expression of the synthetic polynucleotide include, but are not limited to, a promoter, an enhancer, and a transcriptional terminator. Such regulatory polynucleotides are known to those of skill in the art. The construct

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preferably comprises at least one promoter. Suitable promoters that can be utilized to induce expression of the synthetic polynucleotides of the invention include constitutive promoters and inducible promoters.

5 Synthetic polynucleotides according to the invention may be operably linked to one or more regulatory sequences in the form of an expression vector.

10 The invention also contemplates synthetic polynucleotides encoding one or more desired portions of the protein to be expressed. A polynucleotide encodes a domain of the protein having a function associated therewith, or which is otherwise detectable, and preferably encodes at least 10, 20, 50, 100, 150, or 500 contiguous amino acid residues of the protein.

15 *4. Synthetic polynucleotides for enhanced protein expression in a particular cell or tissue*

In contrast to differential protein expression between different cells/tissues, it will be appreciated that a synthetic polynucleotide may be tailored with synonymous
20 codons such that expression of a protein in a target cell is enhanced. In this regard, the difference in level of protein expressed in the target cell/tissue from a synthetic polynucleotide relative to that expressed from a parent polynucleotide depends on the percentage of existing codons
25 replaced by synonymous codons, and the difference in translational efficiencies between the existing codons and the synonymous codons in the target cell/tissue. Put another way, the fewer such replacements, and/or the smaller the difference in translational efficiencies between the
30 synonymous and existing codons, the smaller the difference in protein expression between the synthetic polynucleotide and parent polynucleotide will be. Conversely, the more such replacements, and/or the greater the difference in

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translational efficiencies between the synonymous and existing codons, the greater the difference in protein expression between the synthetic polynucleotide and parent polynucleotide will be. The inventors have found in this
5 respect that a protein can be expressed from a synthetic polynucleotide in a target cell/tissue at levels greater than 10,000-fold than from a parent polynucleotide.

Preferably, the at least one existing codon and the synonymous codon are selected such that said protein is
10 expressed from said synthetic polynucleotide in said target cell or tissue at a level which is at least 110%, preferably at least 200%, more preferably at least 500%, and most preferably at least 1000%, of that expressed from said parent polynucleotide in said target cell or tissue.

15

The invention is further described with reference to the following non-limiting examples.

EXAMPLE 1

*Construction of expression vectors for determining
20 relative codon preferences in mammalian cells.*

Synthetic *gfp* genes were constructed in which a single artificial start codon (ATG) followed by a stretch of five identical codons is fused in frame immediately upstream of a *gfp* coding sequence. A reverse oligonucleotide primer (SEQ
25 ID NO:185; sequence complementary to the termination codon for GFP, is underlined), and a suite of forward oligonucleotide primers (SEQ ID NO: 126 through 184; the first codon of GFP, is underlined) were synthesized and used for PCR amplification of a humanized *gfp* gene (SEQ ID NO:124)
30 (GIBCO) as template with *Taq* DNA polymerase (Amplification parameters: 95°C/30 sec; 52°C/30 sec; 72°C/1 min; 30 cycles). The amplified fragments have nucleic acid sequences and

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deduced amino acid sequences as shown in SEQ ID NO:1 through 124.

In summary, the synthetic fragments contain an artificial start codon followed by a tandem repeat of five identical codons specific for a given iso-tRNA species. The tandem repeat immediately precedes the second codon of the *gfp* gene. The synthetic fragments by SEQ ID NO, and encoded tandem repeat, are presented in the TABLE 1.

The amplified fragments were cloned between the *EcoRI* and *KpnI* sites of the mammalian expression vector pCDNA3 containing SV40 *ori* (Invitrogen) and the CMV promoter.

Transfection of COS-1 cells

COS-1 cells were grown continuously in DMEM media supplemented with 10% fetal calf serum (FCS), glutamine, penicillin and streptomycin. Cells were passaged from a 150 cm² flask into multiple 25 cm² flasks. Cells were transfected using a QIAGEN Effectene™ transfection kit (and the manufacturer's instructions) when confluency of the cells was between 60-80%. Briefly, 1 µg of plasmid DNA was diluted into 10 µL of filtered TE buffer and 140 µL of QIAGEN™ Buffer EC. Eight microliters of QIAGEN™ Enhancer was added followed by vortexing and incubation at room temperature for 2-5 min. QIAGEN™ Effectene (10 µL) was added followed by vortexing for 10 seconds and a further incubation at room temperature for 10 min. The cells were washed once in 1x PBS followed by re-suspension in fresh media (1 mL). After 48 hrs, cells were harvested and washed in 1x PBA (phosphate buffered saline plus azide). Cells adhering to the flask were removed by scraping with a cell scraper. Cells were then filtered through a 70 µm filter before addition of 300 µL of 2% paraformaldehyde and 300 µL of 10x FCS. Cells were kept on ice in the dark until FACS analysis.

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Synthetic *gfp* mRNA expression of transfected cells was tested by reverse transcriptase PCR. GFP protein expression was analyzed by confocal microscopy and flow cytometry.

Confocal microscopy

5 Transfected COS-1 cells were examined using a Bio-Rad MRC-600 laser-scanning confocal microscope equipped with a krypton-argon laser and filter sets suitable for the detection of fluorescein and Texas red dyes (Bio-Rad KlyK2), and a Nikon 603 PlanApo™ numerical aperture 1.2 water-
10 immersion objective. Dual-channel confocal images and video montages of the transfected cells can be suitably composed using ADOBE PhotoShop™.

Flow cytometry

Transfected COS-1 cells were analyzed with a Becton
15 Dickinson™ Flow cytometer Elite II. Omega Filters™ allowed detection of green fluorescence emission (EMI510/20 - collects light from 490-530 nm) and yellow fluorescence emission (EM2 550/30 - collects light form 525-580 nm) from the transfected cells.

20 Results

A series of 64 reporter constructs (see TABLE 1) was made and validated, in which the *gfp* gene is preceded in frame by a tandem repeat of 5 identical codons. Together, the series covers the entire set of isoaccepting codon
25 triplets.

The series was transfected into a single cell line, and expression levels measured by flow cytometry (see TABLE 2). Overall, the expression level of the reporter gene constructs in the cell line varied over a range of 20-fold, according to
30 the triplet used in the reporter construct. Repeated determinations on the same construct showed excellent inter-assay reproducibility ($r^2 = 0.9$). Variation in expression

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levels across the isoaccepting codons for a single amino acid ranged from 1.4-fold for valine to 13-fold for threonine, with a median of about 4-fold. Variation in expression between amino acids was of the same order of magnitude. The order of magnitude of the effect is defined as an average of 4 fold per amino acid if 5 copies are incorporated, compatible with an extreme in range of expression levels of up to $(1.6)^{200} = 10^{86}$ over an average 200-amino acid residues protein. This figure is derived as:

$$[1 + ((4-1) (\text{range of reporter construct expression}) / 5 (\text{no of triplets in the reporter construct}))]^{200 (\text{no of amino acid residues in the protein})}$$

and is more than sufficient to explain the observed differences in expression of mammalian genes according to codon usage.

The results presented in TABLE 2 also show that various codons in the undifferentiated epithelial cells (COS-1) have translational efficiencies at least two-fold higher or two-fold lower relative to those of their corresponding synonymous codons. Representative codons having at least a two-fold higher translational efficiency relative to at least one of their corresponding synonymous codons include aga (Arg), cgg (Arg), tgc (Cys), gga (Gly), ggc (Gly), ccg (Pro), cga (Pro), aca (Thr), acg (Thr), and act (Thr). Thus, these codons appear to be preferred for translation in the undifferentiated epithelial cells. By contrast, representative codons having at least a two-fold lower translational efficiency relative to at least one of their corresponding synonymous codons include agg (Arg), tgt (Cys), ggg (Gly), ggt (Gly), ccc (Pro), cct (Pro), and acc (Thr). These latter codons would therefore appear to be less preferred for translation in the undifferentiated epithelial cells. Accordingly, if higher protein expression is required within undifferentiated epithelial cells such as COS-1 cells,

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the preferred codons should be used to replace any existing codons of a parent polynucleotide encoding the protein that correspond to the less preferred codons. In this respect, a codon substitution algorithm for increasing protein
5 expression in non-differentiated epithelial cells is presented in TABLE 3. However, if lower protein expression is required in non-differentiated epithelial cells, the less preferred codons should be used to replace any existing codons of the parent polynucleotide that correspond to the
10 preferred codons.

The present invention has been described in terms of particular embodiments found or proposed by the present inventors to comprise preferred modes for the practice of the
15 invention. Those of skill in the art will appreciate that, in light of the present disclosure, numerous modifications and changes can be made in the particular embodiments exemplified without departing from the scope of the invention. All such modifications are intended to be
20 included within the scope of the appended claims.

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TABLE 1

Synthetic *gfp* constructs are tabulated by SEQ ID NO and by the codon corresponding to the tandem repeat of five identical codons immediately upstream of the *gfp* gene.

