US 20180201656A1

(19) **United States**

(12) **Patent Application Publication**

Møller et al.

(10) **Pub. No.: US 2018/0201656 A1**

(43) **Pub. Date: Jul. 19, 2018**

(54) **PROTEINS AND NUCLEIC ACIDS USEFUL IN VACCINES TARGETING PSEUDOMONAS AERUGINOSA**

(71) Applicant: **Evaxion Biotech ApS**, Copenhagen K (DK)

(72) Inventors: **Niels Iversen Møller**, Vedbæk (DK); **Andreas Holm Mattsson**, København N (DK)

(21) Appl. No.: **15/741,881**

(22) PCT Filed: **Jul. 4, 2016**

(86) PCT No.: **PCT/EP2016/065647**

§ 371 (c)(1),
(2) Date: **Jan. 4, 2018**

(30) **Foreign Application Priority Data**

Jul. 4, 2015 (EP) 15175365.4

Publication Classification

(51) **Int. Cl.**

C07K 14/21	(2006.01)
A61K 47/64	(2006.01)
A61K 39/104	(2006.01)
A61P 31/04	(2006.01)
C07K 16/12	(2006.01)

(52) **U.S. Cl.**

CPC ***C07K 14/21*** (2013.01); ***A61K 47/646*** (2017.08); ***A61K 47/643*** (2017.08); *A61K 2039/575* (2013.01); ***A61K 39/104*** (2013.01); ***A61P 31/04*** (2018.01); ***C07K 16/1214*** (2013.01); ***A61K 47/6415*** (2017.08)

(57) **ABSTRACT**

Disclosed are immunogenic proteins from *Pseudomonas aeruginosa* as well as nucleic acids, vectors and transformed cells useful for expression of the proteins. Also disclosed are methods for prophylaxis of infection with *Pseudomonas aeruginosa* using the proteins, nucleic acids, vectors or transformed cells.

Fig. 1

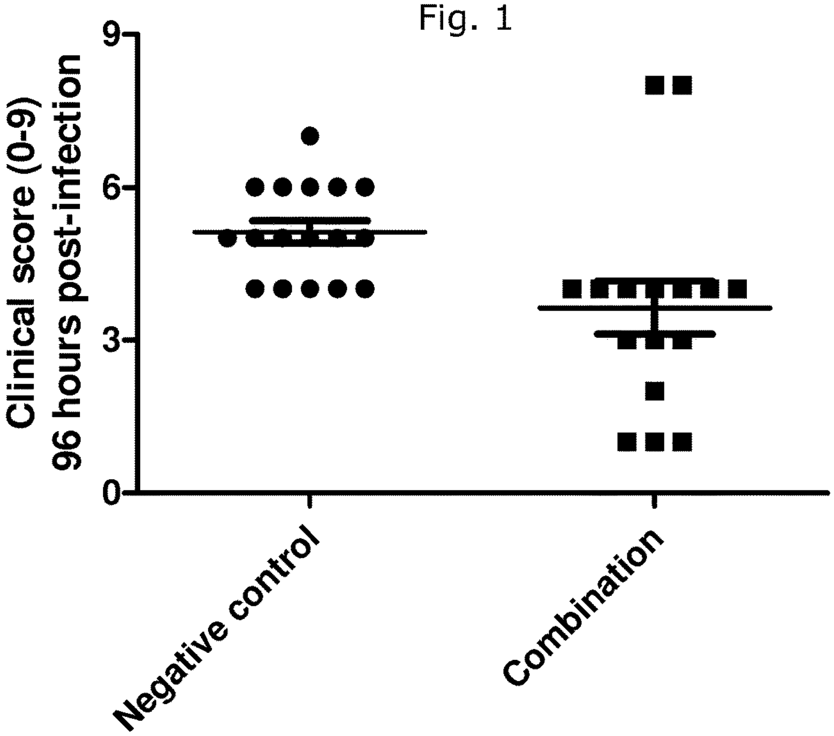

Clinical score (0-9)
96 hours post-infection
9
6
3
0
Negative control
Combination

Fig. 2

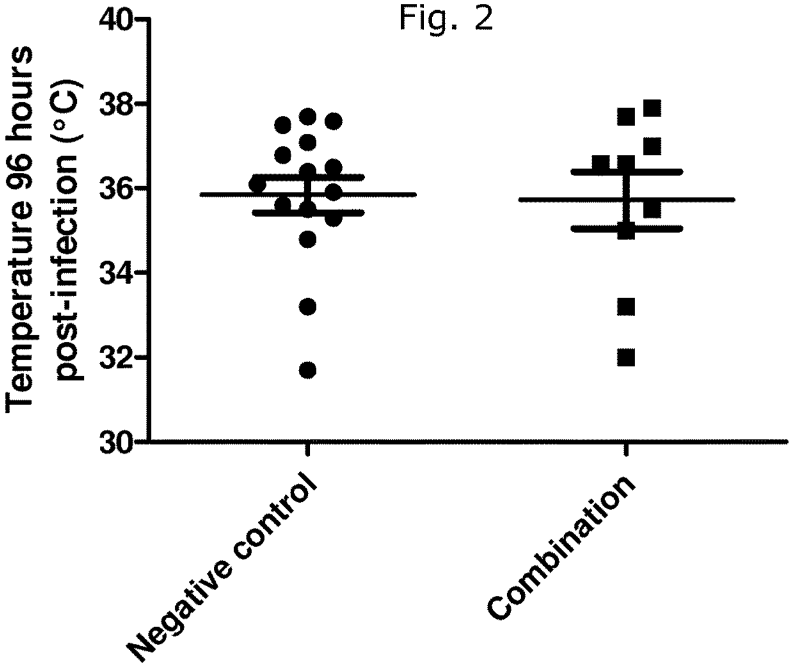

Temperature 96 hours
post-infection (°C)
40
38
36
34
32
30
Negative control
Combination

Fig. 3

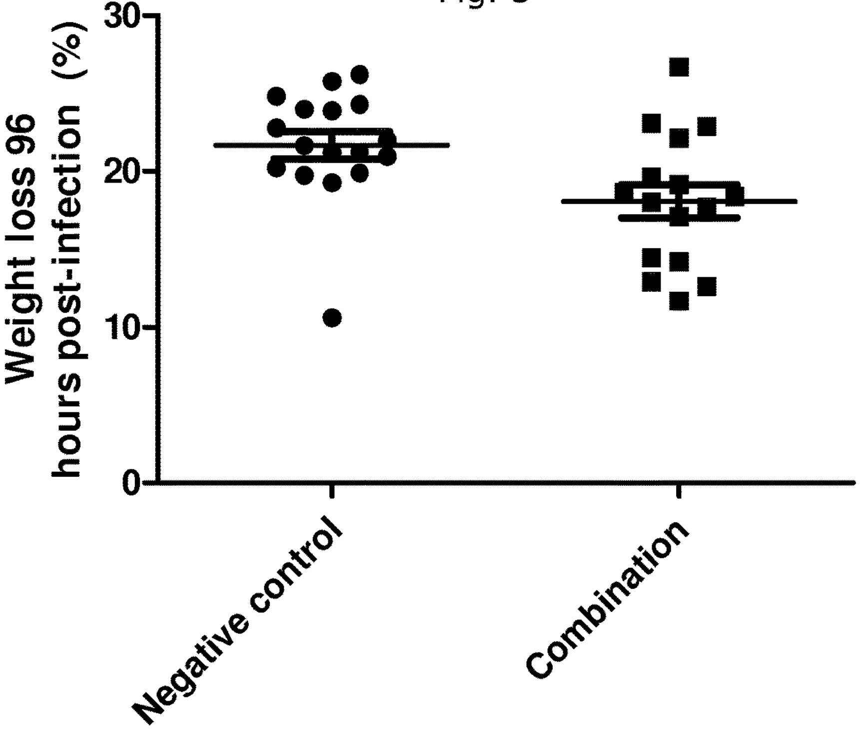

Weight loss 96 hours post-infection (%)
30
20
10
0
Negative control
Combination

Fig. 4

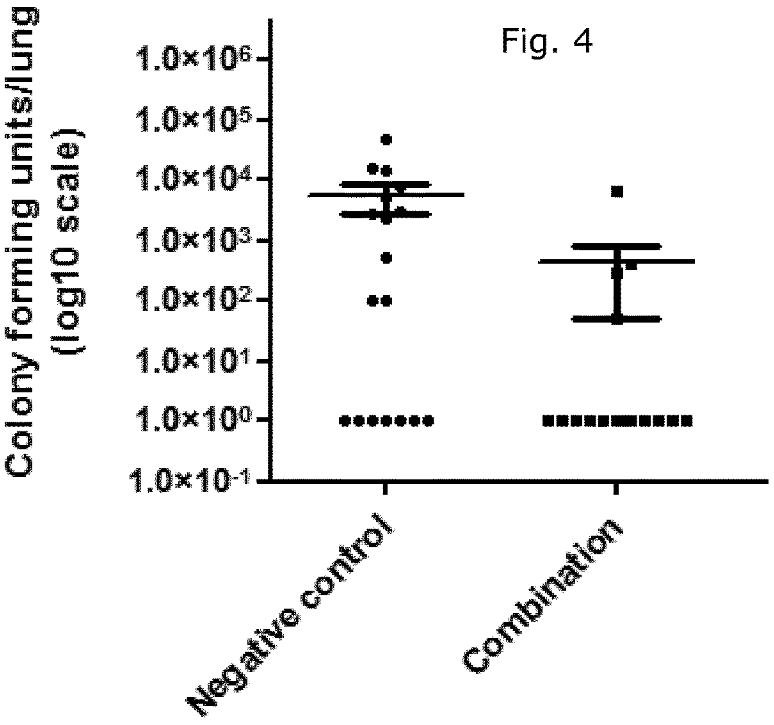

Colony forming units/lung (log10 scale)
1.0×10⁶
1.0×10⁵
1.0×10⁴
1.0×10³
1.0×10²
1.0×10¹
1.0×10⁰
1.0×10⁻¹
Negative control
Combination

Fig. 5

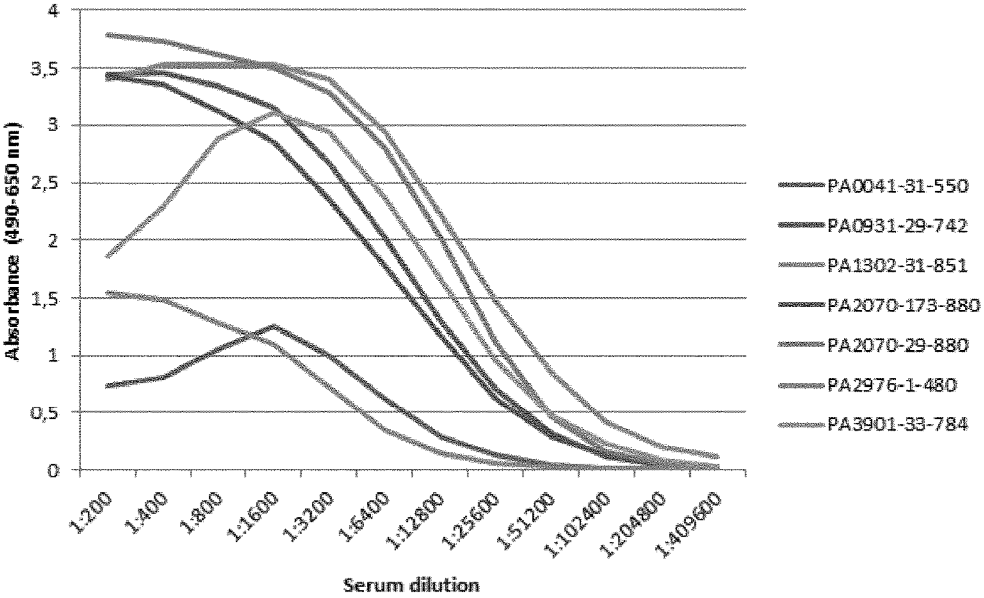

4
3,5
3
2,5
2
1,5
1
0,5
0
Absorbance (490-650 nm)
1:200
1:400
1:800
1:1600
1:3200
1:6400
1:12800
1:25600
1:51200
1:102400
1:204800
1:409600
Serum dilution
PA0041-31-550
PA0931-29-742
PA1302-31-851
PA2070-173-880
PA2070-29-880
PA2976-1-480
PA3901-33-784

Fig. 6

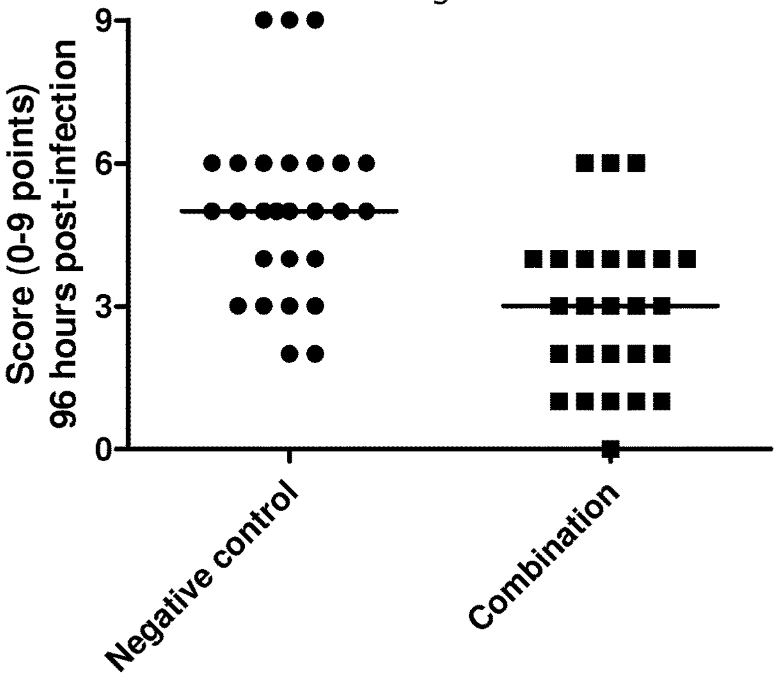

9
6
3
0
Score (0-9 points)
96 hours post-infection
Negative control
Combination

Fig. 7

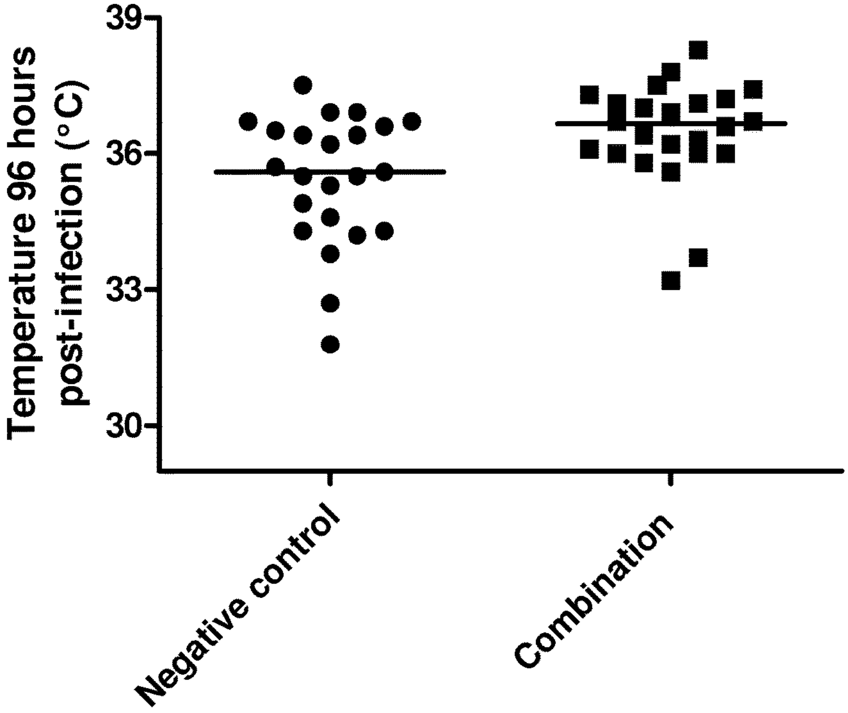

39
36
33
30
Temperature 96 hours post-infection (°C)
Negative control
Combination

Fig. 8

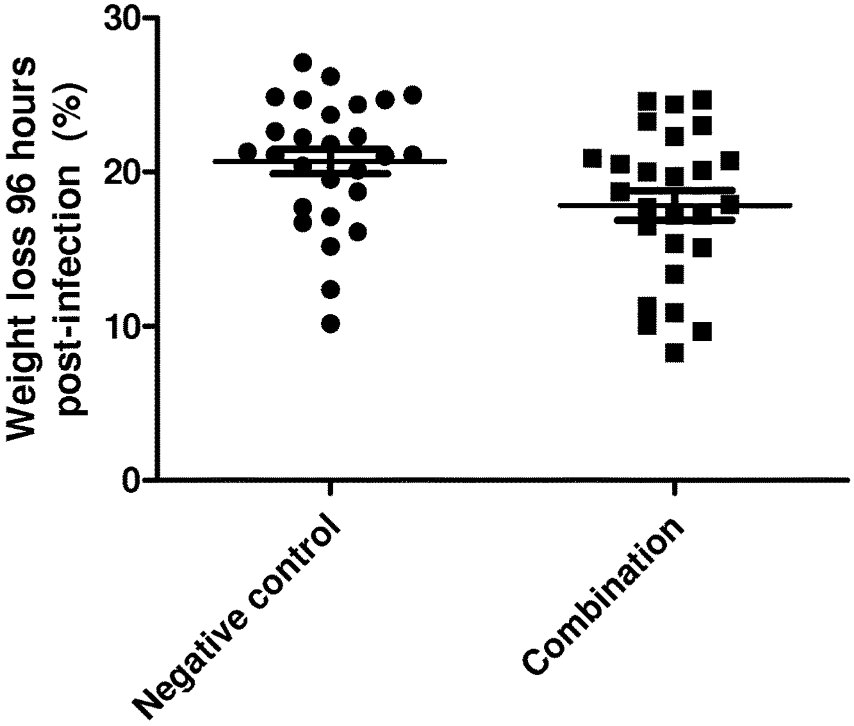

30
20
10
0
Weight loss 96 hours post-infection (%)
Negative control
Combination

Fig. 9

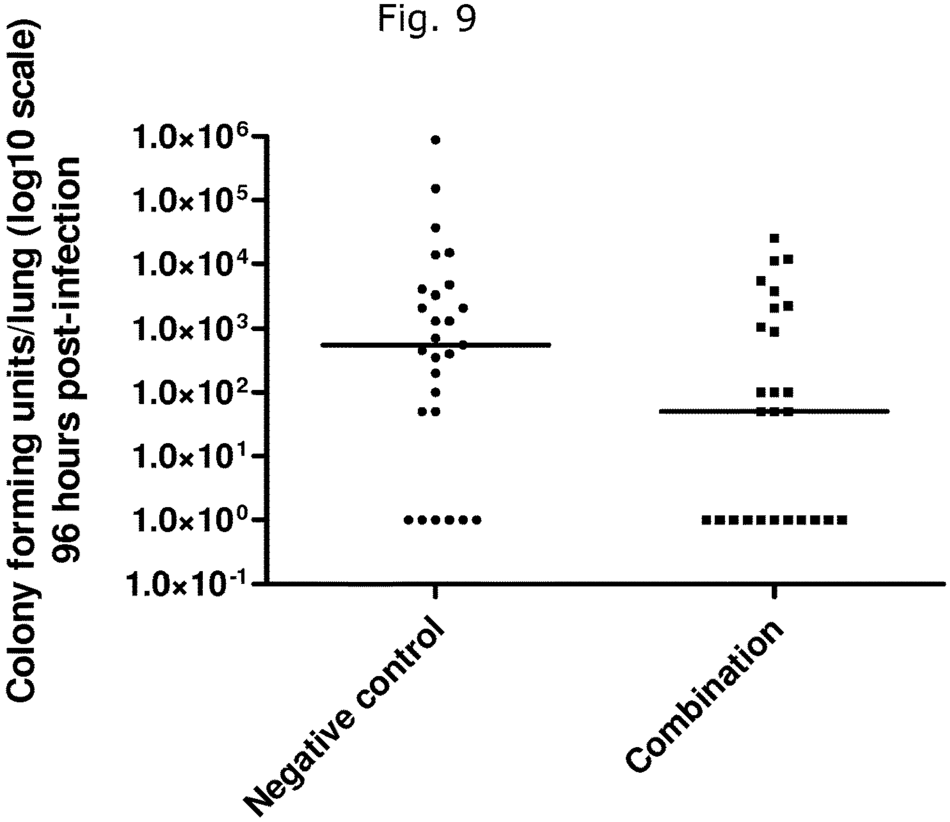

Colony forming units/lung (log10 scale)
96 hours post-infection
1.0×10⁶
1.0×10⁵
1.0×10⁴
1.0×10³
1.0×10²
1.0×10¹
1.0×10⁰
1.0×10⁻¹
Negative control
Combination

Fig. 10

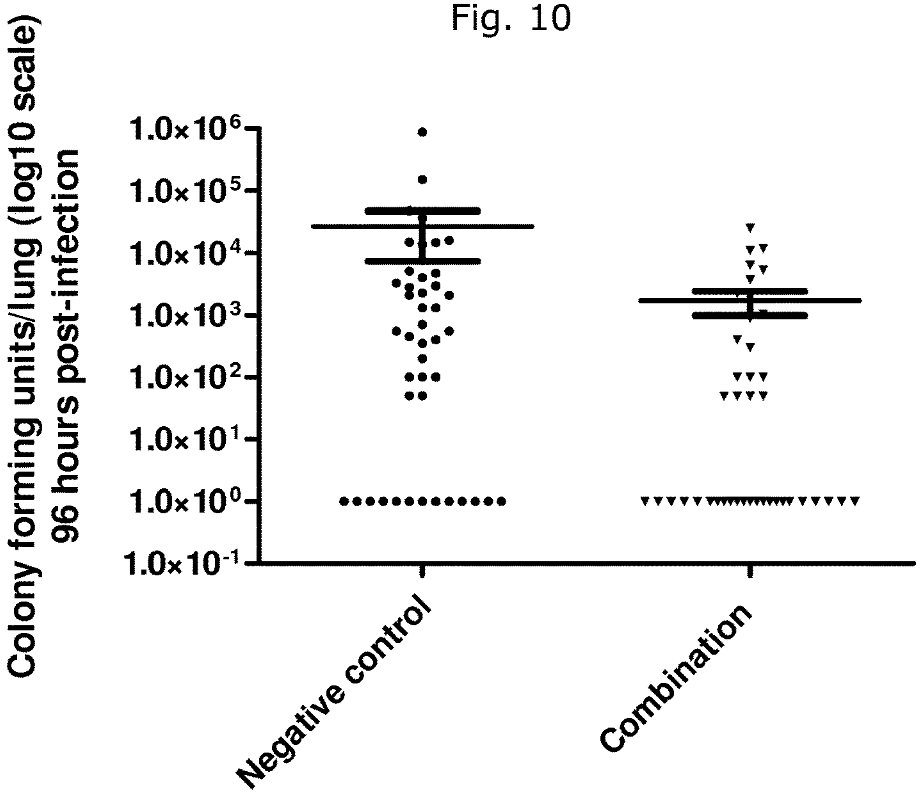
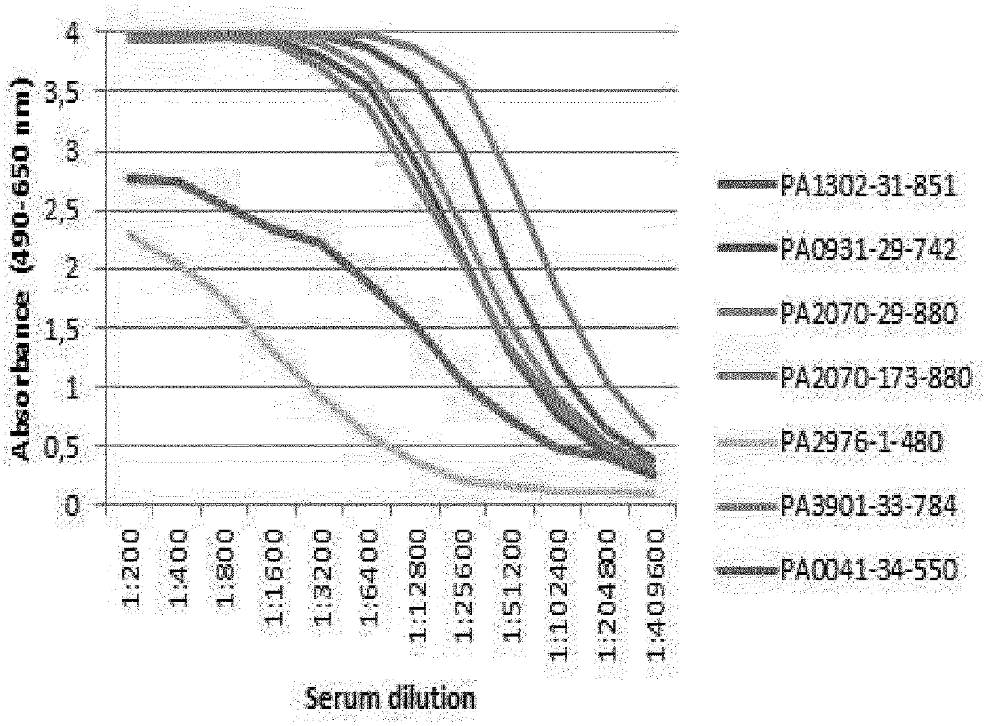

Colony forming units/lung (log10 scale)
96 hours post-infection
1.0×10⁶
1.0×10⁵
1.0×10⁴
1.0×10³
1.0×10²
1.0×10¹
1.0×10⁰
1.0×10⁻¹
Negative control
Combination

Fig. 11


4
3,5
3
2,5
2
1,5
1
0,5
0
Absorbance (490-650 nm)
1:200
1:400
1:800
1:1600
1:3200
1:6400
1:12800
1:25600
1:51200
1:102400
1:204800
1:409600
Serum dilution
PA1302-31-851
PA0931-29-742
PA2070-29-880
PA2070-173-880
PA2976-1-480
PA3901-33-784
PA0041-34-550

PROTEINS AND NUCLEIC ACIDS USEFUL IN VACCINES TARGETING PSEUDOMONAS AERUGINOSA

FIELD OF THE INVENTION

[0001] The present invention relates to the field of anti-microbial prophylaxis and therapy. In particular the present invention relates to novel proteins and polynucleotides derived from *Pseudomonoas aeruginosa*. The invention further relates to vectors comprising the polynucleotides, transformed host organisms expressing the polynucleotides, antibodies (mono- or polyclonal) specific for the polypeptides as well as diagnostic, prophylactic and therapeutic uses and methods. Finally, also methods of preparation are part of the invention.

BACKGROUND OF THE INVENTION

[0002] *Pseudomonas aeruginosa* is an opportunistic gram-negative pathogen. It represents a major course of hospital-aquired infections, especially in burnt and other immuno-compromised patients, including transplant or cancer patients. Therefore, it is regarded as a "problem microbe" in human medicine.