5

TABLE 2

Mean fluorescence intensities of up to four different samples of transiently transfected COS-1 cells are shown (Green mean 1-4). Synthetic *gfp* constructs are tabulated by SEQ ID NO and by the codon corresponding to the tandem repeat immediately upstream of the *gfp* gene.

10

TABLE 3

Input codons and output codons represent, respectively, synonymous codons and existing (*i.e.*, "first") codons according to the invention. Change means an actual change of a codon.

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TABLES

TABLE 1

Synthetic fragments and tandem repeats encoded thereby.

<i>SEQ ID NO</i>	<i>Tandem repeat</i>	<i>SEQ ID NO</i>	<i>Tandem repeat</i>
1	Ala (GCA) x 5	65	Leu (CTT) x 5
3	Ala (GCC) x 5	67	Leu (TTA) x 5
5	Ala (GCG) x 5	69	Leu (TTG) x 5
7	Ala (GCT) x 5	71	Lys (AAA) x 5
9	Arg (AGA) x 5	73	Lys (AAG) x 5
11	Arg (AGG) x 5	75	Phe (TTT) x 5
13	Arg (CGA) x 5	77	Phe (TTC) x 5
15	Arg (CGC) x 5	79	Pro (CCC) x 5
17	Arg (CGG) x 5	81	Pro (CCG) x 5
19	Arg (CGT) x 5	83	Pro (CCT) x 5
21	Asn (AAC) x 5	85	Pro (CGA) x 5
23	Asn (AAT) x 5	87	Ser (AGC) x 5
25	Asp (GAC) x 5	89	Ser (AGT) x 5
27	Asp (GAT) x 5	91	Ser (TCA) x 5
29	Cys (TGC) x 5	93	Ser (TCC) x 5
31	Cys (TGT) x 5	95	Ser (TCG) x 5
33	Gln (CAA) x 5	97	Ser (TCT) x 5
35	Gln (CAG) x 5	99	Thr (ACA) x 5
37	Gly (GAA) x 5	101	Thr (ACC) x 5
39	Gly (GAG) x 5	103	Thr (ACG) x 5
41	Gly (GGA) x 5	105	Thr (ACT) x 5

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<i>SEQ ID NO</i>	<i>Tandem repeat</i>	<i>SEQ ID NO</i>	<i>Tandem repeat</i>
43	Gly (GGC) x 5	107	Trp (TGG) x 5
45	Gly (GGG) x 5	109	Tyr (TAT) x 5
47	Gly (GGT) x 5	111	Tyr (TAC) x 5
49	His (CAC) x 5	113	Val (GTA) x 5
51	His (CAT) x 5	115	Val (GTC) x 5
53	Ile (ATA) x 5	117	Val (GTG) x 5
55	Ile (ATC) x 5	119	Val (GTT) x 5
57	Ile (ATT) x 5	121	Stop (TAA) x 5
59	Leu (CTA) x 5	122	Stop (TAG) x 5
61	Leu (CTC) x 5	123	Stop (TGA) x 5
63	Leu (CTG) x 5	124	control

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TABLE 2

GFP protein expression in transiently transfected COS-1 cells

SEQ ID NO	Codon	[DNA] ($\mu\text{g/mL}$)	Green mean 1	Green mean 2	Green mean 3	Green mean 4	Average
1	Ala (GCA)	1.07	45.70	54.40			50.05
3	Ala (GCC)	1.10	43.70	50.00			46.85
5	Ala (GCG)	0.03	28.50	42.40			35.45
7	Ala (GCT)	0.56	11.60	48.30			29.95
9	Arg (AGA)	0.90	29.00	33.00			31.00
11	Arg (AGG)	0.34	7.35	2.88			5.12
13	Arg (CGA)	1.00	18.30	14.20			16.25
15	Arg (CGC)	0.86	14.60	16.00			15.30
17	Arg (CGG)	1.00	22.50	20.60			21.55
19	Arg (CGT)	0.68	21.70	32.20			26.95
21	Asn (AAC)	0.02					
23	Asn (AAT)	0.38	28.30	8.22			18.26
25	Asp (GAC)	0.46	24.90	17.80			21.35
27	Asp (GAT)	1.39	14.50	18.90			16.70
29	Cys (TGC)	0.68	21.90	16.10			19.00
31	Cys (TGT)	1.14	5.95	5.89			5.92
33	Gln (CAA)	0.28	26.50	43.50			35.00
35	Gln (CAG)	1.98	44.70	48.60			46.65
37	Glu (GAA)	0.60	10.30	22.70			16.50
39	Glu (GAG)	0.43	3.86				
41	Gly (GGA)	0.33	28.80	36.30			32.55
43	Gly (GGC)	1.62	17.80	28.10			22.95
45	Gly (GGG)	1.15	6.43	4.96			5.70
47	Gly (GGT)	1.39	7.12	4.02			5.57
49	His (CAC)	1.62	29.90	39.70			34.80
51	His (CAT)	1.69	43.40	37.20			40.30
53	Ile (ATA)	0.69	2.76	3.98			3.37

- 36 -

SEQ ID NO	Codon	[DNA] (µg/mL)	Green mean 1	Green mean 2	Green mean 3	Green mean 4	Average
55	Ile (ATC)	1.52	4.12	2.83			3.48
57	Ile (ATT)	1.77	3.19	3.16			3.18
59	Leu (CTA)	0.10	15.00	3.01	5.26	2.44	6.43
61	Leu (CTC)	1.74	2.70	2.92	2.56		2.73
63	Leu (CTG)	0.41	2.80	7.51	2.63		4.31
65	Leu (CTT)	1.43	3.17	3.56	2.70		3.14
67	Leu (TTA)	0.62	3.85	3.91	2.66		3.47
69	Leu (TTG)	0.70	2.87	4.63	2.85		3.45
71	Lys (AAA)	0.10	11.90	8.24			10.07
73	Lys (AAG)	0.56	19.20	16.00			17.60
75	Phe (TTT)	2.28	2.67				
77	Phe (TTC)	1.65	4.35				
79	Pro (CCC)	0.40	12.00	8.95			10.48
81	Pro (CCG)	0.13	17.40	25.40			21.40
83	Pro (CCT)	0.40	10.60	9.89			10.25
85	Pro (CGA)	0.17	27.20	34.80			31.00
87	Ser (AGC)	0.03	62.40				
89	Ser (AGT)	0.81	23.10				
91	Ser (TCA)	0.08	30.70	37.20			33.95
93	Ser (TCC)	1.68	32.90				
95	Ser (TCG)	1.58	60.00				
97	Ser (TCT)	0.62	26.80	40.70			33.75
99	Thr (ACA)	1.70	37.80	39.90			38.85
101	Thr (ACC)	7.69	3.48	2.75			3.12
103	Thr (ACG)	1.06	36.10	44.10			40.10
105	Thr (ACT)	1.42	38.80	42.60			40.70
107	Trp (TGG)	1.19	5.21	4.29			4.75
109	Tyr (TAT)	0.02					
111	Tyr (TAC)	1.07	12.00	15.00			13.50
113	Val (GTA)	0.16	10.50	3.81			7.16
115	Val (GTC)	0.66	15.20	4.55	3.65	5.06	7.12
117	Val (GTG)	0.10	9.17	4.29	7.03	2.36	5.71

- 37 -

SEQ ID NO	Codon	[DNA] ($\mu\text{g/mL}$)	Green mean 1	Green mean 2	Green mean 3	Green mean 4	Average
119	Val (GTT)	0.49	14.10	2.63	3.70	2.49	5.73
121	stop (TAA)	1.88	39.40	35.30			37.35
122	stop (TAG)	2.86	2.88	3.28			3.08
123	stop (TGA)	0.02					
124			9.34	61.60	30.40	55.00	39.09
GFP alone control			2.33	2.21	2.16	2.00	2.18

TABLE 3

Substitution algorithm used for high level expression in non-differentiated epithelial cells

Input Codon	Output Codon	Amino Acid	Change
AAA	AAG	LYS	Yes
AAC	AAC	ASN	No
AAG	AAG	LYS	No
AAT	AAC	ASN	Yes
AAU	AAC	ASN	Yes
ACA	ACC	THR	Yes
ACC	ACC	THR	No
ACG	ACC	THR	Yes
ACT	ACC	THR	Yes
ACU	ACC	THR	Yes
AGA	AGG	ARG	Yes
AGC	AGC	SER	No
AGG	AGG	ARG	No
AGT	AGC	SER	Yes
AGU	AGC	SER	Yes
ATA	ATC	ILE	Yes
ATC	ATC	ILE	No
ATG	ATG	MET	No
ATT	ATC	ILE	Yes
AUA	ATC	ILE	Yes
AUC	ATC	ILE	No
AUG	ATG	MET	No
AUU	ATC	ILE	Yes
CAA	CAG	GLN	Yes
CAC	CAC	HIS	No
CAG	CAG	GLN	No
CAT	CAC	HIS	Yes
CAU	CAC	HIS	Yes
CCA	CCC	PRO	Yes
CCC	CCC	PRO	No
CCG	CCC	PRO	Yes
CCT	CCC	PRO	Yes
CCU	CCC	PRO	Yes
CGA	CGC	ARG	Yes

- 39 -

Input Codon	Output Codon	Amino Acid	Change
CGC	CGC	ARG	No
CGG	CGC	ARG	Yes
CGT	CGC	ARG	Yes
CGU	CGC	ARG	Yes
CTA	CTG	LEU	Yes
CTC	CTG	LEU	Yes
CTG	CTG	LEU	No
CTT	CTG	LEU	Yes
CUA	CTG	LEU	Yes
CUC	CTG	LEU	Yes
CUG	CTG	LEU	No
CUU	CTG	LEU	Yes
GAA	GAG	GLU	Yes
GAC	GAC	ASP	No
GAG	GAG	GLU	No
GAT	GAC	ASP	Yes
GAU	GAC	ASP	Yes
GCA	GCC	ALA	Yes
GCC	GCC	ALA	No
GCG	GCC	ALA	Yes
GCT	GCC	ALA	Yes
GCU	GCC	ALA	Yes
GGA	GGC	GLY	Yes
GGC	GGC	GLY	No
GGG	GGG	GLY	No
GGT	GGC	GLY	Yes
GGU	GGC	GLY	Yes
GTA	GTG	VAL	Yes
GTC	GTG	VAL	Yes
GTG	GTG	VAL	No
GTT	GTG	VAL	Yes
GUA	GTG	VAL	Yes
GUC	GTG	VAL	Yes
GUG	GTG	VAL	No
GUU	GTG	VAL	Yes
TAA	TAA	XXX	No
TAC	TAC	TYR	No
TAG	TAG	XXX	No
TAT	TAC	TYR	Yes
TCA	TCC	SER	Yes

- 40 -

Input Codon	Output Codon	Amino Acid	Change
TCC	TCC	SER	No
TCG	TCC	SER	Yes
TCT	TCC	SER	Yes
TGA	TGA	XXX	No
TGC	TGC	CYS	No
TGG	TGG	TRP	No
TGT	TGT	CYS	No
TTA	CTG	LEU	Yes
TTC	TTC	PHE	No
TTG	CTG	LEU	Yes
TTT	TTC	PHE	No
UAA	TAA	XXX	No
UAC	TAC	TYR	No
UAG	TAG	XXX	No
UAU	TAC	TYR	Yes
UCA	TCC	SER	Yes
UCC	TCC	SER	No
UCG	TCC	SER	Yes
UCU	TCC	SER	Yes
UGA	TGA	XXX	No
UGC	TGC	CYS	No
UGG	TGG	TRP	No
UGU	TGT	CYS	No
UUA	CTG	LEU	Yes
UUC	TTC	PHE	No
UUG	CTG	LEU	Yes
UUU	TTC	PHE	Yes

SEQUENCE LISTING

<110> The University of Queensland (all designated States except US)
Frazer, Ian Hector and Zhou, Jian (US only)

<120> METHOD AND POLYNUCLEOTIDES FOR DETERMINING TRANSLATIONAL
EFFICIENCY OF A CODON

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<151> 1999-01-08

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gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	

tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
		100						105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145					150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
			165						170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
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Leu	Tyr	Lys														

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

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
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 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
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ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
	65				70					75					80	
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggt	gac	acc	ctg	gtg	aat	aga	atc	384
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Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
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Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
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aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
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      35                      40                      45
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
      50                      55                      60
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
      65                      70                      75                      80
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
      85                      90                      95
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
      100                     105                     110
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
      115                     120                     125
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
      130                     135                     140
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
      145                     150                     155                     160
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
      165                     170                     175
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
      180                     185                     190
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
      195                     200                     205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
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gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
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85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
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Leu Tyr Lys

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

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<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ala(GCT)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 7

atg gct gct gct gct gct agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Ala Ala Ala Ala Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

ctg tac aag tga 732
 Leu Tyr Lys

<210> 8
 <211> 243
 <212> PRT
 <213> Artificial Sequence

<400> 8
 Met Ala Ala Ala Ala Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15

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

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80

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

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240

Leu Tyr Lys

<210> 9
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Arg(AGA)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 9
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Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
130 135 140

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aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                      150                      155                      160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                      165                      170                      175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                      180                      185                      190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                      195                      200                      205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                      210                      215                      220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                      230                      235                      240

ctg tac aag tga
Leu Tyr Lys
732

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<210> 10
<211> 243
<212> PRT
<213> Artificial Sequence

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<400> 10
Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1                      5                      10                      15

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

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                35                      40                      45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
  50                      55                      60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
  65                      70                      75                      80

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

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                100                      105                      110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                115                      120                      125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
  130                      135                      140

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12

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240

Leu Tyr Lys

<210> 11

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Arg(AGG)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 11

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

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95

tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
		130				135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145					150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
			165					170					175			
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195				200						205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
		210				215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
225					230				235						240	
ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 12

<211> 243

<212> PRT

<213> Artificial Sequence

<400> 12

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

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

Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr
		35					40					45			

Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr
	50					55					60				

Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro
65					70					75					80

14

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

Leu Tyr Lys

<210> 13
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Arg(CGA)5GFP

<220>
 <221> CDS
 <222> (1)..(732)

<400> 13
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 Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
	65				70					75					80	
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggc	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
	145				150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
	225				230				235						240	
ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 14

<211> 243

<212> PRT

<213> Artificial Sequence

<400> 14

Met	Arg	Arg	Arg	Arg	Arg	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val
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16

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

<210> 15

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Arg(CGC)5GFP

<220>

<221> CDS

<222> (1)..(732)

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<400> 15
atg cgc cgc cgc cgc cgc agc aag ggc gag gaa ctg ttc act ggc gtg 48
Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1             5             10             15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
             20             25             30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
             35             40             45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
             50             55             60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
             65             70             75             80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
             85             90             95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
             100            105            110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
             115            120            125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
             130            135            140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
             145            150            155            160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
             165            170            175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
             180            185            190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
             195            200            205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
             210            215            220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
             225            230            235            240

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ctg tac aag tga
Leu Tyr Lys

732

<210> 16
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 16
Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
130 135 140
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240
Leu Tyr Lys

<210> 17
<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Arg(CGG)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 17

atg cgg cgg cgg cgg cgg agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	

<400> 18																
Met	Arg	Arg	Arg	Arg	Arg	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	
1				5					10					15		
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
			20					25					30			
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		35					40					45				
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
65					70					75					80	
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145					150					155					160	
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

Leu Tyr Lys

<210> 19

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Arg(CGT)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 19

atg cgt cgt cgt cgt cgt agc aag ggc gag gaa ctg ttc act ggc gtg 48
 Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

ctg tac aag tga 732
 Leu Tyr Lys

<210> 20
 <211> 243
 <212> PRT
 <213> Artificial Sequence

<400> 20
 Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240
 Leu Tyr Lys

<210> 21
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Asn(AAC)5GFP

<220>
 <221> CDS
 <222> (1)..(732)

<400> 21
 atg aac aac aac aac aac agc aag ggc gag gaa ctg ttc act ggc gtg 48
 Met Asn Asn Asn Asn Asn Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80
 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95

tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145					150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
225					230				235						240	
ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 22

<211> 243

<212> PRT

<213> Artificial Sequence

<400> 22

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

25

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

Leu Tyr Lys

<210> 23
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Asn(AAT)5GFP

<220>
 <221> CDS
 <222> (1)..(732)

<400> 23
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 Met Asn Asn Asn Asn Asn Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
	65				70					75					80	
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggc	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
	145				150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
			165						170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
	225				230					235					240	
ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 24

<211> 243

<212> PRT

<213> Artificial Sequence

<400> 24

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

27

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

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Leu Tyr Lys

<210> 25

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Asp(GAC)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 25

atg gac gac gac gac gac agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Asp Asp Asp Asp Asp Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	

ctg tac aag tga
Leu Tyr Lys

732

<210> 26
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 26
Met Asp Asp Asp Asp Asp Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
130 135 140
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240
Leu Tyr Lys

<210> 27
<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Asp(GAT)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 27

atg gat gat gat gat gat agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Asp Asp Asp Asp Asp Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	

<400> 28																
Met	Asp	Asp	Asp	Asp	Asp	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	
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Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
			20					25					30			
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		35					40					45				
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
65					70					75					80	
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145				150					155						160	
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

Leu Tyr Lys

<210> 29

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Cys(TGC)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 29

atg tgc tgc tgc tgc tgc agc aag ggc gag gaa ctg ttc act ggc gtg 48
 Met Cys Cys Cys Cys Cys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

ctg tac aag tga 732
 Leu Tyr Lys

<210> 30

<211> 243

<212> PRT

<213> Artificial Sequence

<400> 30

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

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

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80

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

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240

Leu Tyr Lys

<210> 31

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Cys(TGT)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 31

atg tgt tgt tgt tgt tgt agc aag ggc gag gaa ctg ttc act ggc gtg 48
Met Cys Cys Cys Cys Cys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95