[0003] Many efforts have been made so far in order to develop a vaccine against *Pseudomonas aeruginosa*. For example, in the EP-0 297 291 the complete amino acid-sequence of the outer membrane protein F, as well as the nucleotide sequence coding for OprF is disclosed. In the EP-0 357 024 the complete amino acid sequence of the outer membrane protein I and, additionally, the nucleotide sequence coding for Oprl is shown. Furthermore, with both proteins it was shown that they may be useful for conferring immunoprotection against *Pseudomonas aeruginosa* to an animal or human proband. However, improvement of procedures of vaccination against and treatment of a lethal *Pseudomonas aeruginosa* infection is still an object.

[0004] Vaccination is considered to be a very effective method of preventing infectious diseases in human and veterinary health care. Vaccination is the administration of immungenically effective amounts of antigenic material (the vaccine) to produce immunity to a disease/disease-causing pathogenic agent. Vaccines have contributed to the eradication of smallpox, the near eradication of polio, and the control of a variety of diseases, including rubella, measles, mumps, chickenpox, typhoid fever.

[0005] Before "the genomic era", vaccines were based on killed or live attenuated, microorganisms, or parts purified from them. Subunit vaccines are considered as a modern upgrade of these types of vaccine, as the subunit vaccines contain one or more protective antigens, which are more or less the weak spot of the pathogen. Hence, in order to develop subunit vaccines, it is critical to identify the proteins, which are important for inducing protection and to eliminate others.

[0006] An antigen is said to be protective if it is able to induce protection from subsequent challenge by a disease-causing infectious agent in an appropriate animal model following immunization.

[0007] The empirical approach to subunit vaccine development, which includes several steps, begins with pathogen cultivation, followed by purification into components, and then testing of antigens for protection. Apart from being time and labour consuming, this approach has several limitations that can lead to failure. It is not possible to develop vaccines using this approach for microorganisms, which cannot easily be cultured and only allows for the identification of the antigens, which can be obtained in sufficient quantities. The empirical approach has a tendency to focus on the most abundant proteins, which in some cases are not immuno-protective. In other cases, the antigen expressed during in vivo infection is not expressed during in vitro cultivation. Furthermore, antigen discovery by use of the empirical approach demands an extreme amount of proteins in order to discover the protective antigens, which are like finding needles in the haystack. This renders it a very expensive approach, and it limits the vaccine development around diseases, which is caused by pathogens with a large genome or disease areas, which perform badly in a cost-effective perspective.

OBJECT OF THE INVENTION

[0008] It is an object of embodiments of the invention to provide *Pseudomonas aeruginosa* derived antigenic polypeptides that may serve as constituents in vaccines against *Pseudomonas aeruginosa* infections and in diagnosis of *Pseudomonas aeruginosa* infections. It is also an object to provide nucleic acids, vectors, transformed cells, vaccine compositions, and other useful means for molecular cloning as well as for therapy and diagnosis with relevance for *Pseudomonas aeruginosa*.

SUMMARY OF THE INVENTION

[0009] It has been found by the present inventor(s) that *Pseudomonas aeruginosa* expresses a number of hitherto unknown putatively surface exposed proteins which are candidates as vaccine targets as well as candidates as immunizing agents for preparation of antibodies that target *Pseudomonas aeruginosa*.

[0010] So, in a first aspect the present invention relates to a polypeptide comprising

a) an amino acid sequence selected from the group consisting of any one of SEQ ID NOs: 1-30, or

b) an amino acid sequence consisting of at least 5 contiguous amino acid residues from any one of SEQ ID NOs: 1-30, or

c) an amino acid sequence having a sequence identity of at least 60% with the amino acid sequence of a),

d) an amino acid sequence having a sequence identity of at least 60% with the amino acid sequence of b), or

e) an assembly of amino acids derived from any one of SEQ ID NOs: 1-30 which has essentially the same 3D conformation as in the protein from whicht said assembly is derived so as to constitute a B-cell epitope, said polypeptide being antigenic in a mammal.

[0011] In another aspect, the invention relates to an isolated nucleic acid fragment, which comprises

i) a nucleotide sequence encoding a polypeptide of the invention, or

ii) a nucleotide sequence consisting of any one of SEQ ID NOs: 31-90.

iii) a nucleotide sequence consisting of at least 10 consecutive nucleotides in any one of SEQ ID NOs: 31-90,

iv) a nucleotide sequence having a sequence identity of at least 60% with the nucleotide sequence in i) or ii),

v) a nucleotide sequence having a sequence identity of at least 60% with the nucleotide sequence in iii),

vi) a nucleotide sequence complementary to the nucleotide sequence in i)-v), or

vii) a nucleotide sequence which hybridizes under stringent conditions with the nucleotide sequence in i)-vi).

[0012] In a third aspect, the invention relates to a vector comprising the nucleic acid of the invention, such as a cloning vector or an expression vector.

[0013] In fourth aspect, the invention relates to a cell which is transformed so as to carry the vector of the invention.

[0014] In a fifth aspect, the invention relates to a pharmaceutical composition comprising a polypeptide of the invention, a nucleic acid fragment of the invention, a vector of the invention, or a transformed cell of the invention, and a pharmaceutically acceptable carrier, vehicle or diluent.

[0015] In a sixth aspect, the invention relates to a method for inducing immunity in an animal by administering at least once an immunogenically effective amount of a polypeptide of the invention, a nucleic acid fragment of the invention, a vector of the invention, a transformed cell of the invention, or a pharmaceutical composition of the fifth aspect of the invention so as to induce adaptive immunity against *Pseudomonas aeruginosa* in the animal.

[0016] In a seventh and eighth aspect, the invention relatas to 1) a polyclonal antibody in which the antibodies specifically bind to at least one polypeptide of the invention, and which is essentially free from antibodies binding specifically to other *Pseudomonas aeruginosa* polypeptides, and to 2) an isolated monoclonal antibody or antibody analogue which binds specifically to a polypeptide of the invention. In a related ninth aspect, the invention relates to a pharmaceutical composition comprising such a polyclonal or monoclona antibody and a pharmaceutically acceptable carrier, vehicle or diluent.

[0017] In a 10th aspect, the invention relates to a method for prophylaxis, treatment or amelioration of infection with *Pseudomonas aeruginosa*, comprising administering a therapeutically effective amount of an antibody of the 7th or 8th aspect of the invention or a pharmaceutical composition of the eighth aspect to an individual in need thereof.

[0018] In an 11th aspect, the invention relates to a method for determining, quantitatively or qualitatively, the presence of *Pseudomonas aeruginosa*, in a sample, the method comprising contacting the sample with an antibody of aspects 8 or 9 of the invention and detecting the presence of antibody bound to material in the sample.

[0019] In an 12th aspect of the invention is provided a method for determining, quantitatively or qualitatively, the presence of antibodies specific for *Pseudomonas aeruginosa* in a sample, the method comprising contacting the sample with a polypeptide of the invention and detecting the presence of antibody that specifically bind said polypeptide.

[0020] In a 13th aspect, the invention relates to a method for determining, quantitatively or qualitatively, the presence of a nucleic acid characteristic of *Pseudomonas aeruginosa*, in particular the presence of a nucleic acid characteristic of *Pseudomonas aeruginosa*, in a sample, the method comprising contacting the sample with a nucleic acid fragment of the invention and detecting the presence of nucleic acid in the sample that hybridizes to said nucleic acid fragment.

[0021] In a 14th aspect, the invention relates to a method for the preparation of the polypeptide of the invention, comprising

[0022] culturing a transformed cell of the present invention, which is capable of expressing the nucleic acid of the invention, under condiditions that facilitate that the transformed cell expresses the nucleic acid fragment of the invention, which encodes a polypeptide of the invention, and subsequently recovering said polypeptide, or

[0023] preparing said polypeptide by means of solid or liquid phase peptide synthesis.

[0024] In a 15th aspect, the invention relates to a method for determining whether a substance, such as an antibody, is potentially useful for treating infection with *Pseudomonas aeruginosa*, the method comprising contacting the polypeptide of the invention with the substance and subsequently establishing whether the substance has at least one of the following characteristics:

1) the ability to bind specifically to said polypeptide,

2) the ability to compeed with said polypeptide for specific binding to a ligand/receptor, and 3) the ability to specifically inactivate said polypeptide.

[0025] Finally, in a 16th aspect, the invention relates to a method for determining whether a substance, such as a nucleic acid, is potentially useful for treating infection with *Pseudomonas aeruginosa*, the method comprising contacting the substance with the nucleic acid fragment of claim of the invention and subsequently establishing whether the substance has either the ability to

1) bind specifically to the nucleic acid fragment, or

2) bind specifically to a nucleic acid that hybridizes specifically with the nucleic acid fragment.

LEGENDS TO THE FIGURE

[0026] FIG. **1**. Graph of clinical score four days post-infection, Example 1.

[0027] Mice immunized with the 7-valent combination vaccine had a significantly lower clinical score 96 hours post-infection compared to the control group immunized with adjuvant. The data were analysed using Student's t-test, P=0.0109.

[0028] FIG. **2**. Graph of body temperature four days post-infection, Example 1.

[0029] Comparison of body temperature, measured in the two groups of mice four days post-infection, showed that there was no significant difference in body temperature. The data were analyzed using the Mann Whitney test, P=0.8814.

[0030] FIG. **3**. Weight loss 96 hours post-infection, Example 1.

[0031] The group of mice immunized with the 7-valent combination vaccine had a significantly smaller weight loss than the control group. The data were analyzed using the Mann Whitney test, P=0.0081.

[0032] FIG. **4**. Lung bacteriology, Example 1.

[0033] The number of colony forming units was significantly smaller in lung homogenates from mice immunized with the 7-valent combination vaccine compared to the control group. Note that in this figure the CFU values equaled 0 are altered to 1, this is purely for illustrative purposes as a value of 0 cannot be shown on a logarithmic scale. The CFU data are given in appendix 4. The data were analyzed using the Mann Whitney test, P=0.0176.

[0034] FIG. **5**. Mean antibody responses to the seven antigens tested in Example 1.

[0035] The Y-axis represents the absorbance measured at 490 nm-650 nm (reference), and the X-axis shows the serum dilution. In general, the antibody response to five of the seven antigens was high, while the antibody response to PA2976-1-480 and PA0041-34-550 was quite low.

[0036] FIG. **6**. Clinical score four days post-infection, Example 2.

[0037] The mice immunized with the 7-valent combination vaccine had a significantly lower clinical score 96 hours post-infection compared to the control group immunized with adjuvant. The data were analysed using a two-tailed t-test, $P<0.0001$.

[0038] FIG. **7**. Body temperature four days post-infection, Example 2.

[0039] Comparison of body temperature, measured in the two groups of mice four days post-infection, showed that mice immunized with the 7-valent combination vaccine had a significantly higher body temperature compared to controls. The data were analyzed using the Mann Whitney test, $P=0.0085$.

[0040] FIG. **8**. Weight loss 96 hours post-infection, Example 2.

[0041] The group of mice immunized with the 7-valent combination vaccine had a significantly smaller weight loss than the control group. The data were analyzed using a two-tailed t-test, $P=0.0262$.

[0042] FIG. **4**. Lung bacteriology, Example 2.

[0043] There was no significant difference when comparing CFU in lung homogenates from mice immunized with the 7-valent combination vaccine and the control group. Note that in this figure the CFU values equaled 0 are altered to 1, this is purely for illustrative purposes as a value of 0 cannot be shown on a logarithmic scale. The CFU data are given in appendix 4. The data were analyzed using the Mann Whitney test, $P=0.0888$. In relation to this note that the high number of animals having complete clearance complicates statistical test of bacterial load, hence no significant p-value<0.05. However, a higher number of animals in the vaccinated group (11/26) experienced total clearance of bacteria in the kidneys compared to control (6/27).

[0044] FIG. **10**. Lung bacteriology—combined results from Examples 1 and 2.

[0045] When pooling the CFU results obtained in ER_0039 and ER_0040, two completely identical experiments, the mice immunized with the 7-valent vaccine exhibit a significantly lower lung CFU compared to controls. Note that in this figure, the CFU values equaled 0 are altered to 1, this is purely for illustrative purposes as a value of 0 cannot be shown on a logarithmic scale. The data were analyzed using the Mann Whitney test, $P=0.0044$.

[0046] FIG. **11**. Mean antibody responses to the seven antigens. The Y-axis represents the absorbance measured at 490 nm-650 nm (reference), and the X-axis shows the serum dilution. In general, the antibody responses to five of the seven antigens were high, while the antibody responses to PA2976-1-480 and PA0041-34-550 were quite low.

DETAILED DISCLOSURE OF THE INVENTION

Definitions

[0047] The term "polypeptide" is in the present context intended to mean both short peptides of from 2 to 10 amino acid residues, oligopeptides of from 11 to 100 amino acid residues, and polypeptides of more than 100 amino acid residues. Further-more, the term is also intended to include proteins, i.e. functional biomolecules comprising at least one polypeptide; when comprising at least two polypeptides, these may form complexes, be covalently linked, or may be non-covalently linked. The polypeptide (s) in a protein can be glycosylated and/or lipidated and/or comprise prosthetic groups.

[0048] The term "subsequence" means any consecutive stretch of at least 3 amino acids or, when relevant, of at least 3 nucleotides, derived directly from a naturally occurring amino acid sequence or nucleic acid sequence, respectively

[0049] The term "amino acid sequence" s the order in which amino acid residues, connected by peptide bonds, lie in the chain in peptides and proteins.

[0050] The term "adjuvant" has its usual meaning in the art of vaccine technology, i.e. a substance or a composition of matter which is 1) not in itself capable of mounting a specific immune response against the immunogen of the vaccine, but which is 2) nevertheless capable of enhancing the immune response against the immunogen. Or, in other words, vaccination with the adjuvant alone does not provide an immune response against the immunogen, vaccination with the immunogen may or may not give rise to an immune response against the immunogen, but the combined vaccination with immunogen and adjuvant induces an immune response against the immunogen which is stronger than that induced by the immunogen alone.

[0051] "Sequence identity" is in the context of the present invention determined by comparing 2 optimally aligned sequences of equal length (e.g. DNA, RNA or amino acid) according to the following formula: $(N_{ref}-N_{dif})\cdot 100/N_{ref}$, wherein N_{ref} is the number of residues in one of the 2 sequences and N_{dif} is the number of residues which are non-identical in the two sequences when they are aligned over their entire lengths and in the same direction. So, two sequences 5'-ATTCGGAAC-3' and 5'-ATACGGGAC-3' will provide the sequence identity 77.8% ($N_{ref}=9$ and $N_{dif}=2$). It will be understood that such a sequence identity determination requires that the two aligned sequences are aligned so that there are no overhangs between the two sequences: each amino acid in each sequence will have to be matched with a counterpart in the other sequence.

[0052] An "assembly of amino acids" means two or more amino acids bound together by physical or chemical means.

[0053] The "3D conformation" is the 3 dimensional structure of a biomolecule such as a protein. In monomeric polypeptides/proteins, the 3D conformation is also termed "the tertiary structure" and denotes the relative locations in 3 dimensional space of the amino acid residues forming the polypeptide.

[0054] "An immunogenic carrier" is a molecule or moiety to which an immunogen or a hapten can be coupled in order to enhance or enable the elicitation of an immune response against the immunogen/hapten. Immunogenic carriers are in classical cases relatively large molecules (such as tetanus toxoid, KLH, diphtheria toxoid etc.) which can be fused or conjugated to an immunogen/hapten, which is not sufficiently immunogenic in its own right—typically, the immunogenic carrier is capable of eliciting a strong T-helper lymphocyte response against the combined substance constituted by the immunogen and the immunogenic carrier, and this in turn provides for improved responses against the immungon by B-lymphocytes and cytotoxic lymphocytes. More recently, the large carrier molecules have to a certain extent been substituted by so-called promiscuous T-helper epitopes, i.e. shorter peptides that are recognized by a large fraction of HLA haplotypes in a population, and which elicit T-helper lymphocyte responses.

[0055] A "T-helper lymphocyte response" is an immune response elicited on the basis of a peptide, which is able to bind to an MHC class II molecule (e.g. an HLA class II molecule) in an antigen-presenting cell and which stimulates T-helper lymphocytes in an animal species as a consequence of T-cell receptor recognition of the complex between the peptide and the MHC Class II molecule prese

[0056] An "immunogen" is a substance of matter which is capable of inducing an adaptive immune response in a host, whose immune system is confronted with the immunogen. As such, immunogens are a subset of the larger genus "antigens", which are substances that can be recognized specifically by the immune system (e.g. when bound by antibodies or, alternatively, when fragments of the are antigens bound to MHC molecules are being recognized by T-cell receptors) but which are not necessarily capable of inducing immunity—an antigen is, however, always capable of eliciting immunity, meaning that a host that has an established memory immunity against the antigen will mount a specific immune response against the antigen.

[0057] A "hapten" is a small molecule, which can neither induce or elicit an immune response, but if conjugated to an immunogenic carrier, antibodies or TCRs that recognize the hapten can be induced upon confrontation of the immune system with the hapten carrier conjugate.

[0058] An "adaptive immune response" is an immune response in response to confrontation with an antigen or immunogen, where the immune response is specific for antigenc determinants of the antigen/immunogen—examples of adaptive immune responses are induction of antigen specific antibody production or antigen specific induction/activation of T helper lymphocytes or cytotoxic lymphocytes.

[0059] A "protective, adaptive immune response" is an antigen-specific immune response induced in a subject as a reaction to immunization (artificial or natural) with an antigen, where the immune response is capable of protecting the subject against subsequent challenges with the antigen or a pathology-related agent that includes the antigen. Typically, prophylactic vaccination aims at establishing a protective adaptive immune response against one or several pathogens.

[0060] "Stimulation of the immune system" means that a substance or composition of matter exhibits a general, non-specific immunostimulatory effect. A number of adjuvants and putative adjuvants (such as certain cytokines) share the ability to stimulate the immune system. The result of using an immunostimulating agent is an increased "alertness" of the immune system meaning that simultaneous or subsequent immunization with an immunogen induces a significantly more effective immune response compared to isolated use of the immunogen.

[0061] Hybridization under "stringent conditions" is herein defined as hybridization performed under conditions by which a probe will hybridize to its target sequence, to a detectably greater degree than to other sequences. Stringent conditions are target-sequence-dependent and will differ depending on the structure of the polynucleotide. By controlling the stringency of the hybridization and/or washing conditions, target sequences can be identified which are 100% complementary to a probe (homologous probing). Alternatively, stringency conditions can be adjusted to allow some mismatching in sequences so that lower degrees of similarity are detected (heterologous probing). Specificity is typically the function of post-hybridization washes, the critical factors being the ionic strength and temperature of the final wash solution. Generally, stringent wash temperature conditions are selected to be about 5° C. to about 2° C. lower than the melting point (Tm) for the specific sequence at a defined ionic strength and pH. The melting point, or denaturation, of DNA occurs over a narrow temperature range and represents the disruption of the double helix into its complementary single strands. The process is described by the temperature of the midpoint of transition, Tm, which is also called the melting temperature. Formulas are available in the art for the determination of melting temperatures.

[0062] The term "animal" is in the present context in general intended to denote an animal species (preferably mammalian), such as *Homo sapiens, Canis domesticus*, etc. and not just one single animal. However, the term also denotes a population of such an animal species, since it is important that the individuals immunized according to the method of the invention substantially all will mount an immune response against the immunogen of the present invention.

[0063] As used herein, the term "antibody" refers to a polypeptide or group of polypeptides composed of at least one antibody combining site. An "antibody combining site" is the three-dimensional binding space with an internal surface shape and charge distribution complementary to the features of an epitope of an antigen, which allows a binding of the antibody with the antigen. "Antibody" includes, for example, vertebrate antibodies, hybrid antibodies, chimeric antibodies, humanised antibodies, altered antibodies, univalent antibodies, Fab proteins, and single domain antibodies.

[0064] "Specific binding" denotes binding between two substances which goes beyond binding of either substance to randomly chosen substances and also goes beyond simple association between substances that tend to aggregate because they share the same overall hydrophobicity or hydrophilicity. As such, specific binding usually involves a combination of electrostatic and other interactions between two conformationally complementary areas on the two substances, meaning that the substances can "recognize" each other in a complex mixture.

[0065] The term "vector" is used to refer to a carrier nucleic acid molecule into which a heterologous nucleic acid sequence can be inserted for introduction into a cell where it can be replicated and expressed. The term further denotes certain biological vehicles useful for the same purpose, e.g. viral vectors and phage—both these infectious agents are capable of introducing a heterelogous nucleic acid sequence

[0066] The term "expression vector" refers to a vector containing a nucleic acid sequence coding for at least part of a gene product capable of being transcribed. In some cases, when the transcription product is an mRNA molecule, this is in trun translated into a protein, polypeptide, or peptide.

Specific Embodiments of the Invention

The Polypeptides of the Invention

[0067] In some embodiments the at least 5 contiguous amino acids referred to in option b) in the definition of the first aspect of the invention constitute at least or exactly or at most 6, such as at least or exactly or at most 7, at least or exactly or at most 8, at least or exactly or at most 9, at least or exactly or at most 10, at least or exactly or at most 11, at least or exactly or at most 12, at least or exactly or at most 13, at least or exactly or at most 14, at least or exactly or at most 15, at least or exactly or at most 16, at least or exactly or at most 17, at least or exactly or at most 18, at least or exactly or at most 19, at least or exactly or at most 20, at least or exactly or at most 21, at least or exactly or at most 22, at least or exactly or at most 23, at least or exactly or at most 24, at least or exactly or at most 25, at least or exactly or at most 26, at least or exactly or at most 27 at least or exactly or at most 28, at least or exactly or at most 29, at least or exactly or at most 30, at least or exactly or at most 31, at least or exactly or at most 32, at least or exactly or at most 33, at least or exactly or at most 34, at least or exactly or at most 35, at least or exactly or at most 36, at least or exactly or at most 37, at least or exactly or at most 38, at least or exactly or at most 39, at least or exactly or at most 40, at least or exactly or at most 41, at least or exactly or at most 42, at least or exactly or at most 43, at least or exactly or at most 44, at least or exactly or at most 45, at least or exactly or at most 46, at least or exactly or at most 47, at least or exactly or at most 48, at least or exactly or at most 49, at least or exactly or at most 50, at least or exactly or at most 51, at least or exactly or at most 52, at least or exactly or at most 53, at least or exactly or at most 54, at least or exactly or at most 55, at least or exactly or at most 56, at least or exactly or at most 57, at least or exactly or at most 58, at least or exactly or at most 59, at least or exactly or at most 60, at least or exactly or at most 61, at least or exactly or at most 62, at least or exactly or at most 63, at least or exactly or at most 64 and at least or exactly or at most 65 contiguous amino acid residues.

[0068] The number of contiguous amino acids in option b) can be higher, for all of SEQ ID NOs. 2-30. Another way to phrase this is that for each of SEQ ID NOs: 1-30, the number of the contiguous amino acid residues is at least or exactly or at most N-n, where N is the length of the sequence ID in question and n is any integer between 1 and N-5; that is, the at least or exactly 5 contiguous amino acids can be at least any number between 5 and the length of the reference sequence minus one, in increments of one.

[0069] Insofar as embodiment b relates to SEQ ID NOs: 2-30, the at least 5 contiguous amino acids referred to in option b) in the definition of the first aspect of the invention may also constitute at least or exactly or at most 66, at least or exactly or at most 67, at least or exactly or at most 68, at least or exactly or at most 69, at least or exactly or at most 70, at least or exactly or at most 71, at least or exactly or at most 72, at least or exactly or at most 73, at least or exactly or at most 74, at least or exactly or at most 75, at least or exactly or at most 76, or at least or exactly or at most 77 contiguous amino acid residues.

[0070] Insofar as embodiment b relates to SEQ ID NOs: 3-30, the at least 5 contiguous amino acids referred to in option b) in the definition of the first aspect of the invention may also constitute at least or exactly or at most 78, at least or exactly or at most 79, at least or exactly or at most 80, at least or exactly or at most 81, at least or exactly or at most 82, at least or exactly or at most 83, at least or exactly or at most 84, at least or exactly or at most 85, at least or exactly or at most 86, at least or exactly or at most 87, at least or exactly or at most 88, at least or exactly or at most 89, at least or exactly or at most 90, at least or exactly or at most 91, at least or exactly or at most 92, at least or exactly or at most 93, at least or exactly or at most 94, at least or exactly or at most 95, at least or exactly or at most 96, at least or exactly or at most 97, at least or exactly or at most 98, at least or exactly or at most 99, at least or exactly or at most 100, at least or exactly or at most 101, at least or exactly or at most 102, or at least or exactly or at most 103 contiguous amino acid residues.

[0071] Insofar as embodiment b relates to SEQ ID NOs: 4-30, the at least 5 contiguous amino acids referred to in option b) in the definition of the first aspect of the invention may also constitute at least or exactly or at most 104, at least or exactly or at most 105, at least or exactly or at most 106, at least or exactly or at most 107, at least or exactly or at most 108, at least or exactly or at most 109, at least or exactly or at most 110, at least or exactly or at most 111, at least or exactly or at most 112, at least or exactly or at most 113, at least or exactly or at most 114, at least or exactly or at most 115, at least or exactly or at most 116, at least or exactly or at most 117, at least or exactly or at most 118, at least or exactly or at most 119, at least or exactly or at most 120, at least or exactly or at most 121, at least or exactly or at most 122, at least or exactly or at most 123, at least or exactly or at most 124, at least or exactly or at most 125, at least or exactly or at most 126, at least or exactly or at most 127, at least or exactly or at most 128, at least or exactly or at most 129, at least or exactly or at most 130, at least or exactly or at most 131, at least or exactly or at most 132, at least or exactly or at most 133, at least or exactly or at most 134, at least or exactly or at most 135, at least or exactly or at most 136, at least or exactly or at most 137, at least or exactly or at most 138, at least or exactly or at most 139, at least or exactly or at most 140, at least or exactly or at most 141, at least or exactly or at most 142, at least or exactly or at most 143, at least or exactly or at most 144, at least or exactly or at most 145, at least or exactly or at most 146, at least or exactly or at most 147, at least or exactly or at most 148, at least or exactly or at most 149, at least or exactly or at most 150, at least or exactly or at most 151, at least or exactly or at most 152, at least or exactly or at most 153, or at least or exactly or at most 154 contiguous amino acid residues.

[0072] Insofar as embodiment b relates to SEQ ID NOs: 5-30, the at least 5 contiguous amino acids referred to in option b) in the definition of the first aspect of the invention may also constitute at least or exactly or at most 155, at least or exactly or at most 156, at least or exactly or at most 157, at least or exactly or at most 158, at least or exactly or at most 159, at least or exactly or at most 160, at least or exactly or at most 161, at least or exactly or at most 162, at least or exactly or at most 163, at least or exactly or at most 164, at least or exactly or at most 165, at least or exactly or at most 166, at least or exactly or at most 167, at least or exactly or at most 168, at least or exactly or at most 169, at least or exactly or at most 170, at least or exactly or at most 171, at least or exactly or at most 172, at least or exactly or at most 173, at least or exactly or at most 174, at least or exactly or at most 175, at least or exactly or at most 176, at least or exactly or at most 177, or at least or exactly or at most 178 contiguous amino acid residues.