35

tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
		100					105					110				
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
	115						120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145					150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
			165						170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
	195					200						205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
225					230				235						240	
ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 32

<211> 243

<212> PRT

<213> Artificial Sequence

<400> 32

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

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240
 Leu Tyr Lys

<210> 33
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Gln(CAA)5GFP

<220>
 <221> CDS
 <222> (1)..(732)

<400> 33
 atg caa caa caa caa caa agc aag ggc gag gaa ctg ttc act ggc gtg 48
 Met Gln Gln Gln Gln Gln Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
65					70					75					80	
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggt	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145					150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
225					230					235					240	
ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 34

<211> 243

<212> PRT

<213> Artificial Sequence

<400> 34

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

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

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Leu Tyr Lys

<210> 35

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Gln(CAG)5GFP

<220>

<221> CDS

<222> (1) .. (732)

<400> 35

atg cag cag cag cag cag agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Gln Gln Gln Gln Gln Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	

40

ctg tac aag tga
Leu Tyr Lys

732

<210> 36
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 36
Met Gln Gln Gln Gln Gln Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
130 135 140
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240
Leu Tyr Lys

<210> 37
<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Glu(GAA)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 37

atg gaa gaa gaa gaa gaa agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Glu Glu Glu Glu Glu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	

ctg tac aag tga	732
Leu Tyr Lys	

<210> 38
 <211> 243
 <212> PRT
 <213> Artificial Sequence

<400> 38
Met Glu Glu Glu Glu Glu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15

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

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80

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

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

Leu Tyr Lys

<210> 39

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Glu(GAG)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 39

atg gag gag gag gag gag agc aag ggc gag gaa ctg ttc act ggc gtg 48
 Met Glu Glu Glu Glu Glu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140

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aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                      150                      155                      160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                      165                      170                      175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                      180                      185                      190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                      195                      200                      205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                      210                      215                      220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                      230                      235                      240

ctg tac aag tga 732
Leu Tyr Lys

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<210> 40
<211> 243
<212> PRT
<213> Artificial Sequence

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<400> 40
Met Glu Glu Glu Glu Glu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1                      5                      10                      15

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

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                35                      40                      45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
                50                      55                      60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
        65                      70                      75                      80

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

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                100                      105                      110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                115                      120                      125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130                      135                      140

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45

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240
 Leu Tyr Lys

<210> 41
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Gly(GGA)5GFP

<220>
 <221> CDS
 <222> (1)..(732)

<400> 41
 atg gga gga gga gga gga agc aag ggc gag gaa ctg ttc act ggc gtg 48
 Met Gly Gly Gly Gly Gly Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80
 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95

46

tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145					150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
			165					170						175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195				200						205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
225					230					235					240	
ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 42

<211> 243

<212> PRT

<213> Artificial Sequence

<400> 42

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

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

Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr
		35					40					45			

Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr
	50					55					60				

Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro
65						70				75					80

47

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

Leu Tyr Lys

<210> 43
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Gly(GGC)5GFP

<220>
 <221> CDS
 <222> (1)..(732)

<400> 43
 atg ggc ggc ggc ggc ggc agc aag ggc gag gaa ctg ttc act ggc gtg 48
 Met Gly Gly Gly Gly Gly Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
	65				70					75					80	
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggc	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
	145				150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
	225				230					235					240	
ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 44

<211> 243

<212> PRT

<213> Artificial Sequence

<400> 44

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

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

<210> 45

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Gly(GGG)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 45

atg ggg ggg ggg ggg ggg agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Gly Gly Gly Gly Gly Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	

ctg tac aag tga
Leu Tyr Lys

732

<210> 46
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 46
Met Gly Gly Gly Gly Gly Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
130 135 140
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240
Leu Tyr Lys

<210> 47
<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Gly(GGT)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 47

atg ggt ggt ggt ggt ggt agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Gly Gly Gly Gly Gly Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	

<400> 48																
Met	Gly	Gly	Gly	Gly	Gly	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	
1				5					10					15		
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
			20					25					30			
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		35					40					45				
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
65					70					75					80	
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145					150					155					160	
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240

Leu Tyr Lys

<210> 49

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: His(CAC)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 49

atg cac cac cac cac cac agc aag ggc gag gaa ctg ttc act ggc gtg 48
Met His His His His His Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
130 135 140

55

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

ctg tac aag tga 732
 Leu Tyr Lys

<210> 50

<211> 243

<212> PRT

<213> Artificial Sequence

<400> 50

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

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

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80

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

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140

56

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240

Leu Tyr Lys

<210> 51

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: His(CAT)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 51

atg cat cat cat cat cat agc aag ggc gag gaa ctg ttc act ggc gtg 48
Met His His His His His Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95

tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
		130				135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
					150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
		210				215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
		225			230				235						240	
ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 52

<211> 243

<212> PRT

<213> Artificial Sequence

<400> 52

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

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

Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr
		35					40					45			

Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr
	50					55					60				

Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro
	65					70				75					80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

Leu Tyr Lys

<210> 53
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ile(ATA)5GFP

<220>
 <221> CDS
 <222> (1)..(732)

<400> 53
 atg ata ata ata ata ata agc aag ggc gag gaa ctg ttc act ggc gtg 48
 Met Ile Ile Ile Ile Ile Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
	65				70					75					80	
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
		100					105					110				
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggc	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
	145				150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
	225				230					235					240	
ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 54

<211> 243

<212> PRT

<213> Artificial Sequence

<400> 54

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

1

5

10

15

60

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

Leu Tyr Lys

<210> 55

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ile(ATC)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 55

atg atc atc atc atc atc agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Ile Ile Ile Ile Ile Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	

ctg tac aag tga
Leu Tyr Lys

732

<210> 56
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 56
Met Ile Ile Ile Ile Ile Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
130 135 140
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240
Leu Tyr Lys

<210> 57
<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ile(ATT)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 57

atg att att att att att agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Ile Ile Ile Ile Ile Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	

<400> 58															
Met	Ile	Ile	Ile	Ile	Ile	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val
1				5					10					15	
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe
			20					25					30		
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr
		35					40					45			
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr
	50					55					60				
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro
65					70					75					80
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly
				85					90					95	
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys
			100					105					110		
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile
		115					120					125			
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His
	130					135					140				
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp
145				150						155					160
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile
			165						170					175	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro
			180					185					190		
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr
		195					200					205			

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

Leu Tyr Lys

<210> 59

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Leu(CTA)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 59

atg cta cta cta cta cta agc aag ggc gag gaa ctg ttc act ggc gtg 48
 Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

ctg tac aag tga 732
 Leu Tyr Lys

<210> 60

<211> 243

<212> PRT

<213> Artificial Sequence

<400> 60

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

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

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80

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

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240
 Leu Tyr Lys

<210> 61
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Leu(CTC)5GFP

<220>
 <221> CDS
 <222> (1)..(732)

<400> 61
 atg ctc ctc ctc ctc ctc agc aag ggc gag gaa ctg ttc act ggc gtg 48
 Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80
 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95

68

tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggt	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
		130				135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
					150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
		210				215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
		225			230					235					240	
ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 62

<211> 243

<212> PRT

<213> Artificial Sequence

<400> 62

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

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

Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr
		35					40					45			

Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr
	50					55					60				

Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro
	65					70				75					80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

Leu Tyr Lys

<210> 63
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Leu(CTG)5GFP

<220>
 <221> CDS
 <222> (1)..(732)

<400> 63
 atg ctg ctg ctg ctg ctg agc aag ggc gag gaa ctg ttc act ggc gtg 48
 Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
	65				70					75					80	
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggc	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
	145				150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
			165						170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
	225				230					235					240	
ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 64

<211> 243

<212> PRT

<213> Artificial Sequence

<400> 64

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

71

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

Leu Tyr Lys

<210> 65

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Leu(CTT)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 65

atg ctt ctt ctt ctt ctt agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	

ctg tac aag tga
Leu Tyr Lys

732

<210> 66
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 66
Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
130 135 140
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240
Leu Tyr Lys

<210> 67
<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Leu(TTA)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 67

atg tta tta tta tta tta agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	

<400> 68															
Met	Leu	Leu	Leu	Leu	Leu	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val
1				5					10					15	
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe
			20					25					30		
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr
		35					40					45			
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr
	50					55					60				
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro
65					70					75					80
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly
				85					90					95	
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys
			100					105					110		
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile
		115					120					125			
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His
	130					135					140				
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp
145					150					155					160
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile
				165					170					175	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro
			180					185					190		
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr
		195					200					205			