[0073] Insofar as embodiment b relates to SEQ ID NOs: 6-30, the at least 5 contiguous amino acids referred to in option b) in the definition of the first aspect of the invention may also constitute at least or exactly or at most 179, at least or exactly or at most 180, at least or exactly or at most 181, at least or exactly or at most 182, at least or exactly or at most 183, at least or exactly or at most 184, at least or exactly or at most 185, at least or exactly or at most 186, at least or exactly or at most 187, at least or exactly or at most 188, at least or exactly or at most 189, at least or exactly or at most 190, at least or exactly or at most 191, at least or exactly or at most 192, at least or exactly or at most 193, at least or exactly or at most 194, at least or exactly or at most 195, at least or exactly or at most 196, at least or exactly or at most 197, at least or exactly or at most 198, at least or exactly or at most 199, at least or exactly or at most 200, at least or exactly or at most 201, at least or exactly or at most 202, at least or exactly or at most 203, at least or exactly or at most 204, at least or exactly or at most 205, at least or exactly or at most 206, at least or exactly or at most 207, at least or exactly or at most 208, at least or exactly or at most 209, at least or exactly or at most 210, at least or exactly or at most 211, at least or exactly or at most 212, at least or exactly or at most 213, at least or exactly or at most 214, at least or exactly or at most 215, at least or exactly or at most 216, at least or exactly or at most 217, at least or exactly or at most 218, at least or exactly or at most 219, at least or exactly or at most 220, at least or exactly or at most 221, at least or exactly or at most 222, at least or exactly or at most 223, at least or exactly or at most 224, at least or exactly or at most 225, at least or exactly or at most 226, at least or exactly or at most 227, at least or exactly or at most 228, at least or exactly or at most 229, at least or exactly or at most 230, at least or exactly or at most 231, at least or exactly or at most 232, at least or exactly or at most 233, at least or exactly or at most 234, at least or exactly or at most 235, at least or exactly or at most 236, at least or exactly or at most 237, at least or exactly or at most 238, at least or exactly or at most 239, at least or exactly or at most 240, at least or exactly or at most 241, at least or exactly or at most 242, at least or exactly or at most 243, at least or exactly or at most 244, at least or exactly or at most 245, at least or exactly or at most 246, at least or exactly or at most 247, at least or exactly or at most 248, at least or exactly or at most 249, at least or exactly or at most 250, at least or exactly or at most 251, at least or exactly or at most 252, at least or exactly or at most 253, at least or exactly or at most 254, at least or exactly or at most 255, at least or exactly or at most 256, at least or exactly or at most 257, at least or exactly or at most 258, at least or exactly or at most 259, at least or exactly or at most 260, at least or exactly or at most 261, at least or exactly or at most 262, at least or exactly or at most 263, at least or exactly or at most 264, at least or exactly or at most 265, at least or exactly or at most 266, at least or exactly or at most 267, at least or exactly or at most 268, at least or exactly or at most 269, at least or exactly or at most 270, at least or exactly or at most 271, at least or exactly or at most 272, at least or exactly or at most 273, at least or exactly or at most 274, at least or exactly or at most 275, at least or exactly or at most 276, at least or exactly or at most 277, at least or exactly or at most 278, at least or exactly or at most 279, at least or exactly or at most 280, at least or exactly or at most 281, at least or exactly or at most 282, at least or exactly or at most 283, at least or exactly or at most 284, at least or exactly or at most 285, at least or exactly or at most 286, at least or exactly or at most 287, at least or exactly or at most 288, at least or exactly or at most 289, at least or exactly or at most 290, at least or exactly or at most 291, at least or exactly or at most 292, at least or exactly or at most 293, at least or exactly or at most 294, at least or exactly or at most 295, at least or exactly or at most 296, at least or exactly or at most 297, at least or exactly or at most 298, at least or exactly or at most 299, at least or exactly or at most 300, at least or exactly or at most 301, at least or exactly or at most 302, or at least or exactly or at most 303 contiguous amino acid residues.

[0074] Insofar as embodiment b relates to SEQ ID NOs: 7-30, the at least 5 contiguous amino acids referred to in option b) in the definition of the first aspect of the invention may also constitute at least or exactly or at most 304, at least or exactly or at most 305, at least or exactly or at most 306, at least or exactly or at most 307, or at least or exactly or at most 308 contiguous amino acid residues.

[0075] Insofar as embodiment b relates to SEQ ID NOs: 8-30, the at least 5 contiguous amino acids referred to in option b) in the definition of the first aspect of the invention may also constitute at least or exactly or at most 309, at least or exactly or at most 310, at least or exactly or at most 311, at least or exactly or at most 312, at least or exactly or at most 313, at least or exactly or at most 314, at least or exactly or at most 315, at least or exactly or at most 316, at least or exactly or at most 317, at least or exactly or at most 318, at least or exactly or at most 319, at least or exactly or at most 320, at least or exactly or at most 321, at least or exactly or at most 322, at least or exactly or at most 323, at least or exactly or at most 324, at least or exactly or at most 325, at least or exactly or at most 326, at least or exactly or at most 327, at least or exactly or at most 328, at least or exactly or at most 329, at least or exactly or at most 330, at least or exactly or at most 331, at least or exactly or at most 332, at least or exactly or at most 333, at least or exactly or at most 334, at least or exactly or at most 335, at least or exactly or at most 336, at least or exactly or at most 337, at least or exactly or at most 338, or at least or exactly or at most 339 contiguous amino acid residues.

[0076] Insofar as embodiment b relates to SEQ ID NOs: 9-30, the at least 5 contiguous amino acids referred to in option b) in the definition of the first aspect of the invention may also constitute at least or exactly or at most 340, at least or exactly or at most 341, at least or exactly or at most 342, at least or exactly or at most 343, at least or exactly or at most 344, at least or exactly or at most 345, or at least or exactly or at most 346 contiguous amino acid residues.

[0077] Insofar as embodiment b relates to SEQ ID NOs: 10-30, the at least 5 contiguous amino acids referred to in option b) in the definition of the first aspect of the invention may also constitute at least or exactly or at most 347, at least or exactly or at most 348, at least or exactly or at most 349, at least or exactly or at most 350, or at least or exactly or at most 351 contiguous amino acid residues.

[0078] Insofar as embodiment b relates to SEQ ID NOs: 11-30, the at least 5 contiguous amino acids referred to in option b) in the definition of the first aspect of the invention may also constitute at least or exactly or at most 352, at least or exactly or at most 353, at least or exactly or at most 354, at least or exactly or at most 355, at least or exactly or at most 356, at least or exactly or at most 357, at least or exactly or at most 358, at least or exactly or at most 359, at least or exactly or at most 360, at least or exactly or at most 361, at least or exactly or at most 362, at least or exactly or at most 363, at least or exactly or at most 364, at least or exactly or at most 365, at least or exactly or at most 366, at least or exactly or at most 367, at least or exactly or at most

368, at least or exactly or at most 369, at least or exactly or at most 370, at least or exactly or at most 371, at least or exactly or at most 372, at least or exactly or at most 373, at least or exactly or at most 374, at least or exactly or at most 375, at least or exactly or at most 376, at least or exactly or at most 377, at least or exactly or at most 378, at least or exactly or at most 379, at least or exactly or at most 380, at least or exactly or at most 381, at least or exactly or at most 382, at least or exactly or at most 383, at least or exactly or at most 384, at least or exactly or at most 385, at least or exactly or at most 386, at least or exactly or at most 387, at least or exactly or at most 388, at least or exactly or at most 389, at least or exactly or at most 390, at least or exactly or at most 391, at least or exactly or at most 392, at least or exactly or at most 393, at least or exactly or at most 394, at least or exactly or at most 395, at least or exactly or at most 396, at least or exactly or at most 397, at least or exactly or at most 398, at least or exactly or at most 399, at least or exactly or at most 400, at least or exactly or at most 401, at least or exactly or at most 402, at least or exactly or at most 403, at least or exactly or at most 404, at least or exactly or at most 405, at least or exactly or at most 406, at least or exactly or at most 407, at least or exactly or at most 408, at least or exactly or at most 409, at least or exactly or at most 410, at least or exactly or at most 411, at least or exactly or at most 412, at least or exactly or at most 413, at least or exactly or at most 414, at least or exactly or at most 415, at least or exactly or at most 416, at least or exactly or at most 417, at least or exactly or at most 418, or at least or exactly or at most 419 contiguous amino acid residues.

[0079] Insofar as embodiment b relates to SEQ ID NOs: 12-30, the at least 5 contiguous amino acids referred to in option b) in the definition of the first aspect of the invention may also constitute at least or exactly or at most 420, at least or exactly or at most 421, at least or exactly or at most 422, at least or exactly or at most 423, at least or exactly or at most 424, at least or exactly or at most 425, or at least or exactly or at most 426 contiguous amino acid residues.

[0080] Insofar as embodiment b relates to SEQ ID NOs: 13-30, the at least 5 contiguous amino acids referred to in option b) in the definition of the first aspect of the invention may also constitute at least or exactly or at most 427 contiguous amino acid residues.

[0081] Insofar as embodiment b relates to SEQ ID NOs: 14-30, the at least 5 contiguous amino acids referred to in option b) in the definition of the first aspect of the invention may also constitute at least or exactly or at most 428, at least or exactly or at most 429, at least or exactly or at most 430, at least or exactly or at most 431, at least or exactly or at most 432, at least or exactly or at most 433, at least or exactly or at most 434, at least or exactly or at most 435, at least or exactly or at most 436, at least or exactly or at most 437, at least or exactly or at most 438, at least or exactly or at most 439, at least or exactly or at most 440, at least or exactly or at most 441, at least or exactly or at most 442, at least or exactly or at most 443, at least or exactly or at most 444, at least or exactly or at most 445, at least or exactly or at most 446, at least or exactly or at most 447, at least or exactly or at most 448, at least or exactly or at most 449, at least or exactly or at most 450, at least or exactly or at most 451, at least or exactly or at most 452, at least or exactly or at most 453, at least or exactly or at most 454, at least or exactly or at most 455, at least or exactly or at most 456, at least or exactly or at most 457, at least or exactly or at most 458, at least or exactly or at most 459, at least or exactly or at most 460, at least or exactly or at most 461, at least or exactly or at most 462, at least or exactly or at most 463, at least or exactly or at most 464, at least or exactly or at most 465, at least or exactly or at most 466, at least or exactly or at most 467, at least or exactly or at most 468, at least or exactly or at most 469, at least or exactly or at most 470, at least or exactly or at most 471, at least or exactly or at most 472, at least or exactly or at most 473, at least or exactly or at most 474, at least or exactly or at most 475, at least or exactly or at most 476, at least or exactly or at most 477, at least or exactly or at most 478, at least or exactly or at most 479, at least or exactly or at most 480, at least or exactly or at most 481, at least or exactly or at most 482, at least or exactly or at most 483, at least or exactly or at most 484, at least or exactly or at most 485, at least or exactly or at most 486, at least or exactly or at most 487, at least or exactly or at most 488, at least or exactly or at most 489, at least or exactly or at most 490, at least or exactly or at most 491, at least or exactly or at most 492, at least or exactly or at most 493, at least or exactly or at most 494, at least or exactly or at most 495, at least or exactly or at most 496, at least or exactly or at most 497, at least or exactly or at most 498, at least or exactly or at most 499, at least or exactly or at most 500, at least or exactly or at most 501, at least or exactly or at most 502, at least or exactly or at most 503, at least or exactly or at most 504, at least or exactly or at most 505, at least or exactly or at most 506, at least or exactly or at most 507, at least or exactly or at most 508, at least or exactly or at most 509, at least or exactly or at most 510, at least or exactly or at most 511, at least or exactly or at most 512, at least or exactly or at most 513, at least or exactly or at most 514, at least or exactly or at most 515, at least or exactly or at most 516, at least or exactly or at most 517, at least or exactly or at most 518, at least or exactly or at most 519, at least or exactly or at most 520, at least or exactly or at most 521, at least or exactly or at most 522, at least or exactly or at most 523, at least or exactly or at most 524, at least or exactly or at most 525, at least or exactly or at most 526, at least or exactly or at most 527, at least or exactly or at most 528, at least or exactly or at most 529, at least or exactly or at most 530, at least or exactly or at most 531, at least or exactly or at most 532, at least or exactly or at most 533, at least or exactly or at most 534, at least or exactly or at most 535, at least or exactly or at most 536, at least or exactly or at most 537, at least or exactly or at most 538, at least or exactly or at most 539, at least or exactly or at most 540, at least or exactly or at most 541, at least or exactly or at most 542, at least or exactly or at most 543, at least or exactly or at most 544, at least or exactly or at most 545, at least or exactly or at most 546, at least or exactly or at most 547, at least or exactly or at most 548, at least or exactly or at most 549, at least or exactly or at most 550, at least or exactly or at most 551, at least or exactly or at most 552, at least or exactly or at most 553, at least or exactly or at most 554, at least or exactly or at most 555, at least or exactly or at most 556, at least or exactly or at most 557, at least or exactly or at most 558, at least or exactly or at most 559, at least or exactly or at most 560, at least or exactly or at most 561, at least or exactly or at most 562, at least or exactly or at most 563, at least or exactly or at most 564, at least or exactly or at most 565, at least or exactly or at most 566, or at least or exactly or at most 567 contiguous amino acid residues.

[0082] Insofar as embodiment b relates to SEQ ID NOs: 15-30, the at least 5 contiguous amino acids referred to in option b) in the definition of the first aspect of the invention may also constitute at least or exactly or at most 568, at least or exactly or at most 569, at least or exactly or at most 570, at least or exactly or at most 571, at least or exactly or at most 572, at least or exactly or at most 573, at least or exactly or at most 574, at least or exactly or at most 575, at least or exactly or at most 576, at least or exactly or at most 577, or at least or exactly or at most 578 contiguous amino acid residues.

[0083] Insofar as embodiment b relates to SEQ ID NOs: 16-30, the at least 5 contiguous amino acids referred to in option b) in the definition of the first aspect of the invention may also constitute at least or exactly or at most 579, at least or exactly or at most 580, at least or exactly or at most 581, at least or exactly or at most 582, at least or exactly or at most 583, at least or exactly or at most 584, at least or exactly or at most 585, at least or exactly or at most 586, at least or exactly or at most 587, at least or exactly or at most 588, at least or exactly or at most 589, at least or exactly or at most 590, at least or exactly or at most 591, at least or exactly or at most 592, at least or exactly or at most 593, at least or exactly or at most 594, at least or exactly or at most 595, at least or exactly or at most 596, at least or exactly or at most 597, at least or exactly or at most 598, at least or exactly or at most 599, at least or exactly or at most 600, at least or exactly or at most 601, at least or exactly or at most 602, at least or exactly or at most 603, at least or exactly or at most 604, at least or exactly or at most 605, at least or exactly or at most 606, at least or exactly or at most 607, at least or exactly or at most 608, at least or exactly or at most 609, at least or exactly or at most 610, at least or exactly or at most 611, at least or exactly or at most 612, at least or exactly or at most 613, at least or exactly or at most 614, at least or exactly or at most 615, at least or exactly or at most 616, at least or exactly or at most 617, at least or exactly or at most 618, at least or exactly or at most 619, or at least or exactly or at most 620 contiguous amino acid residues.

[0084] Insofar as embodiment b relates to SEQ ID NOs: 17-30, the at least 5 contiguous amino acids referred to in option b) in the definition of the first aspect of the invention may also constitute at least or exactly or at most 621, at least or exactly or at most 622, at least or exactly or at most 623, at least or exactly or at most 624, at least or exactly or at most 625, at least or exactly or at most 626, at least or exactly or at most 627, at least or exactly or at most 628, at least or exactly or at most 629, at least or exactly or at most 630, at least or exactly or at most 631, at least or exactly or at most 632, at least or exactly or at most 633, at least or exactly or at most 634, at least or exactly or at most 635, at least or exactly or at most 636, at least or exactly or at most 637, at least or exactly or at most 638, at least or exactly or at most 639, at least or exactly or at most 640, at least or exactly or at most 641, at least or exactly or at most 642, at least or exactly or at most 643, at least or exactly or at most 644, at least or exactly or at most 645, at least or exactly or at most 646, at least or exactly or at most 647, at least or exactly or at most 648, at least or exactly or at most 649, at least or exactly or at most 650, at least or exactly or at most 651, at least or exactly or at most 652, at least or exactly or at most 653, at least or exactly or at most 654, at least or exactly or at most 655, at least or exactly or at most 656, at least or exactly or at most 657, at least or exactly or at most 658, at least or exactly or at most 659, at least or exactly or at most 660, at least or exactly or at most 661, at least or exactly or at most 662, at least or exactly or at most 663, at least or exactly or at most 664, at least or exactly or at most 665, at least or exactly or at most 666, at least or exactly or at most 667, at least or exactly or at most 668, at least or exactly or at most 669, at least or exactly or at most 670, at least or exactly or at most 671, at least or exactly or at most 672, at least or exactly or at most 673, at least or exactly or at most 674, at least or exactly or at most 675, at least or exactly or at most 676, at least or exactly or at most 677, at least or exactly or at most 678, at least or exactly or at most 679, at least or exactly or at most 680, at least or exactly or at most 681, at least or exactly or at most 682, at least or exactly or at most 683, at least or exactly or at most 684, at least or exactly or at most 685, at least or exactly or at most 686, or at least or exactly or at most 687 contiguous amino acid residues.

[0085] Insofar as embodiment b relates to SEQ ID NOs: 18-30, the at least 5 contiguous amino acids referred to in option b) in the definition of the first aspect of the invention may also constitute at least or exactly or at most 688, at least or exactly or at most 689, at least or exactly or at most 690, at least or exactly or at most 691, at least or exactly or at most 692, at least or exactly or at most 693, at least or exactly or at most 694, at least or exactly or at most 695, at least or exactly or at most 696, at least or exactly or at most 697, at least or exactly or at most 698, at least or exactly or at most 699, at least or exactly or at most 700, at least or exactly or at most 701, at least or exactly or at most 702, at least or exactly or at most 703, at least or exactly or at most 704, at least or exactly or at most 705, at least or exactly or at most 706, at least or exactly or at most 707, at least or exactly or at most 708, at least or exactly or at most 709, at least or exactly or at most 710, at least or exactly or at most 711, at least or exactly or at most 712, at least or exactly or at most 713, at least or exactly or at most 714, at least or exactly or at most 715, at least or exactly or at most 716, at least or exactly or at most 717, at least or exactly or at most 718, at least or exactly or at most 719, at least or exactly or at most 720, at least or exactly or at most 721, at least or exactly or at most 722, at least or exactly or at most 723, at least or exactly or at most 724, at least or exactly or at most 725, at least or exactly or at most 726, at least or exactly or at most 727, at least or exactly or at most 728, at least or exactly or at most 729, at least or exactly or at most 730, at least or exactly or at most 731, at least or exactly or at most 732, at least or exactly or at most 733, at least or exactly or at most 734, at least or exactly or at most 735, at least or exactly or at most 736, at least or exactly or at most 737, at least or exactly or at most 738, at least or exactly or at most 739, at least or exactly or at most 740, or at least or exactly or at most 741 contiguous amino acid residues.

[0086] Insofar as embodiment b relates to SEQ ID NOs: 19-30, the at least 5 contiguous amino acids referred to in option b) in the definition of the first aspect of the invention may also constitute at least or exactly or at most 742, at least or exactly or at most 743, at least or exactly or at most 744, or at least or exactly or at most 745 contiguous amino acid residues.

[0087] Insofar as embodiment b relates to SEQ ID NOs: 20-30, the at least 5 contiguous amino acids referred to in option b) in the definition of the first aspect of the invention may also constitute at least or exactly or at most 746, at least or exactly or at most 747, at least or exactly or at most 748, at least or exactly or at most 749, at least or exactly or at most 750, at least or exactly or at most 751, at least or exactly or at most 752, at least or exactly or at most 753, at least or exactly or at most 754, at least or exactly or at most 755, at least or exactly or at most 756, at least or exactly or at most 757, at least or exactly or at most 758, at least or exactly or at most 759, at least or exactly or at most 760, at least or exactly or at most 761, at least or exactly or at most 762, at least or exactly or at most 763, at least or exactly or at most 764, at least or exactly or at most 765, at least or exactly or at most 766, at least or exactly or at most 767, at least or exactly or at most 768, at least or exactly or at most 769, at least or exactly or at most 770, at least or exactly or at most 771, at least or exactly or at most 772, at least or exactly or at most 773, at least or exactly or at most 774, at least or exactly or at most 775, at least or exactly or at most 776, at least or exactly or at most 777, at least or exactly or at most 778, at least or exactly or at most 779, at least or exactly or at most 780, at least or exactly or at most 781, at least or exactly or at most 782, or at least or exactly or at most 783 contiguous amino acid residues.

[0088] Insofar as embodiment b relates to SEQ ID NOs: 21-30, the at least 5 contiguous amino acids referred to in option b) in the definition of the first aspect of the invention may also constitute at least or exactly or at most 784, at least or exactly or at most 785, at least or exactly or at most 786, at least or exactly or at most 787, at least or exactly or at most 788, at least or exactly or at most 789, at least or exactly or at most 790, at least or exactly or at most 791, at least or exactly or at most 792, at least or exactly or at most 793, at least or exactly or at most 794, at least or exactly or at most 795, at least or exactly or at most 796, at least or exactly or at most 797, at least or exactly or at most 798, at least or exactly or at most 799, at least or exactly or at most 800, at least or exactly or at most 801, at least or exactly or at most 802, at least or exactly or at most 803, at least or exactly or at most 804, at least or exactly or at most 805, at least or exactly or at most 806, at least or exactly or at most 807, at least or exactly or at most 808, at least or exactly or at most 809, at least or exactly or at most 810, at least or exactly or at most 811, at least or exactly or at most 812, at least or exactly or at most 813, at least or exactly or at most 814, at least or exactly or at most 815, at least or exactly or at most 816, at least or exactly or at most 817, at least or exactly or at most 818, at least or exactly or at most 819, at least or exactly or at most 820, at least or exactly or at most 821, at least or exactly or at most 822, at least or exactly or at most 823, at least or exactly or at most 824, at least or exactly or at most 825, at least or exactly or at most 826, at least or exactly or at most 827, at least or exactly or at most 828, at least or exactly or at most 829, at least or exactly or at most 830, at least or exactly or at most 831, at least or exactly or at most 832, at least or exactly or at most 833, at least or exactly or at most 834, at least or exactly or at most 835, at least or exactly or at most 836, at least or exactly or at most 837, at least or exactly or at most 838, at least or exactly or at most 839, at least or exactly or at most 840, at least or exactly or at most 841, at least or exactly or at most 842, at least or exactly or at most 843, at least or exactly or at most 844, at least or exactly or at most 845, at least or exactly or at most 846, at least or exactly or at most 847, at least or exactly or at most 848, at least or exactly or at most 849, or at least or exactly or at most 850 contiguous amino acid residues.

[0089] Insofar as embodiment b relates to SEQ ID NOs: 22-30, the at least 5 contiguous amino acids referred to in option b) in the definition of the first aspect of the invention may also constitute at least or exactly or at most 851, at least or exactly or at most 852, at least or exactly or at most 853, at least or exactly or at most 854, at least or exactly or at most 855, at least or exactly or at most 856, at least or exactly or at most 857, at least or exactly or at most 858, at least or exactly or at most 859, at least or exactly or at most 860, at least or exactly or at most 861, at least or exactly or at most 862, at least or exactly or at most 863, at least or exactly or at most 864, at least or exactly or at most 865, at least or exactly or at most 866, at least or exactly or at most 867, at least or exactly or at most 868, at least or exactly or at most 869, at least or exactly or at most 870, at least or exactly or at most 871, at least or exactly or at most 872, at least or exactly or at most 873, at least or exactly or at most 874, at least or exactly or at most 875, at least or exactly or at most 876, at least or exactly or at most 877, at least or exactly or at most 878, or at least or exactly or at most 879 contiguous amino acid residues.

[0090] Insofar as embodiment b relates to SEQ ID NOs: 23-30, the at least 5 contiguous amino acids referred to in option b) in the definition of the first aspect of the invention may also constitute at least or exactly or at most 880, at least or exactly or at most 881, at least or exactly or at most 882, at least or exactly or at most 883, at least or exactly or at most 884, at least or exactly or at most 885, at least or exactly or at most 886, at least or exactly or at most 887, at least or exactly or at most 888, at least or exactly or at most 889, at least or exactly or at most 890, at least or exactly or at most 891, at least or exactly or at most 892, at least or exactly or at most 893, at least or exactly or at most 894, at least or exactly or at most 895, at least or exactly or at most 896, at least or exactly or at most 897, at least or exactly or at most 898, at least or exactly or at most 899, at least or exactly or at most 900, at least or exactly or at most 901, at least or exactly or at most 902, at least or exactly or at most 903, at least or exactly or at most 904, at least or exactly or at most 905, at least or exactly or at most 906, at least or exactly or at most 907, at least or exactly or at most 908, at least or exactly or at most 909, at least or exactly or at most 910, at least or exactly or at most 911, at least or exactly or at most 912, at least or exactly or at most 913, at least or exactly or at most 914, at least or exactly or at most 915, at least or exactly or at most 916, at least or exactly or at most 917, or at least or exactly or at most 918 contiguous amino acid residues.

[0091] Insofar as embodiment b relates to SEQ ID NOs: 24-30, the at least 5 contiguous amino acids referred to in option b) in the definition of the first aspect of the invention may also constitute at least or exactly or at most 919, at least or exactly or at most 920, at least or exactly or at most 921, at least or exactly or at most 922, at least or exactly or at most 923, at least or exactly or at most 924, at least or exactly or at most 925, at least or exactly or at most 926, at least or exactly or at most 927, at least or exactly or at most 928, at least or exactly or at most 929, at least or exactly or at most 930, at least or exactly or at most 931, at least or exactly or at most 932, at least or exactly or at most 933, at least or exactly or at most 934, at least or exactly or at most

935, at least or exactly or at most 936, at least or exactly or at most 937, at least or exactly or at most 938, at least or exactly or at most 939, at least or exactly or at most 940, at least or exactly or at most 941, at least or exactly or at most 942, at least or exactly or at most 943, at least or exactly or at most 944, at least or exactly or at most 945, at least or exactly or at most 946, at least or exactly or at most 947, at least or exactly or at most 948, at least or exactly or at most 949, at least or exactly or at most 950, at least or exactly or at most 951, at least or exactly or at most 952, at least or exactly or at most 953, at least or exactly or at most 954, at least or exactly or at most 955, at least or exactly or at most 956, at least or exactly or at most 957, at least or exactly or at most 958, at least or exactly or at most 959, at least or exactly or at most 960, at least or exactly or at most 961, at least or exactly or at most 962, at least or exactly or at most 963, at least or exactly or at most 964, at least or exactly or at most 965, at least or exactly or at most 966, at least or exactly or at most 967, at least or exactly or at most 968, at least or exactly or at most 969, at least or exactly or at most 970, at least or exactly or at most 971, at least or exactly or at most 972, at least or exactly or at most 973, at least or exactly or at most 974, at least or exactly or at most 975, at least or exactly or at most 976, at least or exactly or at most 977, at least or exactly or at most 978, at least or exactly or at most 979, at least or exactly or at most 980, at least or exactly or at most 981, at least or exactly or at most 982, at least or exactly or at most 983, at least or exactly or at most 984, at least or exactly or at most 985, at least or exactly or at most 986, at least or exactly or at most 987, at least or exactly or at most 988, at least or exactly or at most 989, at least or exactly or at most 990, at least or exactly or at most 991, at least or exactly or at most 992, at least or exactly or at most 993, or at least or exactly or at most 994 contiguous amino acid residues.

[0092] Insofar as embodiment b relates to SEQ ID NOs: 25-30, the at least 5 contiguous amino acids referred to in option b) in the definition of the first aspect of the invention may also constitute at least or exactly or at most 995, at least or exactly or at most 996, at least or exactly or at most 997, at least or exactly or at most 998, at least or exactly or at most 999, at least or exactly or at most 1000, at least or exactly or at most 1001, at least or exactly or at most 1002, at least or exactly or at most 1003, at least or exactly or at most 1004, at least or exactly or at most 1005, at least or exactly or at most 1006, at least or exactly or at most 1007, at least or exactly or at most 1008, at least or exactly or at most 1009, at least or exactly or at most 1010, at least or exactly or at most 1011, at least or exactly or at most 1012, at least or exactly or at most 1013, at least or exactly or at most 1014, at least or exactly or at most 1015, at least or exactly or at most 1016, at least or exactly or at most 1017, at least or exactly or at most 1018, at least or exactly or at most 1019, at least or exactly or at most 1020, at least or exactly or at most 1021, at least or exactly or at most 1022, at least or exactly or at most 1023, at least or exactly or at most 1024, at least or exactly or at most 1025, at least or exactly or at most 1026, at least or exactly or at most 1027, at least or exactly or at most 1028, at least or exactly or at most 1029, at least or exactly or at most 1030, at least or exactly or at most 1031, at least or exactly or at most 1032, at least or exactly or at most 1033, at least or exactly or at most 1034, at least or exactly or at most 1035, at least or exactly or at most 1036, at least or exactly or at most 1037, at least or exactly or at most 1038, at least or exactly or at most 1039, at least or exactly or at most 1040, at least or exactly or at most 1041, at least or exactly or at most 1042, at least or exactly or at most 1043, at least or exactly or at most 1044, at least or exactly or at most 1045, at least or exactly or at most 1046, at least or exactly or at most 1047, at least or exactly or at most 1048, at least or exactly or at most 1049, at least or exactly or at most 1050, at least or exactly or at most 1051, at least or exactly or at most 1052, at least or exactly or at most 1053, at least or exactly or at most 1054, at least or exactly or at most 1055, or at least or exactly or at most 1056 contiguous amino acid residues.

[0093] Insofar as embodiment b relates to SEQ ID NOs: 26-30, the at least 5 contiguous amino acids referred to in option b) in the definition of the first aspect of the invention may also constitute at least or exactly or at most 1057, at least or exactly or at most 1058, at least or exactly or at most 1059, at least or exactly or at most 1060, at least or exactly or at most 1061, at least or exactly or at most 1062, at least or exactly or at most 1063, at least or exactly or at most 1064, at least or exactly or at most 1065, at least or exactly or at most 1066, at least or exactly or at most 1067, at least or exactly or at most 1068, at least or exactly or at most 1069, at least or exactly or at most 1070, at least or exactly or at most 1071, at least or exactly or at most 1072, at least or exactly or at most 1073, at least or exactly or at most 1074, at least or exactly or at most 1075, at least or exactly or at most 1076, at least or exactly or at most 1077, at least or exactly or at most 1078, at least or exactly or at most 1079, at least or exactly or at most 1080, at least or exactly or at most 1081, at least or exactly or at most 1082, at least or exactly or at most 1083, at least or exactly or at most 1084, at least or exactly or at most 1085, at least or exactly or at most 1086, at least or exactly or at most 1087, at least or exactly or at most 1088, at least or exactly or at most 1089, at least or exactly or at most 1090, at least or exactly or at most 1091, at least or exactly or at most 1092, at least or exactly or at most 1093, at least or exactly or at most 1094, at least or exactly or at most 1095, at least or exactly or at most 1096, at least or exactly or at most 1097, at least or exactly or at most 1098, at least or exactly or at most 1099, at least or exactly or at most 1100, at least or exactly or at most 1101, at least or exactly or at most 1102, at least or exactly or at most 1103, at least or exactly or at most 1104, at least or exactly or at most 1105, at least or exactly or at most 1106, at least or exactly or at most 1107, at least or exactly or at most 1108, at least or exactly or at most 1109, at least or exactly or at most 1110, at least or exactly or at most 1111, at least or exactly or at most 1112, at least or exactly or at most 1113, at least or exactly or at most 1114, at least or exactly or at most 1115, at least or exactly or at most 1116, at least or exactly or at most 1117, at least or exactly or at most 1118, at least or exactly or at most 1119, at least or exactly or at most 1120, at least or exactly or at most 1121, at least or exactly or at most 1122, at least or exactly or at most 1123, at least or exactly or at most 1124, at least or exactly or at most 1125, at least or exactly or at most 1126, at least or exactly or at most 1127, at least or exactly or at most 1128, at least or exactly or at most 1129, at least or exactly or at most 1130, at least or exactly or at most 1131, at least or exactly or at most 1132, at least or exactly or at most 1133, at least or exactly or at most 1134, at least or exactly or at most 1135, at least or exactly or at most 1136, at least or exactly or at most 1137, at least or exactly or at most 1138, at least or exactly or at most 1139, at least or exactly or at most 1140, at least or exactly or at most 1141, at least or exactly or at most 1142, at least or exactly or at most 1143, at least or exactly or at most 1144, at least or exactly or at most 1145, at least or exactly or at most 1146, at least or exactly or at most 1147, at least or exactly or at most 1148, at least or exactly or at most 1149, at least or exactly or at most 1150, at least or exactly or at most 1151, at least or exactly or at most 1152, at least or exactly or at most 1153, at least or exactly or at most 1154, at least or exactly or at most 1155, at least or exactly or at most 1156, at least or exactly or at most 1157, at least or exactly or at most 1158, at least or exactly or at most 1159, or at least or exactly or at most 1160 contiguous amino acid residues.

[0094] Insofar as embodiment b relates to SEQ ID NOs: 27-30, the at least 5 contiguous amino acids referred to in option b) in the definition of the first aspect of the invention may also constitute at least or exactly or at most 1161, at least or exactly or at most 1162, at least or exactly or at most 1163, at least or exactly or at most 1164, at least or exactly or at most 1165, at least or exactly or at most 1166, at least or exactly or at most 1167, at least or exactly or at most 1168, at least or exactly or at most 1169, at least or exactly or at most 1170, at least or exactly or at most 1171, at least or exactly or at most 1172, at least or exactly or at most 1173, at least or exactly or at most 1174, at least or exactly or at most 1175, at least or exactly or at most 1176, at least or exactly or at most 1177, at least or exactly or at most 1178, at least or exactly or at most 1179, at least or exactly or at most 1180, at least or exactly or at most 1181, at least or exactly or at most 1182, at least or exactly or at most 1183, at least or exactly or at most 1184, at least or exactly or at most 1185, at least or exactly or at most 1186, at least or exactly or at most 1187, at least or exactly or at most 1188, at least or exactly or at most 1189, at least or exactly or at most 1190, at least or exactly or at most 1191, at least or exactly or at most 1192, at least or exactly or at most 1193, at least or exactly or at most 1194, at least or exactly or at most 1195, at least or exactly or at most 1196, at least or exactly or at most 1197, at least or exactly or at most 1198, at least or exactly or at most 1199, at least or exactly or at most 1200, at least or exactly or at most 1201, at least or exactly or at most 1202, at least or exactly or at most 1203, at least or exactly or at most 1204, at least or exactly or at most 1205, at least or exactly or at most 1206, at least or exactly or at most 1207, at least or exactly or at most 1208, at least or exactly or at most 1209, or at least or exactly or at most 1210 contiguous amino acid residues.

[0095] Insofar as embodiment b relates to SEQ ID NOs: 28-30, the at least 5 contiguous amino acids referred to in option b) in the definition of the first aspect of the invention may also constitute at least or exactly or at most 1211, at least or exactly or at most 1212, at least or exactly or at most 1213, at least or exactly or at most 1214, at least or exactly or at most 1215, at least or exactly or at most 1216, at least or exactly or at most 1217, at least or exactly or at most 1218, at least or exactly or at most 1219, at least or exactly or at most 1220, at least or exactly or at most 1221, at least or exactly or at most 1222, at least or exactly or at most 1223, at least or exactly or at most 1224, at least or exactly or at most 1225, at least or exactly or at most 1226, at least or exactly or at most 1227, at least or exactly or at most 1228, at least or exactly or at most 1229, at least or exactly or at most 1230, at least or exactly or at most 1231, at least or exactly or at most 1232, at least or exactly or at most 1233, at least or exactly or at most 1234, at least or exactly or at most 1235, at least or exactly or at most 1236, at least or exactly or at most 1237, at least or exactly or at most 1238, at least or exactly or at most 1239, at least or exactly or at most 1240, at least or exactly or at most 1241, at least or exactly or at most 1242, at least or exactly or at most 1243, at least or exactly or at most 1244, at least or exactly or at most 1245, at least or exactly or at most 1246, at least or exactly or at most 1247, at least or exactly or at most 1248, at least or exactly or at most 1249, at least or exactly or at most 1250, at least or exactly or at most 1251, at least or exactly or at most 1252, at least or exactly or at most 1253, at least or exactly or at most 1254, at least or exactly or at most 1255, at least or exactly or at most 1256, at least or exactly or at most 1257, at least or exactly or at most 1258, at least or exactly or at most 1259, at least or exactly or at most 1260, at least or exactly or at most 1261, at least or exactly or at most 1262, at least or exactly or at most 1263, at least or exactly or at most 1264, at least or exactly or at most 1265, at least or exactly or at most 1266, at least or exactly or at most 1267, at least or exactly or at most 1268, at least or exactly or at most 1269, at least or exactly or at most 1270, at least or exactly or at most 1271, at least or exactly or at most 1272, at least or exactly or at most 1273, at least or exactly or at most 1274, at least or exactly or at most 1275, at least or exactly or at most 1276, at least or exactly or at most 1277, at least or exactly or at most 1278, at least or exactly or at most 1279, at least or exactly or at most 1280, at least or exactly or at most 1281, at least or exactly or at most 1282, at least or exactly or at most 1283, at least or exactly or at most 1284, at least or exactly or at most 1285, at least or exactly or at most 1286, at least or exactly or at most 1287, at least or exactly or at most 1288, at least or exactly or at most 1289, at least or exactly or at most 1290, at least or exactly or at most 1291, at least or exactly or at most 1292, at least or exactly or at most 1293, at least or exactly or at most 1294, at least or exactly or at most 1295, at least or exactly or at most 1296, at least or exactly or at most 1297, at least or exactly or at most 1298, at least or exactly or at most 1299, at least or exactly or at most 1300, at least or exactly or at most 1301, at least or exactly or at most 1302, at least or exactly or at most 1303, at least or exactly or at most 1304, at least or exactly or at most 1305, at least or exactly or at most 1306, at least or exactly or at most 1307, at least or exactly or at most 1308, at least or exactly or at most 1309, at least or exactly or at most 1310, at least or exactly or at most 1311, at least or exactly or at most 1312, at least or exactly or at most 1313, at least or exactly or at most 1314, at least or exactly or at most 1315, at least or exactly or at most 1316, at least or exactly or at most 1317, at least or exactly or at most 1318, at least or exactly or at most 1319, at least or exactly or at most 1320, at least or exactly or at most 1321, at least or exactly or at most 1322, at least or exactly or at most 1323, at least or exactly or at most 1324, at least or exactly or at most 1325, at least or exactly or at most 1326, at least or exactly or at most 1327, at least or exactly or at most 1328, at least or exactly or at most 1329, at least or exactly or at most 1330, at least or exactly or at most 1331, at least or exactly or at most 1332, at least or exactly or at most 1333, at least or exactly or at most 1334, at least or exactly or at most 1335, at least or exactly or at most 1336, at least

or exactly or at most 1337, at least or exactly or at most 1338, at least or exactly or at most 1339, at least or exactly or at most 1340, at least or exactly or at most 1341, at least or exactly or at most 1342, at least or exactly or at most 1343, at least or exactly or at most 1344, at least or exactly or at most 1345, at least or exactly or at most 1346, at least or exactly or at most 1347, at least or exactly or at most 1348, at least or exactly or at most 1349, at least or exactly or at most 1350, at least or exactly or at most 1351, at least or exactly or at most 1352, at least or exactly or at most 1353, at least or exactly or at most 1354, at least or exactly or at most 1355, at least or exactly or at most 1356, at least or exactly or at most 1357, at least or exactly or at most 1358, at least or exactly or at most 1359, at least or exactly or at most 1360, at least or exactly or at most 1361, at least or exactly or at most 1362, at least or exactly or at most 1363, at least or exactly or at most 1364, at least or exactly or at most 1365, at least or exactly or at most 1366, at least or exactly or at most 1367, at least or exactly or at most 1368, at least or exactly or at most 1369, at least or exactly or at most 1370, at least or exactly or at most 1371, at least or exactly or at most 1372, at least or exactly or at most 1373, at least or exactly or at most 1374, at least or exactly or at most 1375, at least or exactly or at most 1376, at least or exactly or at most 1377, at least or exactly or at most 1378, at least or exactly or at most 1379, at least or exactly or at most 1380, at least or exactly or at most 1381, at least or exactly or at most 1382, at least or exactly or at most 1383, at least or exactly or at most 1384, at least or exactly or at most 1385, at least or exactly or at most 1386, at least or exactly or at most 1387, at least or exactly or at most 1388, at least or exactly or at most 1389, at least or exactly or at most 1390, at least or exactly or at most 1391, at least or exactly or at most 1392, at least or exactly or at most 1393, at least or exactly or at most 1394, at least or exactly or at most 1395, at least or exactly or at most 1396, at least or exactly or at most 1397, at least or exactly or at most 1398, at least or exactly or at most 1399, at least or exactly or at most 1400, at least or exactly or at most 1401, at least or exactly or at most 1402, at least or exactly or at most 1403, at least or exactly or at most 1404, at least or exactly or at most 1405, at least or exactly or at most 1406, at least or exactly or at most 1407, at least or exactly or at most 1408, at least or exactly or at most 1409, at least or exactly or at most 1410, at least or exactly or at most 1411, at least or exactly or at most 1412, at least or exactly or at most 1413, at least or exactly or at most 1414, at least or exactly or at most 1415, at least or exactly or at most 1416, at least or exactly or at most 1417, at least or exactly or at most 1418, at least or exactly or at most 1419, at least or exactly or at most 1420, at least or exactly or at most 1421, at least or exactly or at most 1422, at least or exactly or at most 1423, at least or exactly or at most 1424, at least or exactly or at most 1425, at least or exactly or at most 1426, at least or exactly or at most 1427, at least or exactly or at most 1428, at least or exactly or at most 1429, at least or exactly or at most 1430, at least or exactly or at most 1431, at least or exactly or at most 1432, at least or exactly or at most 1433, at least or exactly or at most 1434, at least or exactly or at most 1435, at least or exactly or at most 1436, at least or exactly or at most 1437, at least or exactly or at most 1438, at least or exactly or at most 1439, at least or exactly or at most 1440, at least or exactly or at most 1441, at least or exactly or at most 1442, at least or exactly or at most 1443, at least or exactly or at most 1444, at least or exactly or at most 1445, at least or exactly or at most 1446, at least or exactly or at most 1447, at least or exactly or at most 1448, at least or exactly or at most 1449, at least or exactly or at most 1450, at least or exactly or at most 1451, at least or exactly or at most 1452, at least or exactly or at most 1453, at least or exactly or at most 1454, at least or exactly or at most 1455, at least or exactly or at most 1456, at least or exactly or at most 1457, at least or exactly or at most 1458, at least or exactly or at most 1459, at least or exactly or at most 1460, at least or exactly or at most 1461, at least or exactly or at most 1462, at least or exactly or at most 1463, at least or exactly or at most 1464, at least or exactly or at most 1465, at least or exactly or at most 1466, at least or exactly or at most 1467, at least or exactly or at most 1468, at least or exactly or at most 1469, at least or exactly or at most 1470, at least or exactly or at most 1471, at least or exactly or at most 1472, at least or exactly or at most 1473, at least or exactly or at most 1474, at least or exactly or at most 1475, at least or exactly or at most 1476, at least or exactly or at most 1477, at least or exactly or at most 1478, at least or exactly or at most 1479, at least or exactly or at most 1480, at least or exactly or at most 1481, at least or exactly or at most 1482, at least or exactly or at most 1483, at least or exactly or at most 1484, at least or exactly or at most 1485, at least or exactly or at most 1486, at least or exactly or at most 1487, at least or exactly or at most 1488, at least or exactly or at most 1489, at least or exactly or at most 1490, at least or exactly or at most 1491, at least or exactly or at most 1492, at least or exactly or at most 1493, at least or exactly or at most 1494, at least or exactly or at most 1495, at least or exactly or at most 1496, at least or exactly or at most 1497, at least or exactly or at most 1498, at least or exactly or at most 1499, at least or exactly or at most 1500, at least or exactly or at most 1501, at least or exactly or at most 1502, at least or exactly or at most 1503, at least or exactly or at most 1504, at least or exactly or at most 1505, at least or exactly or at most 1506, at least or exactly or at most 1507, at least or exactly or at most 1508, at least or exactly or at most 1509, at least or exactly or at most 1510, at least or exactly or at most 1511, at least or exactly or at most 1512, at least or exactly or at most 1513, at least or exactly or at most 1514, at least or exactly or at most 1515, at least or exactly or at most 1516, at least or exactly or at most 1517, at least or exactly or at most 1518, at least or exactly or at most 1519, at least or exactly or at most 1520, at least or exactly or at most 1521, at least or exactly or at most 1522, at least or exactly or at most 1523, at least or exactly or at most 1524, at least or exactly or at most 1525, at least or exactly or at most 1526, at least or exactly or at most 1527, at least or exactly or at most 1528, at least or exactly or at most 1529, at least or exactly or at most 1530, at least or exactly or at most 1531, at least or exactly or at most 1532, at least or exactly or at most 1533, at least or exactly or at most 1534, at least or exactly or at most 1535, at least or exactly or at most 1536, at least or exactly or at most 1537, at least or exactly or at most 1538, at least or exactly or at most 1539, at least or exactly or at most 1540, at least or exactly or at most 1541, at least or exactly or at most 1542, at least or exactly or at most 1543, at least or exactly or at most 1544, at least or exactly or at most 1545, at least or exactly or at most 1546, at least or exactly or at most 1547, at least or exactly or at most 1548, at least or exactly or at most 1549, at least or exactly

or at most 1550, at least or exactly or at most 1551, at least or exactly or at most 1552, at least or exactly or at most 1553, at least or exactly or at most 1554, at least or exactly or at most 1555, at least or exactly or at most 1556, at least or exactly or at most 1557, at least or exactly or at most 1558, at least or exactly or at most 1559, at least or exactly or at most 1560, at least or exactly or at most 1561, at least or exactly or at most 1562, at least or exactly or at most 1563, at least or exactly or at most 1564, at least or exactly or at most 1565, at least or exactly or at most 1566, at least or exactly or at most 1567, at least or exactly or at most 1568, at least or exactly or at most 1569, at least or exactly or at most 1570, at least or exactly or at most 1571, at least or exactly or at most 1572, at least or exactly or at most 1573, at least or exactly or at most 1574, at least or exactly or at most 1575, at least or exactly or at most 1576, at least or exactly or at most 1577, at least or exactly or at most 1578, at least or exactly or at most 1579, at least or exactly or at most 1580, at least or exactly or at most 1581, at least or exactly or at most 1582, at least or exactly or at most 1583, at least or exactly or at most 1584, at least or exactly or at most 1585, at least or exactly or at most 1586, at least or exactly or at most 1587, at least or exactly or at most 1588, at least or exactly or at most 1589, at least or exactly or at most 1590, at least or exactly or at most 1591, at least or exactly or at most 1592, at least or exactly or at most 1593, at least or exactly or at most 1594, at least or exactly or at most 1595, at least or exactly or at most 1596, at least or exactly or at most 1597, at least or exactly or at most 1598, at least or exactly or at most 1599, at least or exactly or at most 1600, at least or exactly or at most 1601, at least or exactly or at most 1602, at least or exactly or at most 1603, at least or exactly or at most 1604, at least or exactly or at most 1605, at least or exactly or at most 1606, at least or exactly or at most 1607, at least or exactly or at most 1608, at least or exactly or at most 1609, at least or exactly or at most 1610, at least or exactly or at most 1611, at least or exactly or at most 1612, at least or exactly or at most 1613, at least or exactly or at most 1614, at least or exactly or at most 1615, at least or exactly or at most 1616, at least or exactly or at most 1617, at least or exactly or at most 1618, at least or exactly or at most 1619, at least or exactly or at most 1620, at least or exactly or at most 1621, at least or exactly or at most 1622, at least or exactly or at most 1623, at least or exactly or at most 1624, at least or exactly or at most 1625, at least or exactly or at most 1626, at least or exactly or at most 1627, at least or exactly or at most 1628, at least or exactly or at most 1629, at least or exactly or at most 1630, at least or exactly or at most 1631, at least or exactly or at most 1632, at least or exactly or at most 1633, at least or exactly or at most 1634, at least or exactly or at most 1635, at least or exactly or at most 1636, at least or exactly or at most 1637, at least or exactly or at most 1638, at least or exactly or at most 1639, at least or exactly or at most 1640, at least or exactly or at most 1641, at least or exactly or at most 1642, at least or exactly or at most 1643, at least or exactly or at most 1644, at least or exactly or at most 1645, at least or exactly or at most 1646, at least or exactly or at most 1647, at least or exactly or at most 1648, at least or exactly or at most 1649, at least or exactly or at most 1650, at least or exactly or at most 1651, at least or exactly or at most 1652, at least or exactly or at most 1653, at least or exactly or at most 1654, at least or exactly or at most 1655, at least or exactly or at most 1656, at least or exactly or at most 1657, at least or exactly or at most 1658, at least or exactly or at most 1659, at least or exactly or at most 1660, at least or exactly or at most 1661, at least or exactly or at most 1662, at least or exactly or at most 1663, at least or exactly or at most 1664, at least or exactly or at most 1665, at least or exactly or at most 1666, at least or exactly or at most 1667, at least or exactly or at most 1668, at least or exactly or at most 1669, at least or exactly or at most 1670, at least or exactly or at most 1671, at least or exactly or at most 1672, at least or exactly or at most 1673, at least or exactly or at most 1674, at least or exactly or at most 1675, at least or exactly or at most 1676, at least or exactly or at most 1677, at least or exactly or at most 1678, at least or exactly or at most 1679, at least or exactly or at most 1680, at least or exactly or at most 1681, at least or exactly or at most 1682, at least or exactly or at most 1683, at least or exactly or at most 1684, at least or exactly or at most 1685, at least or exactly or at most 1686, at least or exactly or at most 1687, at least or exactly or at most 1688, at least or exactly or at most 1689, at least or exactly or at most 1690, at least or exactly or at most 1691, at least or exactly or at most 1692, at least or exactly or at most 1693, at least or exactly or at most 1694, at least or exactly or at most 1695, at least or exactly or at most 1696, at least or exactly or at most 1697, at least or exactly or at most 1698, at least or exactly or at most 1699, at least or exactly or at most 1700, at least or exactly or at most 1701, at least or exactly or at most 1702, at least or exactly or at most 1703, at least or exactly or at most 1704, at least or exactly or at most 1705, at least or exactly or at most 1706, at least or exactly or at most 1707, at least or exactly or at most 1708, at least or exactly or at most 1709, at least or exactly or at most 1710, at least or exactly or at most 1711, at least or exactly or at most 1712, at least or exactly or at most 1713, at least or exactly or at most 1714, at least or exactly or at most 1715, at least or exactly or at most 1716, at least or exactly or at most 1717, at least or exactly or at most 1718, at least or exactly or at most 1719, at least or exactly or at most 1720, at least or exactly or at most 1721, at least or exactly or at most 1722, at least or exactly or at most 1723, at least or exactly or at most 1724, at least or exactly or at most 1725, at least or exactly or at most 1726, at least or exactly or at most 1727, at least or exactly or at most 1728, at least or exactly or at most 1729, at least or exactly or at most 1730, at least or exactly or at most 1731, at least or exactly or at most 1732, at least or exactly or at most 1733, at least or exactly or at most 1734, at least or exactly or at most 1735, at least or exactly or at most 1736, at least or exactly or at most 1737, at least or exactly or at most 1738, at least or exactly or at most 1739, at least or exactly or at most 1740, at least or exactly or at most 1741, at least or exactly or at most 1742, at least or exactly or at most 1743, at least or exactly or at most 1744, at least or exactly or at most 1745, at least or exactly or at most 1746, at least or exactly or at most 1747, at least or exactly or at most 1748, at least or exactly or at most 1749, at least or exactly or at most 1750, at least or exactly or at most 1751, at least or exactly or at most 1752, at least or exactly or at most 1753, at least or exactly or at most 1754, at least or exactly or at most 1755, at least or exactly or at most 1756, at least or exactly or at most 1757, at least or exactly or at most 1758, at least or exactly or at most 1759, at least or exactly or at most 1760, at least or exactly or at most 1761, at least or exactly or at most 1762, at least or exactly or at most