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

Leu Tyr Lys

<210> 69

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Leu(TTG)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 69

atg ttg ttg ttg ttg ttg agc aag ggc gag gaa ctg ttc act ggc gtg 48
 Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

ctg tac aag tga 732
 Leu Tyr Lys

<210> 70
 <211> 243
 <212> PRT
 <213> Artificial Sequence

<400> 70
 Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240
 Leu Tyr Lys

<210> 71
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Lys(AAA)5GFP

<220>
 <221> CDS
 <222> (1)..(732)

<400> 71
 atg aaa aaa aaa aaa aaa agc aag ggc gag gaa ctg ttc act ggc gtg 48
 Met Lys Lys Lys Lys Lys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80
 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95

tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
		100					105					110				
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
		130					135					140				
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
						150					155				160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
		210				215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
		225			230					235					240	
ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 72

<211> 243

<212> PRT

<213> Artificial Sequence

<400> 72

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

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

Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr
			35				40					45			

Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr
	50					55					60				

Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro
	65					70				75					80

80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

Leu Tyr Lys

<210> 73
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Lys(AAG)5GFP

<220>
 <221> CDS
 <222> (1)..(732)

<400> 73
 atg aag aag aag aag aag agc aag ggc gag gaa ctg ttc act ggc gtg 48
 Met Lys Lys Lys Lys Lys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
	65				70					75					80	
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggc	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
	145				150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
	225				230					235					240	
ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 74

<211> 243

<212> PRT

<213> Artificial Sequence

<400> 74

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

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

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
      35                      40                      45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
      50                      55                      60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
      65                      70                      75                      80

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

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
      100                     105                     110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
      115                     120                     125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
      130                     135                     140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
      145                     150                     155                     160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
      165                     170                     175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
      180                     185                     190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
      195                     200                     205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
      210                     215                     220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
      225                     230                     235                     240

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Leu Tyr Lys

<210> 75

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Phe(TTT)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 75

atg ttt ttt ttt ttt ttt agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Phe Phe Phe Phe Phe Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	

ctg tac aag tga
Leu Tyr Lys

732

<210> 76
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 76
Met Phe Phe Phe Phe Phe Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
130 135 140
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240
Leu Tyr Lys

<210> 77
<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Phe(TTC)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 77

atg ttc ttc ttc ttc ttc agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Phe Phe Phe Phe Phe Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	

86

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

ctg tac aag tga 732
 Leu Tyr Lys

<210> 78
 <211> 243
 <212> PRT
 <213> Artificial Sequence

<400> 78
 Met Phe Phe Phe Phe Phe Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15

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

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80

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

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

Leu Tyr Lys

<210> 79

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Pro(CCC)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 79

atg ccc ccc ccc ccc ccc agc aag ggc gag gaa ctg ttc act ggc gtg 48
 Met Pro Pro Pro Pro Pro Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140

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aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                150                155                160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                170                175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                180                185                190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                195                200                205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                210                215                220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                230                235                240

ctg tac aag tga 732
Leu Tyr Lys

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<210> 80
<211> 243
<212> PRT
<213> Artificial Sequence

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<400> 80
Met Pro Pro Pro Pro Pro Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1                5                10                15

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

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                35                40                45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
                50                55                60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
  65                70                75                80

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

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                100                105                110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                115                120                125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
  130                135                140

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Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240
 Leu Tyr Lys

<210> 81
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Pro(CCG)5GFP

<220>
 <221> CDS
 <222> (1)..(732)

<400> 81
 atg ccg ccg ccg ccg ccg agc aag ggc gag gaa ctg ttc act ggc gtg 48
 Met Pro Pro Pro Pro Pro Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80
 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95

90

tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145					150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
			165					170						175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195				200						205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
225					230					235					240	
ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 82

<211> 243

<212> PRT

<213> Artificial Sequence

<400> 82

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

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

Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr
		35					40					45			

Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr
	50					55					60				

Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro
65					70					75					80

91

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

Leu Tyr Lys

<210> 83
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Pro(CCT)5GFP

<220>
 <221> CDS
 <222> (1)..(732)

<400> 83
 atg cct cct cct cct cct agc aag ggc gag gaa ctg ttc act ggc gtg 48
 Met Pro Pro Pro Pro Pro Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
	65				70					75					80	
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggt	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
	145				150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
	225				230					235					240	
ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 84

<211> 243

<212> PRT

<213> Artificial Sequence

<400> 84

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

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

Ser  Val  Ser  Gly  Glu  Gly  Glu  Gly  Asp  Ala  Thr  Tyr  Gly  Lys  Leu  Thr
      35                      40                      45

Leu  Lys  Phe  Ile  Cys  Thr  Thr  Gly  Lys  Leu  Pro  Val  Pro  Trp  Pro  Thr
      50                      55                      60

Leu  Val  Thr  Thr  Phe  Ser  Tyr  Gly  Val  Gln  Cys  Phe  Ser  Arg  Tyr  Pro
      65                      70                      75                      80

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

Tyr  Val  Gln  Glu  Arg  Thr  Ile  Phe  Phe  Lys  Asp  Asp  Gly  Asn  Tyr  Lys
      100                      105                      110

Thr  Arg  Ala  Glu  Val  Lys  Phe  Glu  Gly  Asp  Thr  Leu  Val  Asn  Arg  Ile
      115                      120                      125

Glu  Leu  Lys  Gly  Ile  Asp  Phe  Lys  Glu  Asp  Gly  Asn  Ile  Leu  Gly  His
      130                      135                      140

Lys  Leu  Glu  Tyr  Asn  Tyr  Asn  Ser  His  Asn  Val  Tyr  Ile  Met  Ala  Asp
      145                      150                      155                      160

Lys  Gln  Lys  Asn  Gly  Ile  Lys  Val  Asn  Phe  Lys  Ile  Arg  His  Asn  Ile
      165                      170                      175

Glu  Asp  Gly  Ser  Val  Gln  Leu  Ala  Asp  His  Tyr  Gln  Gln  Asn  Thr  Pro
      180                      185                      190

Ile  Gly  Asp  Gly  Pro  Val  Leu  Leu  Pro  Asp  Asn  His  Tyr  Leu  Ser  Thr
      195                      200                      205

Gln  Ser  Ala  Leu  Ser  Lys  Asp  Pro  Asn  Glu  Lys  Arg  Asp  His  Met  Val
      210                      215                      220

Leu  Leu  Glu  Phe  Val  Thr  Ala  Ala  Gly  Ile  Thr  His  Gly  Met  Asp  Glu
      225                      230                      235                      240

Leu  Tyr  Lys

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<210> 85

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Pro(CGA)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 85

atg cga cga cga cga cga agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	

ctg tac aag tga
Leu Tyr Lys

732

<210> 86
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 86
Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
130 135 140
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240
Leu Tyr Lys

<210> 87
<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ser(AGC)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 87

atg agc agc agc agc agc agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

ctg tac aag tga 732
 Leu Tyr Lys

<210> 88
 <211> 243
 <212> PRT
 <213> Artificial Sequence

<400> 88
 Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15

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

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80

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

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240

Leu Tyr Lys

<210> 89

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ser(AGT)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 89

atg agt agt agt agt agt agc aag ggc gag gaa ctg ttc act ggc gtg 48
Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
130 135 140

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aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                      150                      155                      160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                      165                      170                      175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                      180                      185                      190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                      195                      200                      205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                      210                      215                      220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                      230                      235                      240

ctg tac aag tga 732
Leu Tyr Lys

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<210> 90

<211> 243

<212> PRT

<213> Artificial Sequence

<400> 90

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

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

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                      35                      40                      45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
                      50                      55                      60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
                      65                      70                      75                      80

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

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                      100                      105                      110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                      115                      120                      125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
                      130                      135                      140

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100

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240
 Leu Tyr Lys

<210> 91
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ser(TCA)5GFP

<220>
 <221> CDS
 <222> (1)..(732)

<400> 91
 atg tca tca tca tca tca agc aag ggc gag gaa ctg ttc act ggc gtg 48
 Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80
 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95

101

tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
		100					105					110				
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggt	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
	115					120					125					
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145					150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
			165						170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
	195					200						205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
225					230					235					240	
ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 92

<211> 243

<212> PRT

<213> Artificial Sequence

<400> 92

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

102

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

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
      100                    105                    110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
      115                    120                    125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
      130                    135                    140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
      145                    150                    155                    160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
      165                    170                    175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
      180                    185                    190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
      195                    200                    205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
      210                    215                    220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
      225                    230                    235                    240