1763, at least or exactly or at most 1764, at least or exactly or at most 1765, at least or exactly or at most 1766, at least or exactly or at most 1767, at least or exactly or at most 1768, at least or exactly or at most 1769, at least or exactly or at most 1770, at least or exactly or at most 1771, at least or exactly or at most 1772, at least or exactly or at most 1773, at least or exactly or at most 1774, at least or exactly or at most 1775, at least or exactly or at most 1776, at least or exactly or at most 1777, at least or exactly or at most 1778, at least or exactly or at most 1779, at least or exactly or at most 1780, at least or exactly or at most 1781, at least or exactly or at most 1782, at least or exactly or at most 1783, at least or exactly or at most 1784, at least or exactly or at most 1785, at least or exactly or at most 1786, at least or exactly or at most 1787, at least or exactly or at most 1788, at least or exactly or at most 1789, at least or exactly or at most 1790, at least or exactly or at most 1791, at least or exactly or at most 1792, at least or exactly or at most 1793, at least or exactly or at most 1794, at least or exactly or at most 1795, at least or exactly or at most 1796, at least or exactly or at most 1797, at least or exactly or at most 1798, at least or exactly or at most 1799, at least or exactly or at most 1800, at least or exactly or at most 1801, at least or exactly or at most 1802, at least or exactly or at most 1803, at least or exactly or at most 1804, at least or exactly or at most 1805, at least or exactly or at most 1806, at least or exactly or at most 1807, at least or exactly or at most 1808, at least or exactly or at most 1809, at least or exactly or at most 1810, at least or exactly or at most 1811, at least or exactly or at most 1812, at least or exactly or at most 1813, at least or exactly or at most 1814, at least or exactly or at most 1815, at least or exactly or at most 1816, at least or exactly or at most 1817, at least or exactly or at most 1818, at least or exactly or at most 1819, at least or exactly or at most 1820, at least or exactly or at most 1821, at least or exactly or at most 1822, at least or exactly or at most 1823, at least or exactly or at most 1824, at least or exactly or at most 1825, at least or exactly or at most 1826, at least or exactly or at most 1827, at least or exactly or at most 1828, at least or exactly or at most 1829, at least or exactly or at most 1830, at least or exactly or at most 1831, at least or exactly or at most 1832, at least or exactly or at most 1833, at least or exactly or at most 1834, at least or exactly or at most 1835, at least or exactly or at most 1836, at least or exactly or at most 1837, at least or exactly or at most 1838, at least or exactly or at most 1839, at least or exactly or at most 1840, at least or exactly or at most 1841, at least or exactly or at most 1842, at least or exactly or at most 1843, at least or exactly or at most 1844, at least or exactly or at most 1845, at least or exactly or at most 1846, at least or exactly or at most 1847, at least or exactly or at most 1848, at least or exactly or at most 1849, at least or exactly or at most 1850, at least or exactly or at most 1851, at least or exactly or at most 1852, at least or exactly or at most 1853, at least or exactly or at most 1854, at least or exactly or at most 1855, at least or exactly or at most 1856, at least or exactly or at most 1857, at least or exactly or at most 1858, at least or exactly or at most 1859, at least or exactly or at most 1860, at least or exactly or at most 1861, at least or exactly or at most 1862, at least or exactly or at most 1863, at least or exactly or at most 1864, at least or exactly or at most 1865, at least or exactly or at most 1866, at least or exactly or at most 1867, at least or exactly or at most 1868, at least or exactly or at most 1869, at least or exactly or at most 1870, at least or exactly or at most 1871, at least or exactly or at most 1872, at least or exactly or at most 1873, at least or exactly or at most 1874, at least or exactly or at most 1875, at least or exactly or at most 1876, at least or exactly or at most 1877, at least or exactly or at most 1878, at least or exactly or at most 1879, at least or exactly or at most 1880, at least or exactly or at most 1881, at least or exactly or at most 1882, at least or exactly or at most 1883, at least or exactly or at most 1884, at least or exactly or at most 1885, at least or exactly or at most 1886, at least or exactly or at most 1887, at least or exactly or at most 1888, at least or exactly or at most 1889, at least or exactly or at most 1890, at least or exactly or at most 1891, at least or exactly or at most 1892, at least or exactly or at most 1893, at least or exactly or at most 1894, at least or exactly or at most 1895, at least or exactly or at most 1896, at least or exactly or at most 1897, at least or exactly or at most 1898, at least or exactly or at most 1899, at least or exactly or at most 1900, at least or exactly or at most 1901, at least or exactly or at most 1902, at least or exactly or at most 1903, at least or exactly or at most 1904, at least or exactly or at most 1905, at least or exactly or at most 1906, at least or exactly or at most 1907, at least or exactly or at most 1908, at least or exactly or at most 1909, at least or exactly or at most 1910, at least or exactly or at most 1911, at least or exactly or at most 1912, at least or exactly or at most 1913, at least or exactly or at most 1914, at least or exactly or at most 1915, at least or exactly or at most 1916, at least or exactly or at most 1917, at least or exactly or at most 1918, at least or exactly or at most 1919, at least or exactly or at most 1920, at least or exactly or at most 1921, at least or exactly or at most 1922, at least or exactly or at most 1923, at least or exactly or at most 1924, at least or exactly or at most 1925, at least or exactly or at most 1926, at least or exactly or at most 1927, at least or exactly or at most 1928, at least or exactly or at most 1929, at least or exactly or at most 1930, at least or exactly or at most 1931, at least or exactly or at most 1932, at least or exactly or at most 1933, at least or exactly or at most 1934, at least or exactly or at most 1935, at least or exactly or at most 1936, at least or exactly or at most 1937, at least or exactly or at most 1938, at least or exactly or at most 1939, at least or exactly or at most 1940, at least or exactly or at most 1941, at least or exactly or at most 1942, at least or exactly or at most 1943, at least or exactly or at most 1944, at least or exactly or at most 1945, at least or exactly or at most 1946, at least or exactly or at most 1947, at least or exactly or at most 1948, at least or exactly or at most 1949, at least or exactly or at most 1950, at least or exactly or at most 1951, at least or exactly or at most 1952, at least or exactly or at most 1953, at least or exactly or at most 1954, at least or exactly or at most 1955, at least or exactly or at most 1956, at least or exactly or at most 1957, at least or exactly or at most 1958, at least or exactly or at most 1959, at least or exactly or at most 1960, at least or exactly or at most 1961, at least or exactly or at most 1962, at least or exactly or at most 1963, at least or exactly or at most 1964, at least or exactly or at most 1965, at least or exactly or at most 1966, at least or exactly or at most 1967, at least or exactly or at most 1968, at least or exactly or at most 1969, at least or exactly or at most 1970, at least or exactly or at most 1971, at least or exactly or at most 1972, at least or exactly or at most 1973, at least or exactly or at most 1974, at least or exactly or at most 1975, at least or exactly or at most 1976, at least

or exactly or at most 1977, at least or exactly or at most 1978, at least or exactly or at most 1979, at least or exactly or at most 1980, at least or exactly or at most 1981, at least or exactly or at most 1982, at least or exactly or at most 1983, at least or exactly or at most 1984, at least or exactly or at most 1985, at least or exactly or at most 1986, at least or exactly or at most 1987, at least or exactly or at most 1988, at least or exactly or at most 1989, at least or exactly or at most 1990, at least or exactly or at most 1991, at least or exactly or at most 1992, at least or exactly or at most 1993, at least or exactly or at most 1994, at least or exactly or at most 1995, at least or exactly or at most 1996, at least or exactly or at most 1997, at least or exactly or at most 1998, at least or exactly or at most 1999, at least or exactly or at most 2000, at least or exactly or at most 2001, at least or exactly or at most 2002, at least or exactly or at most 2003, at least or exactly or at most 2004, at least or exactly or at most 2005, at least or exactly or at most 2006, at least or exactly or at most 2007, at least or exactly or at most 2008, at least or exactly or at most 2009, at least or exactly or at most 2010, at least or exactly or at most 2011, at least or exactly or at most 2012, at least or exactly or at most 2013, at least or exactly or at most 2014, at least or exactly or at most 2015, at least or exactly or at most 2016, at least or exactly or at most 2017, at least or exactly or at most 2018, at least or exactly or at most 2019, at least or exactly or at most 2020, at least or exactly or at most 2021, at least or exactly or at most 2022, at least or exactly or at most 2023, at least or exactly or at most 2024, at least or exactly or at most 2025, at least or exactly or at most 2026, at least or exactly or at most 2027, at least or exactly or at most 2028, at least or exactly or at most 2029, at least or exactly or at most 2030, at least or exactly or at most 2031, at least or exactly or at most 2032, at least or exactly or at most 2033, at least or exactly or at most 2034, at least or exactly or at most 2035, at least or exactly or at most 2036, at least or exactly or at most 2037, at least or exactly or at most 2038, at least or exactly or at most 2039, at least or exactly or at most 2040, at least or exactly or at most 2041, at least or exactly or at most 2042, at least or exactly or at most 2043, at least or exactly or at most 2044, at least or exactly or at most 2045, at least or exactly or at most 2046, at least or exactly or at most 2047, at least or exactly or at most 2048, at least or exactly or at most 2049, at least or exactly or at most 2050, at least or exactly or at most 2051, at least or exactly or at most 2052, at least or exactly or at most 2053, at least or exactly or at most 2054, at least or exactly or at most 2055, at least or exactly or at most 2056, at least or exactly or at most 2057, at least or exactly or at most 2058, at least or exactly or at most 2059, at least or exactly or at most 2060, at least or exactly or at most 2061, at least or exactly or at most 2062, at least or exactly or at most 2063, at least or exactly or at most 2064, at least or exactly or at most 2065, at least or exactly or at most 2066, at least or exactly or at most 2067, at least or exactly or at most 2068, at least or exactly or at most 2069, at least or exactly or at most 2070, at least or exactly or at most 2071, at least or exactly or at most 2072, at least or exactly or at most 2073, at least or exactly or at most 2074, at least or exactly or at most 2075, at least or exactly or at most 2076, at least or exactly or at most 2077, at least or exactly or at most 2078, at least or exactly or at most 2079, at least or exactly or at most 2080, at least or exactly or at most 2081, at least or exactly or at most 2082, at least or exactly or at most 2083, at least or exactly or at most 2084, at least or exactly or at most 2085, at least or exactly or at most 2086, at least or exactly or at most 2087, at least or exactly or at most 2088, at least or exactly or at most 2089, at least or exactly or at most 2090, at least or exactly or at most 2091, at least or exactly or at most 2092, at least or exactly or at most 2093, at least or exactly or at most 2094, at least or exactly or at most 2095, at least or exactly or at most 2096, at least or exactly or at most 2097, at least or exactly or at most 2098, at least or exactly or at most 2099, at least or exactly or at most 2100, at least or exactly or at most 2101, at least or exactly or at most 2102, at least or exactly or at most 2103, at least or exactly or at most 2104, at least or exactly or at most 2105, at least or exactly or at most 2106, at least or exactly or at most 2107, at least or exactly or at most 2108, at least or exactly or at most 2109, at least or exactly or at most 2110, at least or exactly or at most 2111, at least or exactly or at most 2112, at least or exactly or at most 2113, at least or exactly or at most 2114, at least or exactly or at most 2115, at least or exactly or at most 2116, at least or exactly or at most 2117, at least or exactly or at most 2118, at least or exactly or at most 2119, at least or exactly or at most 2120, at least or exactly or at most 2121, at least or exactly or at most 2122, at least or exactly or at most 2123, at least or exactly or at most 2124, at least or exactly or at most 2125, at least or exactly or at most 2126, at least or exactly or at most 2127, at least or exactly or at most 2128, at least or exactly or at most 2129, at least or exactly or at most 2130, at least or exactly or at most 2131, at least or exactly or at most 2132, at least or exactly or at most 2133, at least or exactly or at most 2134, at least or exactly or at most 2135, at least or exactly or at most 2136, at least or exactly or at most 2137, at least or exactly or at most 2138, at least or exactly or at most 2139, at least or exactly or at most 2140, at least or exactly or at most 2141, at least or exactly or at most 2142, at least or exactly or at most 2143, at least or exactly or at most 2144, at least or exactly or at most 2145, at least or exactly or at most 2146, at least or exactly or at most 2147, at least or exactly or at most 2148, at least or exactly or at most 2149, at least or exactly or at most 2150, at least or exactly or at most 2151, at least or exactly or at most 2152, at least or exactly or at most 2153, at least or exactly or at most 2154, at least or exactly or at most 2155, at least or exactly or at most 2156, at least or exactly or at most 2157, at least or exactly or at most 2158, at least or exactly or at most 2159, at least or exactly or at most 2160, at least or exactly or at most 2161, at least or exactly or at most 2162, at least or exactly or at most 2163, at least or exactly or at most 2164, at least or exactly or at most 2165, at least or exactly or at most 2166, at least or exactly or at most 2167, at least or exactly or at most 2168, at least or exactly or at most 2169, at least or exactly or at most 2170, at least or exactly or at most 2171, at least or exactly or at most 2172, at least or exactly or at most 2173, at least or exactly or at most 2174, at least or exactly or at most 2175, at least or exactly or at most 2176, at least or exactly or at most 2177, at least or exactly or at most 2178, at least or exactly or at most 2179, at least or exactly or at most 2180, at least or exactly or at most 2181, at least or exactly or at most 2182, at least or exactly or at most 2183, at least or exactly or at most 2184, at least or exactly or at most 2185, at least or exactly or at most 2186, at least or exactly or at most 2187, at least or exactly or at most 2188, at least or exactly or at most 2189, at least or exactly

or at most 2190, at least or exactly or at most 2191, at least or exactly or at most 2192, at least or exactly or at most 2193, at least or exactly or at most 2194, at least or exactly or at most 2195, at least or exactly or at most 2196, at least or exactly or at most 2197, at least or exactly or at most 2198, at least or exactly or at most 2199, at least or exactly or at most 2200, at least or exactly or at most 2201, at least or exactly or at most 2202, at least or exactly or at most 2203, at least or exactly or at most 2204, at least or exactly or at most 2205, at least or exactly or at most 2206, at least or exactly or at most 2207, at least or exactly or at most 2208, at least or exactly or at most 2209, at least or exactly or at most 2210, at least or exactly or at most 2211, at least or exactly or at most 2212, at least or exactly or at most 2213, at least or exactly or at most 2214, at least or exactly or at most 2215, at least or exactly or at most 2216, at least or exactly or at most 2217, at least or exactly or at most 2218, at least or exactly or at most 2219, at least or exactly or at most 2220, at least or exactly or at most 2221, at least or exactly or at most 2222, at least or exactly or at most 2223, at least or exactly or at most 2224, at least or exactly or at most 2225, at least or exactly or at most 2226, at least or exactly or at most 2227, at least or exactly or at most 2228, at least or exactly or at most 2229, at least or exactly or at most 2230, at least or exactly or at most 2231, at least or exactly or at most 2232, at least or exactly or at most 2233, at least or exactly or at most 2234, at least or exactly or at most 2235, at least or exactly or at most 2236, at least or exactly or at most 2237, at least or exactly or at most 2238, at least or exactly or at most 2239, at least or exactly or at most 2240, at least or exactly or at most 2241, at least or exactly or at most 2242, at least or exactly or at most 2243, at least or exactly or at most 2244, at least or exactly or at most 2245, at least or exactly or at most 2246, at least or exactly or at most 2247, at least or exactly or at most 2248, at least or exactly or at most 2249, at least or exactly or at most 2250, at least or exactly or at most 2251, at least or exactly or at most 2252, at least or exactly or at most 2253, at least or exactly or at most 2254, at least or exactly or at most 2255, at least or exactly or at most 2256, at least or exactly or at most 2257, at least or exactly or at most 2258, at least or exactly or at most 2259, at least or exactly or at most 2260, at least or exactly or at most 2261, at least or exactly or at most 2262, at least or exactly or at most 2263, at least or exactly or at most 2264, at least or exactly or at most 2265, at least or exactly or at most 2266, at least or exactly or at most 2267, at least or exactly or at most 2268, at least or exactly or at most 2269, at least or exactly or at most 2270, at least or exactly or at most 2271, at least or exactly or at most 2272, at least or exactly or at most 2273, at least or exactly or at most 2274, at least or exactly or at most 2275, at least or exactly or at most 2276, at least or exactly or at most 2277, at least or exactly or at most 2278, at least or exactly or at most 2279, at least or exactly or at most 2280, at least or exactly or at most 2281, at least or exactly or at most 2282, at least or exactly or at most 2283, at least or exactly or at most 2284, at least or exactly or at most 2285, at least or exactly or at most 2286, at least or exactly or at most 2287, at least or exactly or at most 2288, at least or exactly or at most 2289, at least or exactly or at most 2290, at least or exactly or at most 2291, at least or exactly or at most 2292, at least or exactly or at most 2293, at least or exactly or at most 2294, at least or exactly or at most 2295, at least or exactly or at most 2296, at least or exactly or at most 2297, at least or exactly or at most 2298, at least or exactly or at most 2299, at least or exactly or at most 2300, at least or exactly or at most 2301, at least or exactly or at most 2302, at least or exactly or at most 2303, at least or exactly or at most 2304, at least or exactly or at most 2305, at least or exactly or at most 2306, at least or exactly or at most 2307, at least or exactly or at most 2308, at least or exactly or at most 2309, at least or exactly or at most 2310, at least or exactly or at most 2311, at least or exactly or at most 2312, at least or exactly or at most 2313, at least or exactly or at most 2314, at least or exactly or at most 2315, at least or exactly or at most 2316, at least or exactly or at most 2317, at least or exactly or at most 2318, at least or exactly or at most 2319, at least or exactly or at most 2320, at least or exactly or at most 2321, at least or exactly or at most 2322, at least or exactly or at most 2323, at least or exactly or at most 2324, at least or exactly or at most 2325, at least or exactly or at most 2326, at least or exactly or at most 2327, at least or exactly or at most 2328, at least or exactly or at most 2329, at least or exactly or at most 2330, at least or exactly or at most 2331, at least or exactly or at most 2332, at least or exactly or at most 2333, at least or exactly or at most 2334, at least or exactly or at most 2335, at least or exactly or at most 2336, at least or exactly or at most 2337, at least or exactly or at most 2338, at least or exactly or at most 2339, at least or exactly or at most 2340, at least or exactly or at most 2341, at least or exactly or at most 2342, at least or exactly or at most 2343, at least or exactly or at most 2344, at least or exactly or at most 2345, at least or exactly or at most 2346, at least or exactly or at most 2347, at least or exactly or at most 2348, at least or exactly or at most 2349, at least or exactly or at most 2350, at least or exactly or at most 2351, at least or exactly or at most 2352, at least or exactly or at most 2353, at least or exactly or at most 2354, at least or exactly or at most 2355, at least or exactly or at most 2356, at least or exactly or at most 2357, at least or exactly or at most 2358, at least or exactly or at most 2359, at least or exactly or at most 2360, at least or exactly or at most 2361, at least or exactly or at most 2362, at least or exactly or at most 2363, at least or exactly or at most 2364, at least or exactly or at most 2365, at least or exactly or at most 2366, at least or exactly or at most 2367, at least or exactly or at most 2368, at least or exactly or at most 2369, at least or exactly or at most 2370, at least or exactly or at most 2371, at least or exactly or at most 2372, at least or exactly or at most 2373, at least or exactly or at most 2374, at least or exactly or at most 2375, at least or exactly or at most 2376, at least or exactly or at most 2377, at least or exactly or at most 2378, at least or exactly or at most 2379, at least or exactly or at most 2380, at least or exactly or at most 2381, at least or exactly or at most 2382, at least or exactly or at most 2383, at least or exactly or at most 2384, at least or exactly or at most 2385, at least or exactly or at most 2386, at least or exactly or at most 2387, at least or exactly or at most 2388, at least or exactly or at most 2389, at least or exactly or at most 2390, at least or exactly or at most 2391, at least or exactly or at most 2392, at least or exactly or at most 2393, at least or exactly or at most 2394, at least or exactly or at most 2395, at least or exactly or at most 2396, at least or exactly or at most 2397, at least or exactly or at most 2398, at least or exactly or at most 2399, at least or exactly or at most 2400, at least or exactly or at most 2401, at least or exactly or at most 2402, at least or exactly or at most

2403, at least or exactly or at most 2404, at least or exactly or at most 2405, at least or exactly or at most 2406, at least or exactly or at most 2407, at least or exactly or at most 2408, at least or exactly or at most 2409, at least or exactly or at most 2410, at least or exactly or at most 2411, at least or exactly or at most 2412, at least or exactly or at most 2413, at least or exactly or at most 2414, at least or exactly or at most 2415, at least or exactly or at most 2416, at least or exactly or at most 2417, at least or exactly or at most 2418, at least or exactly or at most 2419, at least or exactly or at most 2420, at least or exactly or at most 2421, at least or exactly or at most 2422, at least or exactly or at most 2423, at least or exactly or at most 2424, at least or exactly or at most 2425, at least or exactly or at most 2426, at least or exactly or at most 2427, at least or exactly or at most 2428, at least or exactly or at most 2429, at least or exactly or at most 2430, at least or exactly or at most 2431, at least or exactly or at most 2432, at least or exactly or at most 2433, at least or exactly or at most 2434, at least or exactly or at most 2435, at least or exactly or at most 2436, at least or exactly or at most 2437, at least or exactly or at most 2438, at least or exactly or at most 2439, at least or exactly or at most 2440, at least or exactly or at most 2441, at least or exactly or at most 2442, at least or exactly or at most 2443, at least or exactly or at most 2444, at least or exactly or at most 2445, at least or exactly or at most 2446, at least or exactly or at most 2447, at least or exactly or at most 2448, at least or exactly or at most 2449, at least or exactly or at most 2450, at least or exactly or at most 2451, at least or exactly or at most 2452, at least or exactly or at most 2453, at least or exactly or at most 2454, at least or exactly or at most 2455, at least or exactly or at most 2456, at least or exactly or at most 2457, at least or exactly or at most 2458, at least or exactly or at most 2459, at least or exactly or at most 2460, at least or exactly or at most 2461, at least or exactly or at most 2462, at least or exactly or at most 2463, at least or exactly or at most 2464, at least or exactly or at most 2465, at least or exactly or at most 2466, or at least or exactly or at most 2467 contiguous amino acid residues.

[0096] Insofar as embodiment b relates to SEQ ID NOs: 29-30, the at least 5 contiguous amino acids referred to in option b) in the definition of the first aspect of the invention may also constitute at least or exactly or at most 2468, at least or exactly or at most 2469, at least or exactly or at most 2470, at least or exactly or at most 2471, at least or exactly or at most 2472, at least or exactly or at most 2473, at least or exactly or at most 2474, at least or exactly or at most 2475, at least or exactly or at most 2476, at least or exactly or at most 2477, at least or exactly or at most 2478, at least or exactly or at most 2479, at least or exactly or at most 2480, at least or exactly or at most 2481, at least or exactly or at most 2482, at least or exactly or at most 2483, at least or exactly or at most 2484, at least or exactly or at most 2485, at least or exactly or at most 2486, at least or exactly or at most 2487, at least or exactly or at most 2488, at least or exactly or at most 2489, at least or exactly or at most 2490, at least or exactly or at most 2491, at least or exactly or at most 2492, at least or exactly or at most 2493, at least or exactly or at most 2494, at least or exactly or at most 2495, at least or exactly or at most 2496, at least or exactly or at most 2497, at least or exactly or at most 2498, at least or exactly or at most 2499, at least or exactly or at most 2500, at least or exactly or at most 2501, at least or exactly or at most 2502, at least or exactly or at most 2503, at least or exactly or at most 2504, at least or exactly or at most 2505, at least or exactly or at most 2506, at least or exactly or at most 2507, at least or exactly or at most 2508, at least or exactly or at most 2509, at least or exactly or at most 2510, at least or exactly or at most 2511, at least or exactly or at most 2512, at least or exactly or at most 2513, at least or exactly or at most 2514, at least or exactly or at most 2515, at least or exactly or at most 2516, at least or exactly or at most 2517, at least or exactly or at most 2518, at least or exactly or at most 2519, at least or exactly or at most 2520, at least or exactly or at most 2521, at least or exactly or at most 2522, at least or exactly or at most 2523, at least or exactly or at most 2524, at least or exactly or at most 2525, at least or exactly or at most 2526, at least or exactly or at most 2527, at least or exactly or at most 2528, at least or exactly or at most 2529, at least or exactly or at most 2530, at least or exactly or at most 2531, at least or exactly or at most 2532, at least or exactly or at most 2533, at least or exactly or at most 2534, at least or exactly or at most 2535, at least or exactly or at most 2536, at least or exactly or at most 2537, at least or exactly or at most 2538, at least or exactly or at most 2539, at least or exactly or at most 2540, at least or exactly or at most 2541, at least or exactly or at most 2542, at least or exactly or at most 2543, at least or exactly or at most 2544, at least or exactly or at most 2545, at least or exactly or at most 2546, at least or exactly or at most 2547, at least or exactly or at most 2548, at least or exactly or at most 2549, at least or exactly or at most 2550, at least or exactly or at most 2551, at least or exactly or at most 2552, at least or exactly or at most 2553, at least or exactly or at most 2554, at least or exactly or at most 2555, at least or exactly or at most 2556, at least or exactly or at most 2557, at least or exactly or at most 2558, at least or exactly or at most 2559, at least or exactly or at most 2560, at least or exactly or at most 2561, at least or exactly or at most 2562, at least or exactly or at most 2563, at least or exactly or at most 2564, at least or exactly or at most 2565, at least or exactly or at most 2566, at least or exactly or at most 2567, at least or exactly or at most 2568, at least or exactly or at most 2569, at least or exactly or at most 2570, at least or exactly or at most 2571, at least or exactly or at most 2572, at least or exactly or at most 2573, at least or exactly or at most 2574, at least or exactly or at most 2575, at least or exactly or at most 2576, at least or exactly or at most 2577, at least or exactly or at most 2578, at least or exactly or at most 2579, at least or exactly or at most 2580, at least or exactly or at most 2581, at least or exactly or at most 2582, at least or exactly or at most 2583, at least or exactly or at most 2584, at least or exactly or at most 2585, at least or exactly or at most 2586, at least or exactly or at most 2587, at least or exactly or at most 2588, at least or exactly or at most 2589, at least or exactly or at most 2590, at least or exactly or at most 2591, at least or exactly or at most 2592, at least or exactly or at most 2593, at least or exactly or at most 2594, at least or exactly or at most 2595, at least or exactly or at most 2596, at least or exactly or at most 2597, at least or exactly or at most 2598, at least or exactly or at most 2599, at least or exactly or at most 2600, at least or exactly or at most 2601, at least or exactly or at most 2602, at least or exactly or at most 2603, at least or exactly or at most 2604, at least or exactly or at most 2605, at least or exactly or at most 2606, at least or exactly or at most 2607, at least or exactly or at most 2608, at least or exactly or at most 2609, at least or exactly or at most

2610, at least or exactly or at most 2611, at least or exactly or at most 2612, at least or exactly or at most 2613, at least or exactly or at most 2614, at least or exactly or at most 2615, at least or exactly or at most 2616, at least or exactly or at most 2617, at least or exactly or at most 2618, at least or exactly or at most 2619, at least or exactly or at most 2620, at least or exactly or at most 2621, at least or exactly or at most 2622, at least or exactly or at most 2623, at least or exactly or at most 2624, at least or exactly or at most 2625, at least or exactly or at most 2626, at least or exactly or at most 2627, at least or exactly or at most 2628, at least or exactly or at most 2629, at least or exactly or at most 2630, at least or exactly or at most 2631, at least or exactly or at most 2632, at least or exactly or at most 2633, at least or exactly or at most 2634, at least or exactly or at most 2635, at least or exactly or at most 2636, at least or exactly or at most 2637, at least or exactly or at most 2638, at least or exactly or at most 2639, at least or exactly or at most 2640, at least or exactly or at most 2641, at least or exactly or at most 2642, at least or exactly or at most 2643, at least or exactly or at most 2644, at least or exactly or at most 2645, at least or exactly or at most 2646, at least or exactly or at most 2647, at least or exactly or at most 2648, at least or exactly or at most 2649, at least or exactly or at most 2650, at least or exactly or at most 2651, at least or exactly or at most 2652, at least or exactly or at most 2653, at least or exactly or at most 2654, at least or exactly or at most 2655, at least or exactly or at most 2656, at least or exactly or at most 2657, at least or exactly or at most 2658, at least or exactly or at most 2659, at least or exactly or at most 2660, at least or exactly or at most 2661, at least or exactly or at most 2662, at least or exactly or at most 2663, at least or exactly or at most 2664, at least or exactly or at most 2665, at least or exactly or at most 2666, at least or exactly or at most 2667, at least or exactly or at most 2668, at least or exactly or at most 2669, at least or exactly or at most 2670, at least or exactly or at most 2671, at least or exactly or at most 2672, at least or exactly or at most 2673, at least or exactly or at most 2674, at least or exactly or at most 2675, at least or exactly or at most 2676, at least or exactly or at most 2677, at least or exactly or at most 2678, at least or exactly or at most 2679, at least or exactly or at most 2680, at least or exactly or at most 2681, at least or exactly or at most 2682, at least or exactly or at most 2683, at least or exactly or at most 2684, at least or exactly or at most 2685, at least or exactly or at most 2686, at least or exactly or at most 2687, at least or exactly or at most 2688, at least or exactly or at most 2689, at least or exactly or at most 2690, at least or exactly or at most 2691, at least or exactly or at most 2692, at least or exactly or at most 2693, at least or exactly or at most 2694, at least or exactly or at most 2695, at least or exactly or at most 2696, at least or exactly or at most 2697, at least or exactly or at most 2698, at least or exactly or at most 2699, at least or exactly or at most 2700, at least or exactly or at most 2701, at least or exactly or at most 2702, at least or exactly or at most 2703, at least or exactly or at most 2704, at least or exactly or at most 2705, at least or exactly or at most 2706, at least or exactly or at most 2707, at least or exactly or at most 2708, at least or exactly or at most 2709, at least or exactly or at most 2710, at least or exactly or at most 2711, at least or exactly or at most 2712, at least or exactly or at most 2713, at least or exactly or at most 2714, at least or exactly or at most 2715, at least or exactly or at most 2716, at least or exactly or at most 2717, at least or exactly or at most 2718, at least or exactly or at most 2719, at least or exactly or at most 2720, at least or exactly or at most 2721, at least or exactly or at most 2722, at least or exactly or at most 2723, at least or exactly or at most 2724, at least or exactly or at most 2725, at least or exactly or at most 2726, at least or exactly or at most 2727, at least or exactly or at most 2728, at least or exactly or at most 2729, at least or exactly or at most 2730, at least or exactly or at most 2731, at least or exactly or at most 2732, at least or exactly or at most 2733, at least or exactly or at most 2734, at least or exactly or at most 2735, at least or exactly or at most 2736, at least or exactly or at most 2737, at least or exactly or at most 2738, at least or exactly or at most 2739, at least or exactly or at most 2740, at least or exactly or at most 2741, at least or exactly or at most 2742, at least or exactly or at most 2743, at least or exactly or at most 2744, at least or exactly or at most 2745, at least or exactly or at most 2746, at least or exactly or at most 2747, at least or exactly or at most 2748, at least or exactly or at most 2749, at least or exactly or at most 2750, at least or exactly or at most 2751, at least or exactly or at most 2752, at least or exactly or at most 2753, at least or exactly or at most 2754, at least or exactly or at most 2755, at least or exactly or at most 2756, at least or exactly or at most 2757, at least or exactly or at most 2758, at least or exactly or at most 2759, at least or exactly or at most 2760, at least or exactly or at most 2761, at least or exactly or at most 2762, at least or exactly or at most 2763, at least or exactly or at most 2764, at least or exactly or at most 2765, at least or exactly or at most 2766, at least or exactly or at most 2767, at least or exactly or at most 2768, at least or exactly or at most 2769, at least or exactly or at most 2770, at least or exactly or at most 2771, at least or exactly or at most 2772, at least or exactly or at most 2773, at least or exactly or at most 2774, at least or exactly or at most 2775, at least or exactly or at most 2776, at least or exactly or at most 2777, at least or exactly or at most 2778, at least or exactly or at most 2779, at least or exactly or at most 2780, at least or exactly or at most 2781, at least or exactly or at most 2782, at least or exactly or at most 2783, at least or exactly or at most 2784, at least or exactly or at most 2785, at least or exactly or at most 2786, at least or exactly or at most 2787, at least or exactly or at most 2788, at least or exactly or at most 2789, at least or exactly or at most 2790, at least or exactly or at most 2791, at least or exactly or at most 2792, at least or exactly or at most 2793, at least or exactly or at most 2794, at least or exactly or at most 2795, at least or exactly or at most 2796, at least or exactly or at most 2797, at least or exactly or at most 2798, at least or exactly or at most 2799, at least or exactly or at most 2800, at least or exactly or at most 2801, at least or exactly or at most 2802, at least or exactly or at most 2803, at least or exactly or at most 2804, at least or exactly or at most 2805, at least or exactly or at most 2806, at least or exactly or at most 2807, at least or exactly or at most 2808, at least or exactly or at most 2809, at least or exactly or at most 2810, at least or exactly or at most 2811, at least or exactly or at most 2812, at least or exactly or at most 2813, at least or exactly or at most 2814, at least or exactly or at most 2815, at least or exactly or at most 2816, at least or exactly or at most 2817, at least or exactly or at most 2818, at least or exactly or at most 2819, at least or exactly or at most 2820, at least or exactly or at most 2821, at least or exactly or at most 2822, at least or exactly or at most 2823, at least

or exactly or at most 2824, at least or exactly or at most 2825, at least or exactly or at most 2826, at least or exactly or at most 2827, at least or exactly or at most 2828, at least or exactly or at most 2829, at least or exactly or at most 2830, at least or exactly or at most 2831, at least or exactly or at most 2832, at least or exactly or at most 2833, at least or exactly or at most 2834, at least or exactly or at most 2835, at least or exactly or at most 2836, at least or exactly or at most 2837, at least or exactly or at most 2838, at least or exactly or at most 2839, at least or exactly or at most 2840, at least or exactly or at most 2841, at least or exactly or at most 2842, at least or exactly or at most 2843, at least or exactly or at most 2844, at least or exactly or at most 2845, at least or exactly or at most 2846, at least or exactly or at most 2847, at least or exactly or at most 2848, at least or exactly or at most 2849, at least or exactly or at most 2850, at least or exactly or at most 2851, at least or exactly or at most 2852, at least or exactly or at most 2853, at least or exactly or at most 2854, at least or exactly or at most 2855, at least or exactly or at most 2856, at least or exactly or at most 2857, at least or exactly or at most 2858, at least or exactly or at most 2859, at least or exactly or at most 2860, at least or exactly or at most 2861, at least or exactly or at most 2862, at least or exactly or at most 2863, at least or exactly or at most 2864, at least or exactly or at most 2865, at least or exactly or at most 2866, at least or exactly or at most 2867, at least or exactly or at most 2868, at least or exactly or at most 2869, at least or exactly or at most 2870, at least or exactly or at most 2871, at least or exactly or at most 2872, at least or exactly or at most 2873, at least or exactly or at most 2874, at least or exactly or at most 2875, at least or exactly or at most 2876, at least or exactly or at most 2877, at least or exactly or at most 2878, at least or exactly or at most 2879, at least or exactly or at most 2880, at least or exactly or at most 2881, at least or exactly or at most 2882, at least or exactly or at most 2883, at least or exactly or at most 2884, at least or exactly or at most 2885, at least or exactly or at most 2886, at least or exactly or at most 2887, at least or exactly or at most 2888, at least or exactly or at most 2889, at least or exactly or at most 2890, at least or exactly or at most 2891, at least or exactly or at most 2892, at least or exactly or at most 2893, at least or exactly or at most 2894, at least or exactly or at most 2895, at least or exactly or at most 2896, at least or exactly or at most 2897, at least or exactly or at most 2898, at least or exactly or at most 2899, at least or exactly or at most 2900, at least or exactly or at most 2901, at least or exactly or at most 2902, at least or exactly or at most 2903, at least or exactly or at most 2904, at least or exactly or at most 2905, at least or exactly or at most 2906, at least or exactly or at most 2907, at least or exactly or at most 2908, at least or exactly or at most 2909, at least or exactly or at most 2910, at least or exactly or at most 2911, at least or exactly or at most 2912, at least or exactly or at most 2913, at least or exactly or at most 2914, at least or exactly or at most 2915, at least or exactly or at most 2916, at least or exactly or at most 2917, at least or exactly or at most 2918, at least or exactly or at most 2919, at least or exactly or at most 2920, at least or exactly or at most 2921, at least or exactly or at most 2922, at least or exactly or at most 2923, at least or exactly or at most 2924, at least or exactly or at most 2925, at least or exactly or at most 2926, at least or exactly or at most 2927, at least or exactly or at most 2928, at least or exactly or at most 2929, at least or exactly or at most 2930, at least or exactly or at most 2931, at least or exactly or at most 2932, at least or exactly or at most 2933, at least or exactly or at most 2934, at least or exactly or at most 2935, at least or exactly or at most 2936, at least or exactly or at most 2937, at least or exactly or at most 2938, at least or exactly or at most 2939, at least or exactly or at most 2940, at least or exactly or at most 2941, at least or exactly or at most 2942, at least or exactly or at most 2943, at least or exactly or at most 2944, at least or exactly or at most 2945, at least or exactly or at most 2946, at least or exactly or at most 2947, at least or exactly or at most 2948, at least or exactly or at most 2949, at least or exactly or at most 2950, at least or exactly or at most 2951, at least or exactly or at most 2952, at least or exactly or at most 2953, at least or exactly or at most 2954, at least or exactly or at most 2955, at least or exactly or at most 2956, at least or exactly or at most 2957, at least or exactly or at most 2958, at least or exactly or at most 2959, at least or exactly or at most 2960, at least or exactly or at most 2961, at least or exactly or at most 2962, at least or exactly or at most 2963, at least or exactly or at most 2964, at least or exactly or at most 2965, at least or exactly or at most 2966, at least or exactly or at most 2967, at least or exactly or at most 2968, at least or exactly or at most 2969, at least or exactly or at most 2970, at least or exactly or at most 2971, at least or exactly or at most 2972, at least or exactly or at most 2973, at least or exactly or at most 2974, at least or exactly or at most 2975, at least or exactly or at most 2976, at least or exactly or at most 2977, at least or exactly or at most 2978, at least or exactly or at most 2979, at least or exactly or at most 2980, at least or exactly or at most 2981, at least or exactly or at most 2982, at least or exactly or at most 2983, at least or exactly or at most 2984, at least or exactly or at most 2985, at least or exactly or at most 2986, at least or exactly or at most 2987, at least or exactly or at most 2988, at least or exactly or at most 2989, at least or exactly or at most 2990, at least or exactly or at most 2991, at least or exactly or at most 2992, at least or exactly or at most 2993, at least or exactly or at most 2994, at least or exactly or at most 2995, at least or exactly or at most 2996, at least or exactly or at most 2997, at least or exactly or at most 2998, at least or exactly or at most 2999, at least or exactly or at most 3000, at least or exactly or at most 3001, at least or exactly or at most 3002, at least or exactly or at most 3003, at least or exactly or at most 3004, at least or exactly or at most 3005, at least or exactly or at most 3006, at least or exactly or at most 3007, at least or exactly or at most 3008, at least or exactly or at most 3009, at least or exactly or at most 3010, at least or exactly or at most 3011, at least or exactly or at most 3012, at least or exactly or at most 3013, at least or exactly or at most 3014, at least or exactly or at most 3015, at least or exactly or at most 3016, at least or exactly or at most 3017, at least or exactly or at most 3018, at least or exactly or at most 3019, at least or exactly or at most 3020, at least or exactly or at most 3021, at least or exactly or at most 3022, at least or exactly or at most 3023, at least or exactly or at most 3024, at least or exactly or at most 3025, at least or exactly or at most 3026, at least or exactly or at most 3027, at least or exactly or at most 3028, at least or exactly or at most 3029, at least or exactly or at most 3030, at least or exactly or at most 3031, at least or exactly or at most 3032, at least or exactly or at most 3033, at least or exactly or at most 3034, at least or exactly or at most 3035, at least or exactly or at most 3036, at least or exactly

or at most 3037, at least or exactly or at most 3038, at least or exactly or at most 3039, at least or exactly or at most 3040, at least or exactly or at most 3041, at least or exactly or at most 3042, at least or exactly or at most 3043, at least or exactly or at most 3044, at least or exactly or at most 3045, at least or exactly or at most 3046, at least or exactly or at most 3047, at least or exactly or at most 3048, at least or exactly or at most 3049, at least or exactly or at most 3050, at least or exactly or at most 3051, at least or exactly or at most 3052, at least or exactly or at most 3053, at least or exactly or at most 3054, at least or exactly or at most 3055, at least or exactly or at most 3056, at least or exactly or at most 3057, at least or exactly or at most 3058, at least or exactly or at most 3059, at least or exactly or at most 3060, at least or exactly or at most 3061, at least or exactly or at most 3062, at least or exactly or at most 3063, at least or exactly or at most 3064, at least or exactly or at most 3065, at least or exactly or at most 3066, at least or exactly or at most 3067, at least or exactly or at most 3068, at least or exactly or at most 3069, at least or exactly or at most 3070, at least or exactly or at most 3071, at least or exactly or at most 3072, at least or exactly or at most 3073, at least or exactly or at most 3074, at least or exactly or at most 3075, at least or exactly or at most 3076, at least or exactly or at most 3077, at least or exactly or at most 3078, at least or exactly or at most 3079, at least or exactly or at most 3080, at least or exactly or at most 3081, at least or exactly or at most 3082, at least or exactly or at most 3083, at least or exactly or at most 3084, at least or exactly or at most 3085, at least or exactly or at most 3086, at least or exactly or at most 3087, at least or exactly or at most 3088, at least or exactly or at most 3089, at least or exactly or at most 3090, at least or exactly or at most 3091, at least or exactly or at most 3092, at least or exactly or at most 3093, at least or exactly or at most 3094, at least or exactly or at most 3095, at least or exactly or at most 3096, at least or exactly or at most 3097, at least or exactly or at most 3098, at least or exactly or at most 3099, at least or exactly or at most 3100, at least or exactly or at most 3101, at least or exactly or at most 3102, at least or exactly or at most 3103, at least or exactly or at most 3104, at least or exactly or at most 3105, at least or exactly or at most 3106, at least or exactly or at most 3107, at least or exactly or at most 3108, at least or exactly or at most 3109, at least or exactly or at most 3110, at least or exactly or at most 3111, at least or exactly or at most 3112, at least or exactly or at most 3113, at least or exactly or at most 3114, at least or exactly or at most 3115, at least or exactly or at most 3116, at least or exactly or at most 3117, at least or exactly or at most 3118, at least or exactly or at most 3119, at least or exactly or at most 3120, at least or exactly or at most 3121, at least or exactly or at most 3122, at least or exactly or at most 3123, at least or exactly or at most 3124, at least or exactly or at most 3125, at least or exactly or at most 3126, at least or exactly or at most 3127, at least or exactly or at most 3128, at least or exactly or at most 3129, at least or exactly or at most 3130, at least or exactly or at most 3131, at least or exactly or at most 3132, at least or exactly or at most 3133, at least or exactly or at most 3134, at least or exactly or at most 3135, at least or exactly or at most 3136, at least or exactly or at most 3137, at least or exactly or at most 3138, at least or exactly or at most 3139, at least or exactly or at most 3140, at least or exactly or at most 3141, at least or exactly or at most 3142, at least or exactly or at most 3143, at least or exactly or at most 3144, at least or exactly or at most 3145, at least or exactly or at most 3146, at least or exactly or at most 3147, at least or exactly or at most 3148, at least or exactly or at most 3149, at least or exactly or at most 3150, at least or exactly or at most 3151, at least or exactly or at most 3152, at least or exactly or at most 3153, at least or exactly or at most 3154, at least or exactly or at most 3155, at least or exactly or at most 3156, at least or exactly or at most 3157, at least or exactly or at most 3158, at least or exactly or at most 3159, at least or exactly or at most 3160, at least or exactly or at most 3161, at least or exactly or at most 3162, at least or exactly or at most 3163, at least or exactly or at most 3164, at least or exactly or at most 3165, at least or exactly or at most 3166, at least or exactly or at most 3167, at least or exactly or at most 3168, at least or exactly or at most 3169, at least or exactly or at most 3170, at least or exactly or at most 3171, at least or exactly or at most 3172, at least or exactly or at most 3173, at least or exactly or at most 3174, at least or exactly or at most 3175, at least or exactly or at most 3176, at least or exactly or at most 3177, at least or exactly or at most 3178, at least or exactly or at most 3179, at least or exactly or at most 3180, at least or exactly or at most 3181, at least or exactly or at most 3182, at least or exactly or at most 3183, at least or exactly or at most 3184, at least or exactly or at most 3185, at least or exactly or at most 3186, at least or exactly or at most 3187, at least or exactly or at most 3188, at least or exactly or at most 3189, at least or exactly or at most 3190, at least or exactly or at most 3191, at least or exactly or at most 3192, at least or exactly or at most 3193, at least or exactly or at most 3194, at least or exactly or at most 3195, at least or exactly or at most 3196, at least or exactly or at most 3197, at least or exactly or at most 3198, at least or exactly or at most 3199, at least or exactly or at most 3200, at least or exactly or at most 3201, at least or exactly or at most 3202, at least or exactly or at most 3203, at least or exactly or at most 3204, at least or exactly or at most 3205, at least or exactly or at most 3206, at least or exactly or at most 3207, at least or exactly or at most 3208, at least or exactly or at most 3209, at least or exactly or at most 3210, at least or exactly or at most 3211, at least or exactly or at most 3212, at least or exactly or at most 3213, at least or exactly or at most 3214, at least or exactly or at most 3215, at least or exactly or at most 3216, at least or exactly or at most 3217, at least or exactly or at most 3218, at least or exactly or at most 3219, at least or exactly or at most 3220, at least or exactly or at most 3221, at least or exactly or at most 3222, at least or exactly or at most 3223, at least or exactly or at most 3224, at least or exactly or at most 3225, at least or exactly or at most 3226, at least or exactly or at most 3227, at least or exactly or at most 3228, at least or exactly or at most 3229, at least or exactly or at most 3230, at least or exactly or at most 3231, at least or exactly or at most 3232, at least or exactly or at most 3233, at least or exactly or at most 3234, at least or exactly or at most 3235, at least or exactly or at most 3236, at least or exactly or at most 3237, at least or exactly or at most 3238, at least or exactly or at most 3239, at least or exactly or at most 3240, at least or exactly or at most 3241, at least or exactly or at most 3242, at least or exactly or at most 3243, at least or exactly or at most 3244, at least or exactly or at most 3245, at least or exactly or at most 3246, at least or exactly or at most 3247, at least or exactly or at most 3248, at least or exactly or at most 3249, at least or exactly or at most

3250, at least or exactly or at most 3251, at least or exactly or at most 3252, at least or exactly or at most 3253, at least or exactly or at most 3254, at least or exactly or at most 3255, at least or exactly or at most 3256, at least or exactly or at most 3257, at least or exactly or at most 3258, at least or exactly or at most 3259, at least or exactly or at most 3260, at least or exactly or at most 3261, at least or exactly or at most 3262, at least or exactly or at most 3263, at least or exactly or at most 3264, at least or exactly or at most 3265, at least or exactly or at most 3266, at least or exactly or at most 3267, at least or exactly or at most 3268, at least or exactly or at most 3269, at least or exactly or at most 3270, at least or exactly or at most 3271, at least or exactly or at most 3272, at least or exactly or at most 3273, at least or exactly or at most 3274, at least or exactly or at most 3275, at least or exactly or at most 3276, at least or exactly or at most 3277, at least or exactly or at most 3278, at least or exactly or at most 3279, at least or exactly or at most 3280, at least or exactly or at most 3281, at least or exactly or at most 3282, at least or exactly or at most 3283, at least or exactly or at most 3284, at least or exactly or at most 3285, at least or exactly or at most 3286, at least or exactly or at most 3287, at least or exactly or at most 3288, at least or exactly or at most 3289, at least or exactly or at most 3290, at least or exactly or at most 3291, at least or exactly or at most 3292, at least or exactly or at most 3293, at least or exactly or at most 3294, at least or exactly or at most 3295, at least or exactly or at most 3296, at least or exactly or at most 3297, at least or exactly or at most 3298, at least or exactly or at most 3299, at least or exactly or at most 3300, at least or exactly or at most 3301, at least or exactly or at most 3302, at least or exactly or at most 3303, at least or exactly or at most 3304, at least or exactly or at most 3305, at least or exactly or at most 3306, at least or exactly or at most 3307, at least or exactly or at most 3308, at least or exactly or at most 3309, at least or exactly or at most 3310, at least or exactly or at most 3311, at least or exactly or at most 3312, at least or exactly or at most 3313, at least or exactly or at most 3314, at least or exactly or at most 3315, at least or exactly or at most 3316, at least or exactly or at most 3317, at least or exactly or at most 3318, at least or exactly or at most 3319, at least or exactly or at most 3320, at least or exactly or at most 3321, at least or exactly or at most 3322, at least or exactly or at most 3323, at least or exactly or at most 3324, at least or exactly or at most 3325, at least or exactly or at most 3326, at least or exactly or at most 3327, at least or exactly or at most 3328, at least or exactly or at most 3329, at least or exactly or at most 3330, at least or exactly or at most 3331, at least or exactly or at most 3332, at least or exactly or at most 3333, or at least or exactly or at most 3334 contiguous amino acid residues.

[0097] Insofar as embodiment b relates to SEQ ID NO: 30, the at least 5 contiguous amino acids referred to in option b) in the definition of the first aspect of the invention may also constitute at least or exactly or at most 3535, at least or exactly or at most 3536, at least or exactly or at most 3537, at least or exactly or at most 3538, at least or exactly or at most 3539, at least or exactly or at most 3540, at least or exactly or at most 3541, at least or exactly or at most 3542, at least or exactly or at most 3543, at least or exactly or at most 3544, at least or exactly or at most 3545, at least or exactly or at most 3546, at least or exactly or at most 3547, at least or exactly or at most 3548, at least or exactly or at most 3549, at least or exactly or at most 3550, at least or exactly or at most 3551, at least or exactly or at most 3552, at least or exactly or at most 3553, at least or exactly or at most 3554, at least or exactly or at most 3555, at least or exactly or at most 3556, at least or exactly or at most 3557, at least or exactly or at most 3558, at least or exactly or at most 3559, at least or exactly or at most 3560, at least or exactly or at most 3561, at least or exactly or at most 3562, at least or exactly or at most 3563, at least or exactly or at most 3564, at least or exactly or at most 3565, at least or exactly or at most 3566, at least or exactly or at most 3567, at least or exactly or at most 3568, at least or exactly or at most 3569, at least or exactly or at most 3570, at least or exactly or at most 3571, at least or exactly or at most 3572, at least or exactly or at most 3573, at least or exactly or at most 3574, at least or exactly or at most 3575, at least or exactly or at most 3576, at least or exactly or at most 3577, at least or exactly or at most 3578, at least or exactly or at most 3579, at least or exactly or at most 3580, at least or exactly or at most 3581, at least or exactly or at most 3582, at least or exactly or at most 3583, at least or exactly or at most 3584, at least or exactly or at most 3585, at least or exactly or at most 3586, at least or exactly or at most 3587, at least or exactly or at most 3588, at least or exactly or at most 3589, at least or exactly or at most 3590, at least or exactly or at most 3591, at least or exactly or at most 3592, at least or exactly or at most 3593, at least or exactly or at most 3594, at least or exactly or at most 3595, at least or exactly or at most 3596, at least or exactly or at most 3597, at least or exactly or at most 3598, at least or exactly or at most 3599, at least or exactly or at most 3600, at least or exactly or at most 3601, at least or exactly or at most 3602, at least or exactly or at most 3603, at least or exactly or at most 3604, at least or exactly or at most 3605, at least or exactly or at most 3606, at least or exactly or at most 3607, at least or exactly or at most 3608, at least or exactly or at most 3609, at least or exactly or at most 3610, at least or exactly or at most 3611, at least or exactly or at most 3612, at least or exactly or at most 3613, at least or exactly or at most 3614, at least or exactly or at most 3615, at least or exactly or at most 3616, at least or exactly or at most 3617, at least or exactly or at most 3618, at least or exactly or at most 3619, at least or exactly or at most 3620, at least or exactly or at most 3621, at least or exactly or at most 3622, at least or exactly or at most 3623, at least or exactly or at most 3624, at least or exactly or at most 3625, at least or exactly or at most 3626, at least or exactly or at most 3627, at least or exactly or at most 3628, at least or exactly or at most 3629, at least or exactly or at most 3630, at least or exactly or at most 3631, at least or exactly or at most 3632, at least or exactly or at most 3633, at least or exactly or at most 3634, at least or exactly or at most 3635, at least or exactly or at most 3636, at least or exactly or at most 3637, at least or exactly or at most 3638, at least or exactly or at most 3639, at least or exactly or at most 3640, at least or exactly or at most 3641, at least or exactly or at most 3642, at least or exactly or at most 3643, at least or exactly or at most 3644, at least or exactly or at most 3645, at least or exactly or at most 3646, at least or exactly or at most 3647, at least or exactly or at most 3648, at least or exactly or at most 3649, at least or exactly or at most 3650, at least or exactly or at most 3651, at least or exactly or at most 3652, at least or exactly or at most 3653, at least or exactly or at most 3654, at least or exactly or at most 3655, at least or exactly or at most 3656, at least or exactly or at most 3657,

at least or exactly or at most 3658, at least or exactly or at most 3659, at least or exactly or at most 3660, at least or exactly or at most 3661, at least or exactly or at most 3662, at least or exactly or at most 3663, at least or exactly or at most 3664, at least or exactly or at most 3665, at least or exactly or at most 3666, at least or exactly or at most 3667, at least or exactly or at most 3668, at least or exactly or at most 3669, at least or exactly or at most 3670, at least or exactly or at most 3671, at least or exactly or at most 3672, at least or exactly or at most 3673, at least or exactly or at most 3674, at least or exactly or at most 3675, at least or exactly or at most 3676, at least or exactly or at most 3677, at least or exactly or at most 3678, at least or exactly or at most 3679, at least or exactly or at most 3680, at least or exactly or at most 3681, at least or exactly or at most 3682, at least or exactly or at most 3683, at least or exactly or at most 3684, at least or exactly or at most 3685, at least or exactly or at most 3686, at least or exactly or at most 3687, at least or exactly or at most 3688, at least or exactly or at most 3689, at least or exactly or at most 3690, at least or exactly or at most 3691, at least or exactly or at most 3692, at least or exactly or at most 3693, at least or exactly or at most 3694, at least or exactly or at most 3695, at least or exactly or at most 3696, at least or exactly or at most 3697, at least or exactly or at most 3698, at least or exactly or at most 3699, at least or exactly or at most 3700, at least or exactly or at most 3701, at least or exactly or at most 3702, at least or exactly or at most 3703, at least or exactly or at most 3704, at least or exactly or at most 3705, at least or exactly or at most 3706, at least or exactly or at most 3707, at least or exactly or at most 3708, at least or exactly or at most 3709, at least or exactly or at most 3710, at least or exactly or at most 3711, at least or exactly or at most 3712, at least or exactly or at most 3713, at least or exactly or at most 3714, at least or exactly or at most 3715, at least or exactly or at most 3716, at least or exactly or at most 3717, at least or exactly or at most 3718, at least or exactly or at most 3719, at least or exactly or at most 3720, at least or exactly or at most 3721, at least or exactly or at most 3722, at least or exactly or at most 3723, at least or exactly or at most 3724, at least or exactly or at most 3725, at least or exactly or at most 3726, at least or exactly or at most 3727, at least or exactly or at most 3728, at least or exactly or at most 3729, at least or exactly or at most 3730, at least or exactly or at most 3731, at least or exactly or at most 3732, at least or exactly or at most 3733, at least or exactly or at most 3734, at least or exactly or at most 3735, at least or exactly or at most 3736, at least or exactly or at most 3737, at least or exactly or at most 3738, at least or exactly or at most 3739, at least or exactly or at most 3740, at least or exactly or at most 3741, at least or exactly or at most 3742, at least or exactly or at most 3743, at least or exactly or at most 3744, at least or exactly or at most 3745, at least or exactly or at most 3746, at least or exactly or at most 3747, at least or exactly or at most 3748, at least or exactly or at most 3749, at least or exactly or at most 3750, at least or exactly or at most 3751, at least or exactly or at most 3752, at least or exactly or at most 3753, at least or exactly or at most 3754, at least or exactly or at most 3755, at least or exactly or at most 3756, at least or exactly or at most 3757, at least or exactly or at most 3758, at least or exactly or at most 3759, at least or exactly or at most 3760, at least or exactly or at most 3761, at least or exactly or at most 3762, at least or exactly or at most 3763, at least or exactly or at most 3764, at least or exactly or at most 3765, at least or exactly or at most 3766, at least or exactly or at most 3767, at least or exactly or at most 3768, at least or exactly or at most 3769, at least or exactly or at most 3770, at least or exactly or at most 3771, at least or exactly or at most 3772, at least or exactly or at most 3773, at least or exactly or at most 3774, at least or exactly or at most 3775, at least or exactly or at most 3776, at least or exactly or at most 3777, at least or exactly or at most 3778, at least or exactly or at most 3779, at least or exactly or at most 3780, at least or exactly or at most 3781, at least or exactly or at most 3782, at least or exactly or at most 3783, at least or exactly or at most 3784, at least or exactly or at most 3785, at least or exactly or at most 3786, at least or exactly or at most 3787, at least or exactly or at most 3788, at least or exactly or at most 3789, at least or exactly or at most 3790, at least or exactly or at most 3791, at least or exactly or at most 3792, at least or exactly or at most 3793, at least or exactly or at most 3794, at least or exactly or at most 3795, at least or exactly or at most 3796, at least or exactly or at most 3797, at least or exactly or at most 3798, at least or exactly or at most 3799, at least or exactly or at most 3800, at least or exactly or at most 3801, at least or exactly or at most 3802, at least or exactly or at most 3803, at least or exactly or at most 3804, at least or exactly or at most 3805, at least or exactly or at most 3806, at least or exactly or at most 3807, at least or exactly or at most 3808, at least or exactly or at most 3809, at least or exactly or at most 3810, at least or exactly or at most 3811, at least or exactly or at most 3812, at least or exactly or at most 3813, at least or exactly or at most 3814, at least or exactly or at most 3815, at least or exactly or at most 3816, at least or exactly or at most 3817, at least or exactly or at most 3818, at least or exactly or at most 3819, at least or exactly or at most 3820, at least or exactly or at most 3821, at least or exactly or at most 3822, at least or exactly or at most 3823, at least or exactly or at most 3824, at least or exactly or at most 3825, at least or exactly or at most 3826, at least or exactly or at most 3827, at least or exactly or at most 3828, at least or exactly or at most 3829, at least or exactly or at most 3830, at least or exactly or at most 3831, at least or exactly or at most 3832, at least or exactly or at most 3833, at least or exactly or at most 3834, at least or exactly or at most 3835, at least or exactly or at most 3836, at least or exactly or at most 3837, at least or exactly or at most 3838, at least or exactly or at most 3839, at least or exactly or at most 3840, at least or exactly or at most 3841, at least or exactly or at most 3842, at least or exactly or at most 3843, at least or exactly or at most 3844, at least or exactly or at most 3845, at least or exactly or at most 3846, at least or exactly or at most 3847, at least or exactly or at most 3848, at least or exactly or at most 3849, at least or exactly or at most 3850, at least or exactly or at most 3851, at least or exactly or at most 3852, at least or exactly or at most 3853, at least or exactly or at most 3854, at least or exactly or at most 3855, at least or exactly or at most 3856, at least or exactly or at most 3857, at least or exactly or at most 3858, at least or exactly or at most 3859, at least or exactly or at most 3860, at least or exactly or at most 3861, at least or exactly or at most 3862, at least or exactly or at most 3863, at least or exactly or at most 3864, at least or exactly or at most 3865, at least or exactly or at most 3866, at least or exactly or at most 3867, at least or exactly or at most 3868, at least or exactly or at most 3869, at least or exactly or at most 3870, at least or