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Leu Tyr Lys

```

<210> 93
<211> 732
<212> DNA
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Ser(TCC)5GFP

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<220>
<221> CDS
<222> (1)..(732)

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<400> 93
atg tcc tcc tcc tcc tcc agc aag ggc gag gaa ctg ttc act ggc gtg 48
Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1                      5                      10                      15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
      20                    25                    30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
      35                    40                    45

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103

ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
	65				70					75					80	
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggt	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
	145				150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
	225				230					235					240	
ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 94

<211> 243

<212> PRT

<213> Artificial Sequence

<400> 94

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

104

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

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<210> 95

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ser(TCG)5GFP

<220>

<221> CDS

<222> (1)..(732)

105

<400> 95

atg	tcg	tcg	tcg	tcg	tcg	agc	aag	ggc	gag	gaa	ctg	ttc	act	ggc	gtg	48
Met	Ser	Ser	Ser	Ser	Ser	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	
1				5					10					15		
gtc	cca	att	ctc	gtg	gaa	ctg	gat	ggc	gat	gtg	aat	ggg	cac	aaa	ttt	96
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
			20					25					30			
tct	gtc	agc	gga	gag	ggt	gaa	ggt	gat	gcc	aca	tac	gga	aag	ctc	acc	144
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		35					40					45				
ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
65					70				75						80	
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggt	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145					150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
			165						170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
225					230					235					240	

106

ctg tac aag tga
Leu Tyr Lys

732

<210> 96
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 96

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

<210> 97
<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ser(TCT)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 97

atg tct tct tct tct tct agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	

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atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
      195                      200                      205

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ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
225					230					235					240	

ctg tac aag tga 732
Leu Tyr Lys

<213> Artificial Sequence

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

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

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80

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

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205

109

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

Leu Tyr Lys

<210> 99

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Thr(ACA)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 99

atg aca aca aca aca aca agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Thr Thr Thr Thr Thr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	

110

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aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                      150                      155                      160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                      165                      170                      175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                      180                      185                      190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                      195                      200                      205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                      210                      215                      220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                      230                      235                      240

ctg tac aag tga
Leu Tyr Lys
732

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<210> 100
<211> 243
<212> PRT
<213> Artificial Sequence

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<400> 100
Met Thr Thr Thr Thr Thr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1                      5                      10                      15

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

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
          35                      40                      45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
          50                      55                      60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
          65                      70                      75                      80

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

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
          100                      105                      110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
          115                      120                      125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
          130                      135                      140

```

111

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240

Leu Tyr Lys

<210> 101

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Thr(ACC)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 101

atg acc acc acc acc acc agc aag ggc gag gaa ctg ttc act ggc gtg 48
Met Thr Thr Thr Thr Thr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95

112

tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
		100						105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggt	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145					150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
			165					170						175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
225					230				235						240	
ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 102

<211> 243

<212> PRT

<213> Artificial Sequence

<400> 102

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

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

Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr
		35					40					45			

Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr
	50					55					60				

Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro
65					70					75					80

113

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

Leu Tyr Lys

<210> 103
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Thr(ACG)5GFP

<220>
 <221> CDS
 <222> (1)..(732)

<400> 103
 atg acg acg acg acg acg agc aag ggc gag gaa ctg ttc act ggc gtg 48
 Met Thr Thr Thr Thr Thr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

114

ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
	65				70					75					80	
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggt	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
	145				150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
	225				230				235						240	
ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 104

<211> 243

<212> PRT

<213> Artificial Sequence

<400> 104

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

115

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

<210> 105

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Thr(ACT)5GFP

<220>

<221> CDS

<222> (1)..(732)

116

<400> 105

atg act act act act act agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Thr Thr Thr Thr Thr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	

117

ctg tac aag tga
Leu Tyr Lys

732

<210> 106
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 106
Met Thr Thr Thr Thr Thr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
130 135 140
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240
Leu Tyr Lys

<210> 107
<211> 732

118

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Trp(TGG)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 107

atg tgg tgg tgg tgg tgg agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Trp Trp Trp Trp Trp Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	

<400> 108																
Met	Trp	Trp	Trp	Trp	Trp	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	
1				5					10					15		
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
			20					25					30			
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		35					40					45				
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
65					70					75					80	
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145				150						155					160	
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				

120

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

Leu Tyr Lys

<210> 109

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Tyr(TAT)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 109

atg tat tat tat tat tat agc aag ggc gag gaa ctg ttc act ggc gtg 48
 Met Tyr Tyr Tyr Tyr Tyr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140

121

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aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                      150                      155                      160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                      165                      170                      175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                      180                      185                      190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                      195                      200                      205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                      210                      215                      220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                      230                      235                      240

ctg tac aag tga 732
Leu Tyr Lys

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<210> 110

<211> 243

<212> PRT

<213> Artificial Sequence

<400> 110

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

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

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                      35                      40                      45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
                      50                      55                      60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
                      65                      70                      75                      80

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

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                      100                      105                      110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                      115                      120                      125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
                      130                      135                      140

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122

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240
 Leu Tyr Lys

<210> 111
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Tyr(TAC)5GFP

<220>
 <221> CDS
 <222> (1)..(732)

<400> 111
 atg tac tac tac tac tac agc aag ggc gag gaa ctg ttc act ggc gtg 48
 Met Tyr Tyr Tyr Tyr Tyr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80
 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95

123

tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggt	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145					150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
			165					170						175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195				200						205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
225					230					235					240	
ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 112

<211> 243

<212> PRT

<213> Artificial Sequence

<400> 112

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

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

Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr
		35					40					45			

Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr
	50					55					60				

Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro
65					70					75					80

124

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240
 Leu Tyr Lys

<210> 113
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Val(GTA)5GFP

<220>
 <221> CDS
 <222> (1)..(732)

<400> 113
 atg gta gta gta gta gta agc aag ggc gag gaa ctg ttc act ggc gtg 48
 Met Val Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

125

ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
	65				70					75					80	
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggc	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
	145				150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
	225				230					235					240	
ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 114

<211> 243

<212> PRT

<213> Artificial Sequence

<400> 114

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

126

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

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
      35                      40                      45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
      50                      55                      60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
      65                      70                      75                      80

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

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
      100                      105                      110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
      115                      120                      125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
      130                      135                      140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
      145                      150                      155                      160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
      165                      170                      175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
      180                      185                      190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
      195                      200                      205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
      210                      215                      220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
      225                      230                      235                      240

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Leu Tyr Lys

<210> 115

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Val(GTC)5GFP

<220>

<221> CDS

<222> (1)..(732)

127

<400> 115

atg gtc gtc gtc gtc gtc agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Val Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	

128

ctg tac aag tga
Leu Tyr Lys

732

<210> 116
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 116
Met Val Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
130 135 140
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240
Leu Tyr Lys

<210> 117
<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Val(GTG)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 117

atg gtg gtg gtg gtg gtg agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Val Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	

130

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

ctg tac aag tga 732
 Leu Tyr Lys

<210> 118
 <211> 243
 <212> PRT
 <213> Artificial Sequence

<400> 118
 Met Val Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15

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

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80

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

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205

131

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

Leu Tyr Lys

<210> 119

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Val(GTT)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 119

atg gtt gtt gtt gtt gtt agc aag ggc gag gaa ctg ttc act ggc gtg 48
 Met Val Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140

132

```

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                      150                      155                      160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                      165                      170                      175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                      180                      185                      190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                      195                      200                      205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                      210                      215                      220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                      230                      235                      240

ctg tac aag tga 732
Leu Tyr Lys

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<210> 120
<211> 243
<212> PRT
<213> Artificial Sequence

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<400> 120
Met Val Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1                      5                      10                      15

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

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
    35                      40                      45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                      55                      60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
    65                      70                      75                      80

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

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                100                      105                      110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
    115                      120                      125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                      135                      140

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133

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240
 Leu Tyr Lys

<210> 121
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Stop(TAA)5GFP

<220>
 <221> CDS
 <222> (1)..(732)

<400> 121
 atg taa taa taa taa taa agc aag ggc gag gaa ctg ttc act ggc gtg 48
 Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80
 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95

134

tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145					150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
			165					170						175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195				200						205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
225					230				235						240	
ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 122

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Stop(TAG)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 122

atg	tag	tag	tag	tag	tag	agc	aag	ggc	gag	gaa	ctg	ttc	act	ggc	gtg	48
Met						Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	
1					5				10					15		

[illegible]

136

<210> 123
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Stop(TGA)5GFP

<220>
 <221> CDS
 <222> (1)..(732)

<400> 123
 atg tga tga tga tga tga agc aag ggc gag gaa ctg ttc act ggc gtg 48
 Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175

137

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gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
      180                      185                      190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
      195                      200                      205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
      210                      215                      220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
      225                      230                      235                      240

ctg tac aag tga 732
Leu Tyr Lys

<210> 124
<211> 717
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: GFP humanized
      control

<220>
<221> CDS
<222> (1)..(717)

<400> 124
atg agc aag ggc gag gaa ctg ttc act ggc gtg gtc cca att ctc gtg 48
Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
      1                      5                      10                      15

gaa ctg gat ggc gat gtg aat ggg cac aaa ttt tct gtc agc gga gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
      20                      25                      30

ggt gaa ggt gat gcc aca tac gga aag ctc acc ctg aaa ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
      35                      40                      45

acc act gga aag ctc cct gtg cca tgg cca aca ctg gtc act acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
      50                      55                      60

tct tat ggc gtg cag tgc ttt tcc aga tac cca gac cat atg aag cag 240
Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
      65                      70                      75                      80

cat gac ttt ttc aag agc gcc atg ccc gag ggc tat gtg cag gag aga 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
      85                      90                      95

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138

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acc atc ttt ttc aaa gat gac ggg aac tac aag acc cgc gct gaa gtc 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
      100                      105                      110

aag ttc gaa ggt gac acc ctg gtg aat aga atc gag ctg aag ggc att 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
      115                      120                      125

gac ttt aag gag gat gga aac att ctc ggc cac aag ctg gaa tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
      130                      135                      140

tat aac tcc cac aat gtg tac atc atg gcc gac aag caa aag aat ggc 480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
      145                      150                      155                      160

atc aag gtc aac ttc aag atc aga cac aac att gag gat gga tcc gtg 528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
      165                      170                      175

cag ctg gcc gac cat tat caa cag aac act cca atc ggc gac ggc cct 576
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
      180                      185                      190

gtg ctc ctc cca gac aac cat tac ctg tcc acc cag tct gcc ctg tct 624
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
      195                      200                      205

aaa gat ccc aac gaa aag aga gac cac atg gtc ctg ctg gag ttt gtg 672
Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
      210                      215                      220

acc gct gct ggg atc aca cat ggc atg gac gag ctg tac aag tga 717
Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
      225                      230                      235

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<210> 125

<211> 238

<212> PRT

<213> Artificial Sequence

<400> 125

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

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

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Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
      35                      40                      45

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Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
      50                      55                      60