exactly or at most 3871, at least or exactly or at most 3872, at least or exactly or at most 3873, at least or exactly or at most 3874, at least or exactly or at most 3875, at least or exactly or at most 3876, at least or exactly or at most 3877, at least or exactly or at most 3878, at least or exactly or at most 3879, at least or exactly or at most 3880, at least or exactly or at most 3881, at least or exactly or at most 3882, at least or exactly or at most 3883, at least or exactly or at most 3884, at least or exactly or at most 3885, at least or exactly or at most 3886, at least or exactly or at most 3887, at least or exactly or at most 3888, at least or exactly or at most 3889, at least or exactly or at most 3890, at least or exactly or at most 3891, at least or exactly or at most 3892, at least or exactly or at most 3893, at least or exactly or at most 3894, at least or exactly or at most 3895, at least or exactly or at most 3896, at least or exactly or at most 3897, at least or exactly or at most 3898, at least or exactly or at most 3899, at least or exactly or at most 3900, at least or exactly or at most 3901, at least or exactly or at most 3902, at least or exactly or at most 3903, at least or exactly or at most 3904, at least or exactly or at most 3905, at least or exactly or at most 3906, at least or exactly or at most 3907, at least or exactly or at most 3908, at least or exactly or at most 3909, at least or exactly or at most 3910, at least or exactly or at most 3911, at least or exactly or at most 3912, at least or exactly or at most 3913, at least or exactly or at most 3914, at least or exactly or at most 3915, at least or exactly or at most 3916, at least or exactly or at most 3917, at least or exactly or at most 3918, at least or exactly or at most 3919, at least or exactly or at most 3920, at least or exactly or at most 3921, at least or exactly or at most 3922, at least or exactly or at most 3923, at least or exactly or at most 3924, at least or exactly or at most 3925, at least or exactly or at most 3926, at least or exactly or at most 3927, at least or exactly or at most 3928, at least or exactly or at most 3929, at least or exactly or at most 3930, at least or exactly or at most 3931, at least or exactly or at most 3932, at least or exactly or at most 3933, at least or exactly or at most 3934, at least or exactly or at most 3935, at least or exactly or at most 3936, at least or exactly or at most 3937, at least or exactly or at most 3938, at least or exactly or at most 3939, at least or exactly or at most 3940, at least or exactly or at most 3941, at least or exactly or at most 3942, at least or exactly or at most 3943, at least or exactly or at most 3944, at least or exactly or at most 3945, at least or exactly or at most 3946, at least or exactly or at most 3947, at least or exactly or at most 3948, at least or exactly or at most 3949, at least or exactly or at most 3950, at least or exactly or at most 3951, at least or exactly or at most 3952, at least or exactly or at most 3953, at least or exactly or at most 3954, at least or exactly or at most 3955, at least or exactly or at most 3956, at least or exactly or at most 3957, at least or exactly or at most 3958, at least or exactly or at most 3959, at least or exactly or at most 3960, at least or exactly or at most 3961, at least or exactly or at most 3962, at least or exactly or at most 3963, at least or exactly or at most 3964, at least or exactly or at most 3965, at least or exactly or at most 3966, at least or exactly or at most 3967, at least or exactly or at most 3968, at least or exactly or at most 3969, at least or exactly or at most 3970, at least or exactly or at most 3971, at least or exactly or at most 3972, at least or exactly or at most 3973, at least or exactly or at most 3974, at least or exactly or at most 3975, at least or exactly or at most 3976, at least or exactly or at most 3977, at least or exactly or at most 3978, at least or exactly or at most 3979, at least or exactly or at most 3980, at least or exactly or at most 3981, at least or exactly or at most 3982, at least or exactly or at most 3983, at least or exactly or at most 3984, at least or exactly or at most 3985, at least or exactly or at most 3986, at least or exactly or at most 3987, at least or exactly or at most 3988, at least or exactly or at most 3989, at least or exactly or at most 3990, at least or exactly or at most 3991, at least or exactly or at most 3992, at least or exactly or at most 3993, at least or exactly or at most 3994, at least or exactly or at most 3995, at least or exactly or at most 3996, at least or exactly or at most 3997, at least or exactly or at most 3998, at least or exactly or at most 3999, at least or exactly or at most 4000, at least or exactly or at most 4001, at least or exactly or at most 4002, at least or exactly or at most 4003, at least or exactly or at most 4004, at least or exactly or at most 4005, at least or exactly or at most 4006, at least or exactly or at most 4007, at least or exactly or at most 4008, at least or exactly or at most 4009, at least or exactly or at most 4010, at least or exactly or at most 4011, at least or exactly or at most 4012, at least or exactly or at most 4013, at least or exactly or at most 4014, at least or exactly or at most 4015, at least or exactly or at most 4016, at least or exactly or at most 4017, at least or exactly or at most 4018, at least or exactly or at most 4019, at least or exactly or at most 4020, at least or exactly or at most 4021, at least or exactly or at most 4022, at least or exactly or at most 4023, at least or exactly or at most 4024, at least or exactly or at most 4025, at least or exactly or at most 4026, at least or exactly or at most 4027, at least or exactly or at most 4028, at least or exactly or at most 4029, at least or exactly or at most 4030, at least or exactly or at most 4031, at least or exactly or at most 4032, at least or exactly or at most 4033, at least or exactly or at most 4034, at least or exactly or at most 4035, at least or exactly or at most 4036, at least or exactly or at most 4037, at least or exactly or at most 4038, at least or exactly or at most 4039, at least or exactly or at most 4040, at least or exactly or at most 4041, at least or exactly or at most 4042, at least or exactly or at most 4043, at least or exactly or at most 4044, at least or exactly or at most 4045, at least or exactly or at most 4046, at least or exactly or at most 4047, at least or exactly or at most 4048, at least or exactly or at most 4049, at least or exactly or at most 4050, at least or exactly or at most 4051, at least or exactly or at most 4052, at least or exactly or at most 4053, at least or exactly or at most 4054, at least or exactly or at most 4055, at least or exactly or at most 4056, at least or exactly or at most 4057, at least or exactly or at most 4058, at least or exactly or at most 4059, at least or exactly or at most 4060, at least or exactly or at most 4061, at least or exactly or at most 4062, at least or exactly or at most 4063, at least or exactly or at most 4064, at least or exactly or at most 4065, at least or exactly or at most 4066, at least or exactly or at most 4067, at least or exactly or at most 4068, at least or exactly or at most 4069, at least or exactly or at most 4070, at least or exactly or at most 4071, at least or exactly or at most 4072, at least or exactly or at most 4073, at least or exactly or at most 4074, at least or exactly or at most 4075, at least or exactly or at most 4076, at least or exactly or at most 4077, at least or exactly or at most 4078, at least or exactly or at most 4079, at least or exactly or at most 4080, at least or exactly or at most 4081, at least or exactly or at most 4082, at least or exactly or at most 4083, at least or exactly or at

most 4084, at least or exactly or at most 4085, at least or exactly or at most 4086, at least or exactly or at most 4087, at least or exactly or at most 4088, at least or exactly or at most 4089, at least or exactly or at most 4090, at least or exactly or at most 4091, at least or exactly or at most 4092, at least or exactly or at most 4093, at least or exactly or at most 4094, at least or exactly or at most 4095, at least or exactly or at most 4096, at least or exactly or at most 4097, at least or exactly or at most 4098, at least or exactly or at most 4099, at least or exactly or at most 4100, at least or exactly or at most 4101, at least or exactly or at most 4102, at least or exactly or at most 4103, at least or exactly or at most 4104, at least or exactly or at most 4105, at least or exactly or at most 4106, at least or exactly or at most 4107, at least or exactly or at most 4108, at least or exactly or at most 4109, at least or exactly or at most 4110, at least or exactly or at most 4111, at least or exactly or at most 4112, at least or exactly or at most 4113, at least or exactly or at most 4114, at least or exactly or at most 4115, at least or exactly or at most 4116, at least or exactly or at most 4117, at least or exactly or at most 4118, at least or exactly or at most 4119, at least or exactly or at most 4120, at least or exactly or at most 4121, at least or exactly or at most 4122, at least or exactly or at most 4123, at least or exactly or at most 4124, at least or exactly or at most 4125, at least or exactly or at most 4126, at least or exactly or at most 4127, at least or exactly or at most 4128, at least or exactly or at most 4129, at least or exactly or at most 4130, at least or exactly or at most 4131, at least or exactly or at most 4132, at least or exactly or at most 4133, at least or exactly or at most 4134, at least or exactly or at most 4135, at least or exactly or at most 4136, at least or exactly or at most 4137, at least or exactly or at most 4138, at least or exactly or at most 4139, at least or exactly or at most 4140, at least or exactly or at most 4141, at least or exactly or at most 4142, at least or exactly or at most 4143, at least or exactly or at most 4144, at least or exactly or at most 4145, at least or exactly or at most 4146, at least or exactly or at most 4147, at least or exactly or at most 4148, at least or exactly or at most 4149, at least or exactly or at most 4150, at least or exactly or at most 4151, at least or exactly or at most 4152, at least or exactly or at most 4153, at least or exactly or at most 4154, at least or exactly or at most 4155, at least or exactly or at most 4156, at least or exactly or at most 4157, at least or exactly or at most 4158, at least or exactly or at most 4159, at least or exactly or at most 4160, at least or exactly or at most 4161, at least or exactly or at most 4162, at least or exactly or at most 4163, at least or exactly or at most 4164, at least or exactly or at most 4165, at least or exactly or at most 4166, at least or exactly or at most 4167, at least or exactly or at most 4168, at least or exactly or at most 4169, at least or exactly or at most 4170, at least or exactly or at most 4171, at least or exactly or at most 4172, at least or exactly or at most 4173, at least or exactly or at most 4174, at least or exactly or at most 4175, at least or exactly or at most 4176, at least or exactly or at most 4177, at least or exactly or at most 4178, at least or exactly or at most 4179, at least or exactly or at most 4180, at least or exactly or at most 4181, at least or exactly or at most 4182, at least or exactly or at most 4183, at least or exactly or at most 4184, at least or exactly or at most 4185, at least or exactly or at most 4186, at least or exactly or at most 4187, at least or exactly or at most 4188, at least or exactly or at most 4189, at least or exactly or at most 4190, at least or exactly or at most 4191, at least or exactly or at most 4192, at least or exactly or at most 4193, at least or exactly or at most 4194, at least or exactly or at most 4195, at least or exactly or at most 4196, at least or exactly or at most 4197, at least or exactly or at most 4198, at least or exactly or at most 4199, at least or exactly or at most 4200, at least or exactly or at most 4201, at least or exactly or at most 4202, at least or exactly or at most 4203, at least or exactly or at most 4204, at least or exactly or at most 4205, at least or exactly or at most 4206, at least or exactly or at most 4207, at least or exactly or at most 4208, at least or exactly or at most 4209, at least or exactly or at most 4210, at least or exactly or at most 4211, at least or exactly or at most 4212, at least or exactly or at most 4213, at least or exactly or at most 4214, at least or exactly or at most 4215, at least or exactly or at most 4216, at least or exactly or at most 4217, at least or exactly or at most 4218, at least or exactly or at most 4219, at least or exactly or at most 4220, at least or exactly or at most 4221, at least or exactly or at most 4222, at least or exactly or at most 4223, at least or exactly or at most 4224, at least or exactly or at most 4225, at least or exactly or at most 4226, at least or exactly or at most 4227, at least or exactly or at most 4228, at least or exactly or at most 4229, at least or exactly or at most 4230, at least or exactly or at most 4231, at least or exactly or at most 4232, at least or exactly or at most 4233, at least or exactly or at most 4234, at least or exactly or at most 4235, at least or exactly or at most 4236, at least or exactly or at most 4237, at least or exactly or at most 4238, at least or exactly or at most 4239, at least or exactly or at most 4240, at least or exactly or at most 4241, at least or exactly or at most 4242, at least or exactly or at most 4243, at least or exactly or at most 4244, at least or exactly or at most 4245, at least or exactly or at most 4246, at least or exactly or at most 4247, at least or exactly or at most 4248, at least or exactly or at most 4249, at least or exactly or at most 4250, at least or exactly or at most 4251, at least or exactly or at most 4252, at least or exactly or at most 4253, at least or exactly or at most 4254, at least or exactly or at most 4255, at least or exactly or at most 4256, at least or exactly or at most 4257, at least or exactly or at most 4258, at least or exactly or at most 4259, at least or exactly or at most 4260, at least or exactly or at most 4261, at least or exactly or at most 4262, at least or exactly or at most 4263, at least or exactly or at most 4264, at least or exactly or at most 4265, at least or exactly or at most 4266, at least or exactly or at most 4267, at least or exactly or at most 4268, at least or exactly or at most 4269, at least or exactly or at most 4270, at least or exactly or at most 4271, at least or exactly or at most 4272, at least or exactly or at most 4273, at least or exactly or at most 4274, at least or exactly or at most 4275, at least or exactly or at most 4276, at least or exactly or at most 4277, at least or exactly or at most 4278, at least or exactly or at most 4279, at least or exactly or at most 4280, at least or exactly or at most 4281, at least or exactly or at most 4282, at least or exactly or at most 4283, at least or exactly or at most 4284, at least or exactly or at most 4285, at least or exactly or at most 4286, at least or exactly or at most 4287, at least or exactly or at most 4288, at least or exactly or at most 4289, at least or exactly or at most 4290, at least or exactly or at most 4291, at least or exactly or at most 4292, at least or exactly or at most 4293, at least or exactly or at most 4294, at least or exactly or at most 4295, at least or exactly or at most 4296, at least or exactly or at most 4297,

at least or exactly or at most 4298, at least or exactly or at most 4299, at least or exactly or at most 4300, at least or exactly or at most 4301, at least or exactly or at most 4302, at least or exactly or at most 4303, at least or exactly or at most 4304, at least or exactly or at most 4305, at least or exactly or at most 4306, at least or exactly or at most 4307, at least or exactly or at most 4308, at least or exactly or at most 4309, at least or exactly or at most 4310, at least or exactly or at most 4311, at least or exactly or at most 4312, at least or exactly or at most 4313, at least or exactly or at most 4314, at least or exactly or at most 4315, at least or exactly or at most 4316, at least or exactly or at most 4317, at least or exactly or at most 4318, at least or exactly or at most 4319, at least or exactly or at most 4320, at least or exactly or at most 4321, at least or exactly or at most 4322, at least or exactly or at most 4323, at least or exactly or at most 4324, at least or exactly or at most 4325, at least or exactly or at most 4326, at least or exactly or at most 4327, at least or exactly or at most 4328, at least or exactly or at most 4329, at least or exactly or at most 4330, at least or exactly or at most 4331, at least or exactly or at most 4332, at least or exactly or at most 4333, at least or exactly or at most 4334, at least or exactly or at most 4335, at least or exactly or at most 4336, at least or exactly or at most 4337, at least or exactly or at most 4338, at least or exactly or at most 4339, at least or exactly or at most 4340, at least or exactly or at most 4341, at least or exactly or at most 4342, at least or exactly or at most 4343, at least or exactly or at most 4344, at least or exactly or at most 4345, at least or exactly or at most 4346, at least or exactly or at most 4347, at least or exactly or at most 4348, at least or exactly or at most 4349, at least or exactly or at most 4350, at least or exactly or at most 4351, at least or exactly or at most 4352, at least or exactly or at most 4353, at least or exactly or at most 4354, at least or exactly or at most 4355, at least or exactly or at most 4356, at least or exactly or at most 4357, at least or exactly or at most 4358, at least or exactly or at most 4359, at least or exactly or at most 4360, at least or exactly or at most 4361, at least or exactly or at most 4362, at least or exactly or at most 4363, at least or exactly or at most 4364, at least or exactly or at most 4365, at least or exactly or at most 4366, at least or exactly or at most 4367, at least or exactly or at most 4368, at least or exactly or at most 4369, at least or exactly or at most 4370, at least or exactly or at most 4371, at least or exactly or at most 4372, at least or exactly or at most 4373, at least or exactly or at most 4374, at least or exactly or at most 4375, at least or exactly or at most 4376, at least or exactly or at most 4377, at least or exactly or at most 4378, at least or exactly or at most 4379, at least or exactly or at most 4380, at least or exactly or at most 4381, at least or exactly or at most 4382, at least or exactly or at most 4383, at least or exactly or at most 4384, at least or exactly or at most 4385, at least or exactly or at most 4386, at least or exactly or at most 4387, at least or exactly or at most 4388, at least or exactly or at most 4389, at least or exactly or at most 4390, at least or exactly or at most 4391, at least or exactly or at most 4392, at least or exactly or at most 4393, at least or exactly or at most 4394, at least or exactly or at most 4395, at least or exactly or at most 4396, at least or exactly or at most 4397, at least or exactly or at most 4398, at least or exactly or at most 4399, at least or exactly or at most 4400, at least or exactly or at most 4401, at least or exactly or at most 4402, at least or exactly or at most 4403, at least or exactly or at most 4404, at least or exactly or at most 4405, at least or exactly or at most 4406, at least or exactly or at most 4407, at least or exactly or at most 4408, at least or exactly or at most 4409, at least or exactly or at most 4410, at least or exactly or at most 4411, at least or exactly or at most 4412, at least or exactly or at most 4413, at least or exactly or at most 4414, at least or exactly or at most 4415, at least or exactly or at most 4416, at least or exactly or at most 4417, at least or exactly or at most 4418, at least or exactly or at most 4419, at least or exactly or at most 4420, at least or exactly or at most 4421, at least or exactly or at most 4422, at least or exactly or at most 4423, at least or exactly or at most 4424, at least or exactly or at most 4425, at least or exactly or at most 4426, at least or exactly or at most 4427, at least or exactly or at most 4428, at least or exactly or at most 4429, at least or exactly or at most 4430, at least or exactly or at most 4431, at least or exactly or at most 4432, at least or exactly or at most 4433, at least or exactly or at most 4434, at least or exactly or at most 4435, at least or exactly or at most 4436, at least or exactly or at most 4437, at least or exactly or at most 4438, at least or exactly or at most 4439, at least or exactly or at most 4440, at least or exactly or at most 4441, at least or exactly or at most 4442, at least or exactly or at most 4443, at least or exactly or at most 4444, at least or exactly or at most 4445, at least or exactly or at most 4446, at least or exactly or at most 4447, at least or exactly or at most 4448, at least or exactly or at most 4449, at least or exactly or at most 4450, at least or exactly or at most 4451, at least or exactly or at most 4452, at least or exactly or at most 4453, at least or exactly or at most 4454, at least or exactly or at most 4455, at least or exactly or at most 4456, at least or exactly or at most 4457, at least or exactly or at most 4458, at least or exactly or at most 4459, at least or exactly or at most 4460, at least or exactly or at most 4461, at least or exactly or at most 4462, at least or exactly or at most 4463, at least or exactly or at most 4464, at least or exactly or at most 4465, at least or exactly or at most 4466, at least or exactly or at most 4467, at least or exactly or at most 4468, at least or exactly or at most 4469, at least or exactly or at most 4470, at least or exactly or at most 4471, at least or exactly or at most 4472, at least or exactly or at most 4473, at least or exactly or at most 4474, at least or exactly or at most 4475, at least or exactly or at most 4476, at least or exactly or at most 4477, at least or exactly or at most 4478, at least or exactly or at most 4479, at least or exactly or at most 4480, at least or exactly or at most 4481, at least or exactly or at most 4482, at least or exactly or at most 4483, at least or exactly or at most 4484, at least or exactly or at most 4485, at least or exactly or at most 4486, at least or exactly or at most 4487, at least or exactly or at most 4488, at least or exactly or at most 4489, at least or exactly or at most 4490, at least or exactly or at most 4491, at least or exactly or at most 4492, at least or exactly or at most 4493, at least or exactly or at most 4494, at least or exactly or at most 4495, at least or exactly or at most 4496, at least or exactly or at most 4497, at least or exactly or at most 4498, at least or exactly or at most 4499, at least or exactly or at most 4500, at least or exactly or at most 4501, at least or exactly or at most 4502, at least or exactly or at most 4503, at least or exactly or at most 4504, at least or exactly or at most 4505, at least or exactly or at most 4506, at least or exactly or at most 4507, at least or exactly or at most 4508, at least or exactly or at most 4509, at least or exactly or at most 4510, at least or

exactly or at most 4511, at least or exactly or at most 4512, at least or exactly or at most 4513, at least or exactly or at most 4514, at least or exactly or at most 4515, at least or exactly or at most 4516, at least or exactly or at most 4517, at least or exactly or at most 4518, at least or exactly or at most 4519, at least or exactly or at most 4520, at least or exactly or at most 4521, at least or exactly or at most 4522, at least or exactly or at most 4523, at least or exactly or at most 4524, at least or exactly or at most 4525, at least or exactly or at most 4526, at least or exactly or at most 4527, at least or exactly or at most 4528, at least or exactly or at most 4529, at least or exactly or at most 4530, at least or exactly or at most 4531, at least or exactly or at most 4532, at least or exactly or at most 4533, at least or exactly or at most 4534, at least or exactly or at most 4535, at least or exactly or at most 4536, at least or exactly or at most 4537, at least or exactly or at most 4538, at least or exactly or at most 4539, at least or exactly or at most 4540, at least or exactly or at most 4541, at least or exactly or at most 4542, at least or exactly or at most 4543, at least or exactly or at most 4544, at least or exactly or at most 4545, at least or exactly or at most 4546, at least or exactly or at most 4547, at least or exactly or at most 4548, at least or exactly or at most 4549, at least or exactly or at most 4550, at least or exactly or at most 4551, at least or exactly or at most 4552, at least or exactly or at most 4553, at least or exactly or at most 4554, at least or exactly or at most 4555, at least or exactly or at most 4556, at least or exactly or at most 4557, at least or exactly or at most 4558, at least or exactly or at most 4559, at least or exactly or at most 4560, at least or exactly or at most 4561, at least or exactly or at most 4562, at least or exactly or at most 4563, at least or exactly or at most 4564, at least or exactly or at most 4565, at least or exactly or at most 4566, at least or exactly or at most 4567, at least or exactly or at most 4568, at least or exactly or at most 4569, at least or exactly or at most 4570, at least or exactly or at most 4571, at least or exactly or at most 4572, at least or exactly or at most 4573, at least or exactly or at most 4574, at least or exactly or at most 4575, at least or exactly or at most 4576, at least or exactly or at most 4577, at least or exactly or at most 4578, at least or exactly or at most 4579, at least or exactly or at most 4580, at least or exactly or at most 4581, at least or exactly or at most 4582, at least or exactly or at most 4583, at least or exactly or at most 4584, at least or exactly or at most 4585, at least or exactly or at most 4586, at least or exactly or at most 4587, at least or exactly or at most 4588, at least or exactly or at most 4589, at least or exactly or at most 4590, at least or exactly or at most 4591, at least or exactly or at most 4592, at least or exactly or at most 4593, at least or exactly or at most 4594, at least or exactly or at most 4595, at least or exactly or at most 4596, at least or exactly or at most 4597, at least or exactly or at most 4598, at least or exactly or at most 4599, at least or exactly or at most 4600, at least or exactly or at most 4601, at least or exactly or at most 4602, at least or exactly or at most 4603, at least or exactly or at most 4604, at least or exactly or at most 4605, at least or exactly or at most 4606, at least or exactly or at most 4607, at least or exactly or at most 4608, at least or exactly or at most 4609, at least or exactly or at most 4610, at least or exactly or at most 4611, at least or exactly or at most 4612, at least or exactly or at most 4613, at least or exactly or at most 4614, at least or exactly or at most 4615, at least or exactly or at most 4616, at least or exactly or at most 4617, at least or exactly or at most 4618, at least or exactly or at most 4619, at least or exactly or at most 4620, at least or exactly or at most 4621, at least or exactly or at most 4622, at least or exactly or at most 4623, at least or exactly or at most 4624, at least or exactly or at most 4625, at least or exactly or at most 4626, at least or exactly or at most 4627, at least or exactly or at most 4628, at least or exactly or at most 4629, at least or exactly or at most 4630, at least or exactly or at most 4631, at least or exactly or at most 4632, at least or exactly or at most 4633, at least or exactly or at most 4634, at least or exactly or at most 4635, at least or exactly or at most 4636, at least or exactly or at most 4637, at least or exactly or at most 4638, at least or exactly or at most 4639, at least or exactly or at most 4640, at least or exactly or at most 4641, at least or exactly or at most 4642, at least or exactly or at most 4643, at least or exactly or at most 4644, at least or exactly or at most 4645, at least or exactly or at most 4646, at least or exactly or at most 4647, at least or exactly or at most 4648, at least or exactly or at most 4649, at least or exactly or at most 4650, at least or exactly or at most 4651, at least or exactly or at most 4652, at least or exactly or at most 4653, at least or exactly or at most 4654, at least or exactly or at most 4655, at least or exactly or at most 4656, at least or exactly or at most 4657, at least or exactly or at most 4658, at least or exactly or at most 4659, at least or exactly or at most 4660, at least or exactly or at most 4661, at least or exactly or at most 4662, at least or exactly or at most 4663, at least or exactly or at most 4664, at least or exactly or at most 4665, at least or exactly or at most 4666, at least or exactly or at most 4667, at least or exactly or at most 4668, at least or exactly or at most 4669, at least or exactly or at most 4670, at least or exactly or at most 4671, at least or exactly or at most 4672, at least or exactly or at most 4673, at least or exactly or at most 4674, at least or exactly or at most 4675, at least or exactly or at most 4676, at least or exactly or at most 4677, at least or exactly or at most 4678, at least or exactly or at most 4679, at least or exactly or at most 4680, at least or exactly or at most 4681, at least or exactly or at most 4682, at least or exactly or at most 4683, at least or exactly or at most 4684, at least or exactly or at most 4685, at least or exactly or at most 4686, at least or exactly or at most 4687, at least or exactly or at most 4688, at least or exactly or at most 4689, at least or exactly or at most 4690, at least or exactly or at most 4691, at least or exactly or at most 4692, at least or exactly or at most 4693, at least or exactly or at most 4694, at least or exactly or at most 4695, at least or exactly or at most 4696, at least or exactly or at most 4697, at least or exactly or at most 4698, at least or exactly or at most 4699, at least or exactly or at most 4700, at least or exactly or at most 4701, at least or exactly or at most 4702, at least or exactly or at most 4703, at least or exactly or at most 4704, at least or exactly or at most 4705, at least or exactly or at most 4706, at least or exactly or at most 4707, at least or exactly or at most 4708, at least or exactly or at most 4709, at least or exactly or at most 4710, at least or exactly or at most 4711, at least or exactly or at most 4712, at least or exactly or at most 4713, at least or exactly or at most 4714, at least or exactly or at most 4715, at least or exactly or at most 4716, at least or exactly or at most 4717, at least or exactly or at most 4718, at least or exactly or at most 4719, at least or exactly or at most 4720, at least or exactly or at most 4721, at least or exactly or at most 4722, at least or exactly or at most 4723, at least or exactly or at