```

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Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
      65                      70                      75                      80

```

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

```

139

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

<210> 126
 <211> 54
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ala(GCA)5
 primer

<400> 126
 cggggtacca tggcagcagc agcagcaagc aagggcgagg aactgttcac tggc 54

<210> 127
 <211> 54
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ala(GCC)5
 primer

<400> 127
 cggggtacca tggccgccgc cgccgccagc aagggcgagg aactgttcac tggc 54

<210> 128
 <211> 54
 <212> DNA
 <213> Artificial Sequence

140

<220>

<223> Description of Artificial Sequence: Ala(GCG)5
primer

<400> 128

cggggtacca tggcggcggc ggcggcgagc aagggcgagg aactgttcac tggc 54

<210> 129

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ala(GCT)5
primer

<400> 129

cggggtacca tggctgctgc tgctgctagc aagggcgagg aactgttcac tggc 54

<210> 130

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Arg(AGA)5
primer

<400> 130

cggggtacca tgagaagaag aagaagaagc aagggcgagg aactgttcac tggc 54

<210> 131

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Arg(AGG)5
primer

<400> 131

cggggtacca tgaggaggag gaggaggagc aagggcgagg aactgttcac tggc 54

<210> 132

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Arg(CGA)5
primer

<400> 132

cggggtacca tgcgacgacg acgacgaagc aagggcgagg aactgttcac tggc 54

141

<210> 133
 <211> 54
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Arg(CGC)5
 primer

<400> 133
 cggggtacca tgcgccgccg ccgccgcagc aagggcgagg aactgttcac tggc 54

<210> 134
 <211> 54
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Arg(CGG)5
 primer

<400> 134
 cggggtacca tgcggcgggc gcgccggagc aagggcgagg aactgttcac tggc 54

<210> 135
 <211> 54
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: arg(CGT)5
 primer

<400> 135
 cggggtacca tgcgtcgtcg tcgtcgtagc aagggcgagg aactgttcac tggc 54

<210> 136
 <211> 54
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Asn(AAC)5
 primer

<400> 136
 cggggtacca tgaacaacaa caacaacagc aagggcgagg aactgttcac tggc 54

<210> 137
 <211> 54
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Asn(AAT)5
 primer

142

<400> 137
cgggggtacca tgaataataa taataatagc aagggcgagg aactgttcac tggc 54

<210> 138
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Asp(GAC)5
primer

<400> 138
cgggggtacca tggacgacga cgacgacagc aagggcgagg aactgttcac tggc 54

<210> 139
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Asp(GAT)5
primer

<400> 139
cgggggtacca tggatgatga tgatgatagc aagggcgagg aactgttcac tggc 54

<210> 140
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Cys(TGC)5
primer

<400> 140
cgggggtacca tgtgctgctg ctgctgcagc aagggcgagg aactgttcac tggc 54

<210> 141
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Cys(TGT)5
primer

<400> 141
cgggggtacca tgtgttggtg ttgttgtagc aagggcgagg aactgttcac tggc 54

<210> 142
<211> 54
<212> DNA
<213> Artificial Sequence

143

<220>

<223> Description of Artificial Sequence: Gln(CAA)5
primer

<400> 142

cggggtacca tgcaacaaca acaacaaagc aagggcgagg aactgttcac tggc 54

<210> 143

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Gln(CAG)5
primer

<400> 143

cggggtacca tgcagcagca gcagcagagc aagggcgagg aactgttcac tggc 54

<210> 144

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Glu(GAA)5
primer

<400> 144

cggggtacca tggaagaaga agaagaaagc aagggcgagg aactgttcac tggc 54

<210> 145

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Glu(GAG)5
primer

<400> 145

cggggtacca tggaggagga ggaggagagc aagggcgagg aactgttcac tggc 54

<210> 146

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Gly(GGA)5
primer

<400> 146

cggggtacca tgggaggagg aggaggaagc aagggcgagg aactgttcac tggc 54

144

<210> 147
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Gly(GGC)5
primer

<400> 147
cggggtacca tgggcgggcgg cggcgggcagc aagggcgagg aactgttcac tggc 54

<210> 148
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Gly(GGG)5
primer

<400> 148
cggggtacca tgggggggggg ggggggggagc aagggcgagg aactgttcac tggc 54

<210> 149
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Gly(GGT)5
primer

<400> 149
cggggtacca tgggtggtgg tggtagtagc aagggcgagg aactgttcac tggc 54

<210> 150
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: His(CAC)5
primer

<400> 150
cggggtacca tgcaccacca ccaccacagc aagggcgagg aactgttcac tggc 54

<210> 151
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: His(CAT)5
primer

145

<400> 151
cgggggtacca tgcatacatca tcatacatagc aagggcgagg aactgttcac tggc 54

<210> 152
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ile(ATA)5
primer

<400> 152
cgggggtacca tgataataat aataataagc aagggcgagg aactgttcac tggc 54

<210> 153
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ile(ATC)5
primer

<400> 153
cgggggtacca tgatcatcat catcatcagc aagggcgagg aactgttcac tggc 54

<210> 154
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ile(ATT)5
primer

<400> 154
cgggggtacca tgattattat tattattagc aagggcgagg aactgttcac tggc 54

<210> 155
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Leu(CTA)5
primer

<400> 155
cgggggtacca tgctactact actactaagc aagggcgagg aactgttcac tggc 54

<210> 156
<211> 54
<212> DNA
<213> Artificial Sequence

146

<220>

<223> Description of Artificial Sequence: Leu(CTC)5
primer

<400> 156

cggggtacca tgctcctcct cctcctcagc aagggcgagg aactgttcac tggc 54

<210> 157

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Leu(CTG)5
primer

<400> 157

cggggtacca tgctgctgct gctgctgagc aagggcgagg aactgttcac tggc 54

<210> 158

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Leu(CTT)5
primer

<400> 158

cggggtacca tgcttcttct tcttcttagc aagggcgagg aactgttcac tggc 54

<210> 159

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Leu(TTA)5
primer

<400> 159

cggggtacca tgttattatt attattaagc aagggcgagg aactgttcac tggc 54

<210> 160

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Leu(TTG)5
primer

<400> 160

cggggtacca tgttgttggt gttgttgagc aagggcgagg aactgttcac tggc 54

147

<210> 161
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Lys(AAA)5
primer

<400> 161
cggggtacca tgaaaaaaaa aaaaaaaagc aagggcgagg aactgttcac tggc 54

<210> 162
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Lys(AAG)5
primer

<400> 162
cggggtacca tgaagaagaa gaagaagagc aagggcgagg aactgttcac tggc 54

<210> 163
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Phe(CTT)5
primer

<400> 163
cggggtacca tgcttcttct tcttcttagc aagggcgagg aactgttcac tggc 54

<210> 164
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Phe(TTC)5
primer

<400> 164
cggggtacca tgttcttctt cttcttcagc aagggcgagg aactgttcac tggc 54

<210> 165
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Pro(CCC)5
primer

<400> 165
cggggtacca tgcccccccc cccccccagc aagggcgagg aactgttcac tggc 54

<210> 166
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<210> 183
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<220>
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primer

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<210> 184
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<223> Description of Artificial Sequence: Val(GTT)5
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oligonucleotide common primer

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ccggaattct cacttgtaca ggtggtccat gcc 33

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CLAIMS:

1. A synthetic construct comprising a regulatory polynucleotide that is operable in a eukaryotic cell and that is operably linked to a tandem repeat of a codon fused in
5 frame with a reporter polynucleotide that encodes a reporter protein.
2. The construct of claim 1, wherein the tandem repeat comprises at least three copies of the codon.
3. The construct of claim 2, wherein the tandem repeat
10 comprises five copies of the codon.
4. The construct of claim 2, wherein the tandem repeat comprises six copies of the codon.
5. The construct of claim 2, wherein the tandem repeat comprises seven copies of the codon.
- 15 6. The construct of claim 1, wherein the tandem repeat is fused at a location adjacent to, or within, the reporter polynucleotide.
7. The construct of claim 6, wherein the tandem repeat is fused immediately upstream of the reporter polynucleotide.
- 20 8. The construct of claim 1, wherein at least one spacer codon is located adjacent to a tandemly repeated codon.
9. The construct of claim 1, wherein at least one spacer codon is interposed between a pair of tandemly
25 repeated codons.
10. The construct of claim 8 or claim 9, wherein the spacer codon is a neutral amino acid.

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11. The construct of claim 8 or claim 9, wherein the spacer codon is alanine or glycine.

12. The construct of claim 7, wherein the reporter protein is β -galactosidase, firefly luciferase, alkaline
5 phosphatase, chloramphenicol acetyl transferase, β -glucuronidase, green fluorescence protein, or an active portion thereof.

13. The construct of claim 1, wherein the reporter protein is encoded by a bialophos resistance gene that
10 confers resistance to a herbicide containing the active ingredient glufosinate-ammonium.

14. The construct of claim 1, wherein the reporter protein is green fluorescence protein or an active portion thereof.

15 15. A plurality of synthetic constructs for determining the translational efficiencies of different codons, each construct comprising a regulatory polynucleotide that is operable in a eukaryotic cell and that is operably linked to a tandem repeat of a codon fused in frame with a reporter
20 polynucleotide that encodes a reporter protein, wherein the tandemly repeated codon of a first construct is different to the tandemly repeated codon of a second construct.

16. The plurality of synthetic constructs of claim 15, wherein the tandemly repeated codons of the first and second
25 constructs encode the same amino acid.

17. The plurality of synthetic constructs of claim 15, wherein the tandemly repeated codons of the first and second constructs encode different amino acids.

18. The plurality of synthetic constructs of claim 16, comprising a set of synthetic constructs, the number of
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synthetic constructs of the set being equal to the number of synonymous codons that encode a first amino acid, wherein the tandemly repeat codon of each synthetic construct of the set is a synonymous codon that encodes the first amino acid and
5 wherein different synthetic constructs of the set comprise different tandemly repeated codons.

19. The plurality of synthetic constructs of claim 16, comprising a first set of synthetic constructs and a second set of synthetic constructs, the number of synthetic
10 constructs of the first set being equal to the number of synonymous codons that encode a first amino acid, the number of synthetic constructs of the second set being equal to the number of synonymous codons that encode a second amino acid, wherein the tandemly repeated codon of each synthetic
15 construct of the first set is a synonymous codon that encodes the first amino acid, wherein the tandemly repeated codon of each synthetic construct of the second set is a synonymous codon that encodes the second amino acid and wherein different synthetic constructs of the first or second sets
20 comprise different tandemly repeated codons.

20. The plurality of synthetic constructs of claim 15, wherein the tandem repeat of each of the synthetic constructs comprises at least three copies of the corresponding codon.

21. The plurality of synthetic constructs of claim 20,
25 wherein the tandem repeat of each of the synthetic constructs comprises five copies of the corresponding codon.

22. The plurality of synthetic constructs of claim 20, wherein the tandem repeat of each of the synthetic constructs comprises six copies of the corresponding codon.

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23. The plurality of synthetic constructs of claim 20, wherein the tandem repeat of each of the synthetic constructs comprises seven copies of the corresponding codon.

24. The plurality of synthetic constructs of claim 15,
5 wherein the tandem repeat is fused at a location adjacent to, or within, the reporter polynucleotide.

25. The plurality of synthetic constructs of claim 24, wherein the tandem repeat is fused immediately upstream of the reporter polynucleotide.

10 26. The plurality of synthetic constructs of claim 15, wherein at least one spacer codon is located adjacent to a tandemly repeated codon.

27. The plurality of synthetic constructs of claim 15, wherein at least one spacer codon is interposed between a
15 pair of tandemly repeated codons.

28. The plurality of synthetic constructs of claim 26 or claim 27, wherein the spacer codon is a neutral amino acid.

29. The plurality of synthetic constructs of claim 26
20 or claim 27, wherein the spacer codon is alanine or glycine.

30. The plurality of synthetic constructs of claim 15, wherein the reporter protein is β -galactosidase, firefly luciferase, alkaline phosphatase, chloramphenicol acetyl transferase, β -glucuronidase, green fluorescence protein, or
25 an active portion thereof.

31. The plurality of synthetic constructs of claim 15, wherein the reporter protein is encoded by a bialophos resistance gene that confers resistance to a herbicide containing the active ingredient glufosinate-ammonium.

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32. The plurality of synthetic constructs of claim 15, wherein the reporter protein is green fluorescence protein or an active portion thereof.

33. A vector comprising the synthetic construct of any
5 one of claims 1 to 14.

34. A cell *in vitro* comprising the synthetic construct of any one of claims 1 to 14.

35. A cell *in vitro* comprising the vector of claim 33.

36. A method for determining the translational
10 efficiency of a codon in a cell, the method comprising:

- introducing into the cell *in vitro* the synthetic construct according to any one of claims 1 to 14; and

- measuring expression of the reporter protein in the cell to determine the translational efficiency of the
15 codon.

37. The method of claim 36, further comprising comparing in cells of the same type:

- expression of the reporter protein in a cell to which a synthetic construct comprising a tandem repeat of a
20 first codon was provided; and

- expression of the reporter protein in a cell to which a synthetic construct comprising a tandem repeat of a second codon was provided;

to thereby determine the translational efficiency of the
25 first codon relative to the second codon in the cells.

38. The method of claim 36, further comprising comparing:

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- expression of the reporter protein in a first cell type to which a synthetic construct comprising a tandem repeat of a first codon was provided; and

- expression of the reporter protein in a second
5 cell type to which a synthetic construct comprising a tandem repeat of the first codon was provided;

to thereby determine the translational efficiency of the first codon in the first cell type relative to the second cell type.

10 39. The method of claim 36, further comprising:

- introducing the synthetic construct into a progenitor of the cell; and

- producing the cell from the progenitor;

wherein the cell contains the synthetic construct.

15 40. The method of claim 36, further comprising:

- introducing the synthetic construct into a progenitor of the cell; and

- growing a non-human organism or part thereof from the progenitor;

20 wherein the organism comprises the cell containing the synthetic construct.

41. A method of constructing a synthetic polynucleotide, the method comprising:

- selecting a first codon of a parent
25 polynucleotide that encodes a polypeptide for replacement with a synonymous codon, wherein the synonymous codon is

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selected on the basis that it exhibits a higher translational efficiency in a first cell of an organism than in a second cell of the organism; and

- replacing the first codon with the synonymous
5 codon to construct the synthetic polynucleotide,

wherein the first codon and the synonymous codon are selected on the basis of a comparison of translational efficiencies in cells of the same type as the first cell and in cells of the same type as the second cell, wherein the
10 translational efficiencies are compared by:

- separately introducing into cells of a specific type *in vitro* individual synthetic constructs according to any one of claims 1 to 14, each comprising a different tandemly repeated codon than the tandemly repeated codon of
15 other constructs;

- comparing expression of the reporter protein in the cells to determine the relative translational efficiencies of the codons.

42. The method of claim 41, wherein the synonymous
20 codon is selected on the basis that it corresponds to a tandemly repeated codon in a synthetic construct from which the reporter protein is expressed in the first cell at a level that is at least 110% of the level at which it is expressed from the same synthetic construct in the second
25 cell.

43. A method of constructing a synthetic polynucleotide, the method comprising:

- selecting a first codon of a parent polynucleotide that encodes a polypeptide for replacement
30 with a synonymous codon, wherein the synonymous codon is

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selected on the basis that it exhibits a higher translational efficiency in a first cell than the first codon in a comparison of translational efficiencies in cells of the same type as the first cell; and

5 - replacing the first codon with the synonymous codon to construct the synthetic polynucleotide,

 wherein the translational efficiencies in the cells are compared by:

 - separately introducing into the cells *in vitro*
10 individual synthetic constructs according to any one of claims 1 to 14, each comprising a different tandemly repeated codon than the tandemly repeated codon of other constructs;

 - comparing expression of the reporter protein in the cells to determine the relative translational
15 efficiencies of the codons.

44. The method of claim 43, wherein the reporter protein is expressed from the synthetic construct comprising a tandem repeat of the synonymous codon at a level that is at least 110% of the level at which it is expressed from the
20 synthetic construct comprising a tandem repeat of the first codon.

45. The method of any one of claims 41 to 44, wherein the synthetic constructs are introduced into the cells by:

 - introducing the individual synthetic constructs
25 into progenitors of the cells; and

 - producing the cells from the progenitors;

wherein the cells contain the synthetic constructs.