most 4724, at least or exactly or at most 4725, at least or exactly or at most 4726, at least or exactly or at most 4727, at least or exactly or at most 4728, at least or exactly or at most 4729, at least or exactly or at most 4730, at least or exactly or at most 4731, at least or exactly or at most 4732, at least or exactly or at most 4733, at least or exactly or at most 4734, at least or exactly or at most 4735, at least or exactly or at most 4736, at least or exactly or at most 4737, at least or exactly or at most 4738, at least or exactly or at most 4739, at least or exactly or at most 4740, at least or exactly or at most 4741, at least or exactly or at most 4742, at least or exactly or at most 4743, at least or exactly or at most 4744, at least or exactly or at most 4745, at least or exactly or at most 4746, at least or exactly or at most 4747, at least or exactly or at most 4748, at least or exactly or at most 4749, at least or exactly or at most 4750, at least or exactly or at most 4751, at least or exactly or at most 4752, at least or exactly or at most 4753, at least or exactly or at most 4754, at least or exactly or at most 4755, at least or exactly or at most 4756, at least or exactly or at most 4757, at least or exactly or at most 4758, at least or exactly or at most 4759, at least or exactly or at most 4760, at least or exactly or at most 4761, at least or exactly or at most 4762, at least or exactly or at most 4763, at least or exactly or at most 4764, at least or exactly or at most 4765, at least or exactly or at most 4766, at least or exactly or at most 4767, at least or exactly or at most 4768, at least or exactly or at most 4769, at least or exactly or at most 4770, at least or exactly or at most 4771, at least or exactly or at most 4772, at least or exactly or at most 4773, at least or exactly or at most 4774, at least or exactly or at most 4775, at least or exactly or at most 4776, at least or exactly or at most 4777, at least or exactly or at most 4778, at least or exactly or at most 4779, at least or exactly or at most 4780, at least or exactly or at most 4781, at least or exactly or at most 4782, at least or exactly or at most 4783, at least or exactly or at most 4784, at least or exactly or at most 4785, at least or exactly or at most 4786, at least or exactly or at most 4787, at least or exactly or at most 4788, at least or exactly or at most 4789, at least or exactly or at most 4790, at least or exactly or at most 4791, at least or exactly or at most 4792, at least or exactly or at most 4793, at least or exactly or at most 4794, at least or exactly or at most 4795, at least or exactly or at most 4796, at least or exactly or at most 4797, at least or exactly or at most 4798, at least or exactly or at most 4799, at least or exactly or at most 4800, at least or exactly or at most 4801, at least or exactly or at most 4802, at least or exactly or at most 4803, at least or exactly or at most 4804, at least or exactly or at most 4805, at least or exactly or at most 4806, at least or exactly or at most 4807, at least or exactly or at most 4808, at least or exactly or at most 4809, at least or exactly or at most 4810, at least or exactly or at most 4811, at least or exactly or at most 4812, at least or exactly or at most 4813, at least or exactly or at most 4814, at least or exactly or at most 4815, at least or exactly or at most 4816, at least or exactly or at most 4817, at least or exactly or at most 4818, at least or exactly or at most 4819, at least or exactly or at most 4820, at least or exactly or at most 4821, at least or exactly or at most 4822, at least or exactly or at most 4823, at least or exactly or at most 4824, at least or exactly or at most 4825, at least or exactly or at most 4826, at least or exactly or at most 4827, at least or exactly or at most 4828, at least or exactly or at most 4829, at least or exactly or at most 4830, at least or exactly or at most 4831, at least or exactly or at most 4832, at least or exactly or at most 4833, at least or exactly or at most 4834, at least or exactly or at most 4835, at least or exactly or at most 4836, at least or exactly or at most 4837, at least or exactly or at most 4838, at least or exactly or at most 4839, at least or exactly or at most 4840, at least or exactly or at most 4841, at least or exactly or at most 4842, at least or exactly or at most 4843, at least or exactly or at most 4844, at least or exactly or at most 4845, at least or exactly or at most 4846, at least or exactly or at most 4847, at least or exactly or at most 4848, at least or exactly or at most 4849, at least or exactly or at most 4850, at least or exactly or at most 4851, at least or exactly or at most 4852, at least or exactly or at most 4853, at least or exactly or at most 4854, at least or exactly or at most 4855, at least or exactly or at most 4856, at least or exactly or at most 4857, at least or exactly or at most 4858, at least or exactly or at most 4859, at least or exactly or at most 4860, at least or exactly or at most 4861, at least or exactly or at most 4862, at least or exactly or at most 4863, at least or exactly or at most 4864, at least or exactly or at most 4865, at least or exactly or at most 4866, at least or exactly or at most 4867, at least or exactly or at most 4868, at least or exactly or at most 4869, at least or exactly or at most 4870, at least or exactly or at most 4871, at least or exactly or at most 4872, at least or exactly or at most 4873, at least or exactly or at most 4874, at least or exactly or at most 4875, at least or exactly or at most 4876, at least or exactly or at most 4877, at least or exactly or at most 4878, at least or exactly or at most 4879, at least or exactly or at most 4880, at least or exactly or at most 4881, at least or exactly or at most 4882, at least or exactly or at most 4883, at least or exactly or at most 4884, at least or exactly or at most 4885, at least or exactly or at most 4886, at least or exactly or at most 4887, at least or exactly or at most 4888, at least or exactly or at most 4889, at least or exactly or at most 4890, at least or exactly or at most 4891, at least or exactly or at most 4892, at least or exactly or at most 4893, at least or exactly or at most 4894, at least or exactly or at most 4895, at least or exactly or at most 4896, at least or exactly or at most 4897, at least or exactly or at most 4898, at least or exactly or at most 4899, at least or exactly or at most 4900, at least or exactly or at most 4901, at least or exactly or at most 4902, at least or exactly or at most 4903, at least or exactly or at most 4904, at least or exactly or at most 4905, at least or exactly or at most 4906, at least or exactly or at most 4907, at least or exactly or at most 4908, at least or exactly or at most 4909, at least or exactly or at most 4910, at least or exactly or at most 4911, at least or exactly or at most 4912, at least or exactly or at most 4913, at least or exactly or at most 4914, at least or exactly or at most 4915, at least or exactly or at most 4916, at least or exactly or at most 4917, at least or exactly or at most 4918, at least or exactly or at most 4919, at least or exactly or at most 4920, at least or exactly or at most 4921, at least or exactly or at most 4922, at least or exactly or at most 4923, at least or exactly or at most 4924, at least or exactly or at most 4925, at least or exactly or at most 4926, at least or exactly or at most 4927, at least or exactly or at most 4928, at least or exactly or at most 4929, at least or exactly or at most 4930, at least or exactly or at most 4931, at least or exactly or at most 4932, at least or exactly or at most 4933, at least or exactly or at most 4934, at least or exactly or at most 4935, at least or exactly or at most 4936, at least or exactly or at most 4937,

at least or exactly or at most 4938, at least or exactly or at most 4939, at least or exactly or at most 4940, at least or exactly or at most 4941, at least or exactly or at most 4942, at least or exactly or at most 4943, at least or exactly or at most 4944, at least or exactly or at most 4945, at least or exactly or at most 4946, at least or exactly or at most 4947, at least or exactly or at most 4948, at least or exactly or at most 4949, at least or exactly or at most 4950, at least or exactly or at most 4951, at least or exactly or at most 4952, at least or exactly or at most 4953, at least or exactly or at most 4954, at least or exactly or at most 4955, at least or exactly or at most 4956, at least or exactly or at most 4957, at least or exactly or at most 4958, at least or exactly or at most 4959, at least or exactly or at most 4960, at least or exactly or at most 4961, at least or exactly or at most 4962, at least or exactly or at most 4963, at least or exactly or at most 4964, at least or exactly or at most 4965, at least or exactly or at most 4966, at least or exactly or at most 4967, at least or exactly or at most 4968, at least or exactly or at most 4969, at least or exactly or at most 4970, at least or exactly or at most 4971, at least or exactly or at most 4972, at least or exactly or at most 4973, at least or exactly or at most 4974, at least or exactly or at most 4975, at least or exactly or at most 4976, at least or exactly or at most 4977, at least or exactly or at most 4978, at least or exactly or at most 4979, at least or exactly or at most 4980, at least or exactly or at most 4981, at least or exactly or at most 4982, at least or exactly or at most 4983, at least or exactly or at most 4984, at least or exactly or at most 4985, at least or exactly or at most 4986, at least or exactly or at most 4987, at least or exactly or at most 4988, at least or exactly or at most 4989, at least or exactly or at most 4990, at least or exactly or at most 4991, at least or exactly or at most 4992, at least or exactly or at most 4993, at least or exactly or at most 4994, at least or exactly or at most 4995, at least or exactly or at most 4996, at least or exactly or at most 4997, at least or exactly or at most 4998, at least or exactly or at most 4999, at least or exactly or at most 5000, at least or exactly or at most 5001, at least or exactly or at most 5002, at least or exactly or at most 5003, at least or exactly or at most 5004, at least or exactly or at most 5005, at least or exactly or at most 5006, at least or exactly or at most 5007, at least or exactly or at most 5008, at least or exactly or at most 5009, at least or exactly or at most 5010, at least or exactly or at most 5011, at least or exactly or at most 5012, at least or exactly or at most 5013, at least or exactly or at most 5014, at least or exactly or at most 5015, at least or exactly or at most 5016, at least or exactly or at most 5017, at least or exactly or at most 5018, at least or exactly or at most 5019, at least or exactly or at most 5020, at least or exactly or at most 5021, at least or exactly or at most 5022, at least or exactly or at most 5023, at least or exactly or at most 5024, at least or exactly or at most 5025, at least or exactly or at most 5026, at least or exactly or at most 5027, at least or exactly or at most 5028, at least or exactly or at most 5029, at least or exactly or at most 5030, at least or exactly or at most 5031, at least or exactly or at most 5032, at least or exactly or at most 5033, at least or exactly or at most 5034, at least or exactly or at most 5035, at least or exactly or at most 5036, at least or exactly or at most 5037, at least or exactly or at most 5038, at least or exactly or at most 5039, at least or exactly or at most 5040, at least or exactly or at most 5041, at least or exactly or at most 5042, at least or exactly or at most 5043, at least or exactly or at most 5044, at least or exactly or at most 5045, at least or exactly or at most 5046, at least or exactly or at most 5047, at least or exactly or at most 5048, at least or exactly or at most 5049, at least or exactly or at most 5050, at least or exactly or at most 5051, at least or exactly or at most 5052, at least or exactly or at most 5053, at least or exactly or at most 5054, at least or exactly or at most 5055, at least or exactly or at most 5056, at least or exactly or at most 5057, at least or exactly or at most 5058, at least or exactly or at most 5059, at least or exactly or at most 5060, at least or exactly or at most 5061, at least or exactly or at most 5062, at least or exactly or at most 5063, at least or exactly or at most 5064, at least or exactly or at most 5065, at least or exactly or at most 5066, at least or exactly or at most 5067, at least or exactly or at most 5068, at least or exactly or at most 5069, at least or exactly or at most 5070, at least or exactly or at most 5071, at least or exactly or at most 5072, at least or exactly or at most 5073, at least or exactly or at most 5074, at least or exactly or at most 5075, at least or exactly or at most 5076, at least or exactly or at most 5077, at least or exactly or at most 5078, at least or exactly or at most 5079, at least or exactly or at most 5080, at least or exactly or at most 5081, at least or exactly or at most 5082, at least or exactly or at most 5083, at least or exactly or at most 5084, at least or exactly or at most 5085, at least or exactly or at most 5086, at least or exactly or at most 5087, at least or exactly or at most 5088, at least or exactly or at most 5089, at least or exactly or at most 5090, at least or exactly or at most 5091, at least or exactly or at most 5092, at least or exactly or at most 5093, at least or exactly or at most 5094, at least or exactly or at most 5095, at least or exactly or at most 5096, at least or exactly or at most 5097, at least or exactly or at most 5098, at least or exactly or at most 5099, at least or exactly or at most 5100, at least or exactly or at most 5101, at least or exactly or at most 5102, at least or exactly or at most 5103, at least or exactly or at most 5104, at least or exactly or at most 5105, at least or exactly or at most 5106, at least or exactly or at most 5107, at least or exactly or at most 5108, at least or exactly or at most 5109, at least or exactly or at most 5110, at least or exactly or at most 5111, at least or exactly or at most 5112, at least or exactly or at most 5113, at least or exactly or at most 5114, at least or exactly or at most 5115, at least or exactly or at most 5116, at least or exactly or at most 5117, at least or exactly or at most 5118, at least or exactly or at most 5119, at least or exactly or at most 5120, at least or exactly or at most 5121, at least or exactly or at most 5122, at least or exactly or at most 5123, at least or exactly or at most 5124, at least or exactly or at most 5125, at least or exactly or at most 5126, at least or exactly or at most 5127, at least or exactly or at most 5128, at least or exactly or at most 5129, at least or exactly or at most 5130, at least or exactly or at most 5131, at least or exactly or at most 5132, at least or exactly or at most 5133, at least or exactly or at most 5134, at least or exactly or at most 5135, at least or exactly or at most 5136, at least or exactly or at most 5137, at least or exactly or at most 5138, at least or exactly or at most 5139, at least or exactly or at most 5140, at least or exactly or at most 5141, at least or exactly or at most 5142, at least or exactly or at most 5143, at least or exactly or at most 5144, at least or exactly or at most 5145, at least or exactly or at most 5146, at least or exactly or at most 5147, at least or exactly or at most 5148, at least or exactly or at most 5149, at least or exactly or at most 5150, at least or

exactly or at most 5151, at least or exactly or at most 5152, at least or exactly or at most 5153, at least or exactly or at most 5154, at least or exactly or at most 5155, at least or exactly or at most 5156, at least or exactly or at most 5157, at least or exactly or at most 5158, at least or exactly or at most 5159, at least or exactly or at most 5160, at least or exactly or at most 5161, at least or exactly or at most 5162, at least or exactly or at most 5163, at least or exactly or at most 5164, at least or exactly or at most 5165, at least or exactly or at most 5166, at least or exactly or at most 5167, at least or exactly or at most 5168, at least or exactly or at most 5169, at least or exactly or at most 5170, at least or exactly or at most 5171, at least or exactly or at most 5172, at least or exactly or at most 5173, at least or exactly or at most 5174, at least or exactly or at most 5175, at least or exactly or at most 5176, at least or exactly or at most 5177, at least or exactly or at most 5178, at least or exactly or at most 5179, at least or exactly or at most 5180, at least or exactly or at most 5181, at least or exactly or at most 5182, at least or exactly or at most 5183, at least or exactly or at most 5184, at least or exactly or at most 5185, at least or exactly or at most 5186, at least or exactly or at most 5187, at least or exactly or at most 5188, at least or exactly or at most 5189, at least or exactly or at most 5190, at least or exactly or at most 5191, at least or exactly or at most 5192, at least or exactly or at most 5193, at least or exactly or at most 5194, at least or exactly or at most 5195, at least or exactly or at most 5196, at least or exactly or at most 5197, at least or exactly or at most 5198, at least or exactly or at most 5199, at least or exactly or at most 5200, at least or exactly or at most 5201, at least or exactly or at most 5202, at least or exactly or at most 5203, at least or exactly or at most 5204, at least or exactly or at most 5205, at least or exactly or at most 5206, at least or exactly or at most 5207, at least or exactly or at most 5208, at least or exactly or at most 5209, at least or exactly or at most 5210, at least or exactly or at most 5211, at least or exactly or at most 5212, at least or exactly or at most 5213, at least or exactly or at most 5214, at least or exactly or at most 5215, at least or exactly or at most 5216, at least or exactly or at most 5217, at least or exactly or at most 5218, at least or exactly or at most 5219, at least or exactly or at most 5220, at least or exactly or at most 5221, at least or exactly or at most 5222, at least or exactly or at most 5223, at least or exactly or at most 5224, at least or exactly or at most 5225, at least or exactly or at most 5226, at least or exactly or at most 5227, at least or exactly or at most 5228, at least or exactly or at most 5229, at least or exactly or at most 5230, at least or exactly or at most 5231, at least or exactly or at most 5232, at least or exactly or at most 5233, at least or exactly or at most 5234, at least or exactly or at most 5235, at least or exactly or at most 5236, at least or exactly or at most 5237, at least or exactly or at most 5238, at least or exactly or at most 5239, at least or exactly or at most 5240, at least or exactly or at most 5241, at least or exactly or at most 5242, at least or exactly or at most 5243, at least or exactly or at most 5244, at least or exactly or at most 5245, at least or exactly or at most 5246, at least or exactly or at most 5247, at least or exactly or at most 5248, at least or exactly or at most 5249, at least or exactly or at most 5250, at least or exactly or at most 5251, at least or exactly or at most 5252, at least or exactly or at most 5253, at least or exactly or at most 5254, at least or exactly or at most 5255, at least or exactly or at most 5256, at least or exactly or at most 5257, at least or exactly or at most 5258, at least or exactly or at most 5259, at least or exactly or at most 5260, at least or exactly or at most 5261, at least or exactly or at most 5262, at least or exactly or at most 5263, at least or exactly or at most 5264, at least or exactly or at most 5265, at least or exactly or at most 5266, at least or exactly or at most 5267, at least or exactly or at most 5268, at least or exactly or at most 5269, at least or exactly or at most 5270, at least or exactly or at most 5271, at least or exactly or at most 5272, at least or exactly or at most 5273, at least or exactly or at most 5274, at least or exactly or at most 5275, at least or exactly or at most 5276, at least or exactly or at most 5277, at least or exactly or at most 5278, at least or exactly or at most 5279, at least or exactly or at most 5280, at least or exactly or at most 5281, at least or exactly or at most 5282, at least or exactly or at most 5283, at least or exactly or at most 5284, at least or exactly or at most 5285, at least or exactly or at most 5286, at least or exactly or at most 5287, at least or exactly or at most 5288, at least or exactly or at most 5289, at least or exactly or at most 5290, at least or exactly or at most 5291, at least or exactly or at most 5292, at least or exactly or at most 5293, at least or exactly or at most 5294, at least or exactly or at most 5295, at least or exactly or at most 5296, at least or exactly or at most 5297, at least or exactly or at most 5298, at least or exactly or at most 5299, at least or exactly or at most 5300, at least or exactly or at most 5301, at least or exactly or at most 5302, at least or exactly or at most 5303, at least or exactly or at most 5304, at least or exactly or at most 5305, at least or exactly or at most 5306, at least or exactly or at most 5307, at least or exactly or at most 5308, at least or exactly or at most 5309, at least or exactly or at most 5310, at least or exactly or at most 5311, at least or exactly or at most 5312, at least or exactly or at most 5313, at least or exactly or at most 5314, at least or exactly or at most 5315, at least or exactly or at most 5316, at least or exactly or at most 5317, at least or exactly or at most 5318, at least or exactly or at most 5319, at least or exactly or at most 5320, at least or exactly or at most 5321, at least or exactly or at most 5322, at least or exactly or at most 5323, at least or exactly or at most 5324, at least or exactly or at most 5325, at least or exactly or at most 5326, at least or exactly or at most 5327, at least or exactly or at most 5328, at least or exactly or at most 5329, at least or exactly or at most 5330, at least or exactly or at most 5331, at least or exactly or at most 5332, at least or exactly or at most 5333, at least or exactly or at most 5334, at least or exactly or at most 5335, at least or exactly or at most 5336, at least or exactly or at most 5337, at least or exactly or at most 5338, at least or exactly or at most 5339, at least or exactly or at most 5340, at least or exactly or at most 5341, at least or exactly or at most 5342, at least or exactly or at most 5343, at least or exactly or at most 5344, at least or exactly or at most 5345, at least or exactly or at most 5346, at least or exactly or at most 5347, at least or exactly or at most 5348, at least or exactly or at most 5349, at least or exactly or at most 5350, at least or exactly or at most 5351, at least or exactly or at most 5352, at least or exactly or at most 5353, at least or exactly or at most 5354, at least or exactly or at most 5355, at least or exactly or at most 5356, at least or exactly or at most 5357, at least or exactly or at most 5358, at least or exactly or at most 5359, at least or exactly or at most 5360, at least or exactly or at most 5361, at least or exactly or at most 5362, at least or exactly or at most 5363, at least or exactly or at

most 5364, at least or exactly or at most 5365, at least or exactly or at most 5366, at least or exactly or at most 5367, at least or exactly or at most 5368, at least or exactly or at most 5369, at least or exactly or at most 5370, at least or exactly or at most 5371, at least or exactly or at most 5372, at least or exactly or at most 5373, at least or exactly or at most 5374, at least or exactly or at most 5375, at least or exactly or at most 5376, at least or exactly or at most 5377, at least or exactly or at most 5378, at least or exactly or at most 5379, at least or exactly or at most 5380, at least or exactly or at most 5381, at least or exactly or at most 5382, at least or exactly or at most 5383, at least or exactly or at most 5384, at least or exactly or at most 5385, at least or exactly or at most 5386, at least or exactly or at most 5387, at least or exactly or at most 5388, at least or exactly or at most 5389, at least or exactly or at most 5390, at least or exactly or at most 5391, at least or exactly or at most 5392, at least or exactly or at most 5393, at least or exactly or at most 5394, at least or exactly or at most 5395, at least or exactly or at most 5396, at least or exactly or at most 5397, at least or exactly or at most 5398, at least or exactly or at most 5399, at least or exactly or at most 5400, at least or exactly or at most 5401, at least or exactly or at most 5402, at least or exactly or at most 5403, at least or exactly or at most 5404, at least or exactly or at most 5405, at least or exactly or at most 5406, at least or exactly or at most 5407, at least or exactly or at most 5408, at least or exactly or at most 5409, at least or exactly or at most 5410, at least or exactly or at most 5411, at least or exactly or at most 5412, at least or exactly or at most 5413, at least or exactly or at most 5414, at least or exactly or at most 5415, at least or exactly or at most 5416, at least or exactly or at most 5417, at least or exactly or at most 5418, at least or exactly or at most 5419, at least or exactly or at most 5420, at least or exactly or at most 5421, at least or exactly or at most 5422, at least or exactly or at most 5423, at least or exactly or at most 5424, at least or exactly or at most 5425, at least or exactly or at most 5426, at least or exactly or at most 5427, at least or exactly or at most 5428, at least or exactly or at most 5429, at least or exactly or at most 5430, at least or exactly or at most 5431, at least or exactly or at most 5432, at least or exactly or at most 5433, at least or exactly or at most 5434, at least or exactly or at most 5435, at least or exactly or at most 5436, at least or exactly or at most 5437, at least or exactly or at most 5438, at least or exactly or at most 5439, at least or exactly or at most 5440, at least or exactly or at most 5441, at least or exactly or at most 5442, at least or exactly or at most 5443, at least or exactly or at most 5444, at least or exactly or at most 5445, at least or exactly or at most 5446, at least or exactly or at most 5447, at least or exactly or at most 5448, at least or exactly or at most 5449, at least or exactly or at most 5450, at least or exactly or at most 5451, at least or exactly or at most 5452, at least or exactly or at most 5453, at least or exactly or at most 5454, at least or exactly or at most 5455, at least or exactly or at most 5456, at least or exactly or at most 5457, at least or exactly or at most 5458, at least or exactly or at most 5459, at least or exactly or at most 5460, at least or exactly or at most 5461, at least or exactly or at most 5462, at least or exactly or at most 5463, at least or exactly or at most 5464, at least or exactly or at most 5465, at least or exactly or at most 5466, at least or exactly or at most 5467, at least or exactly or at most 5468, at least or exactly or at most 5469, at least or exactly or at most 5470, at least or exactly or at most 5471, at least or exactly or at most 5472, at least or exactly or at most 5473, at least or exactly or at most 5474, at least or exactly or at most 5475, at least or exactly or at most 5476, at least or exactly or at most 5477, at least or exactly or at most 5478, at least or exactly or at most 5479, at least or exactly or at most 5480, at least or exactly or at most 5481, at least or exactly or at most 5482, at least or exactly or at most 5483, at least or exactly or at most 5484, at least or exactly or at most 5485, at least or exactly or at most 5486, at least or exactly or at most 5487, at least or exactly or at most 5488, at least or exactly or at most 5489, at least or exactly or at most 5490, at least or exactly or at most 5491, at least or exactly or at most 5492, at least or exactly or at most 5493, at least or exactly or at most 5494, at least or exactly or at most 5495, at least or exactly or at most 5496, at least or exactly or at most 5497, at least or exactly or at most 5498, at least or exactly or at most 5499, at least or exactly or at most 5500, at least or exactly or at most 5501, at least or exactly or at most 5502, at least or exactly or at most 5503, at least or exactly or at most 5504, at least or exactly or at most 5505, at least or exactly or at most 5506, at least or exactly or at most 5507, at least or exactly or at most 5508, at least or exactly or at most 5509, at least or exactly or at most 5510, at least or exactly or at most 5511, at least or exactly or at most 5512, at least or exactly or at most 5513, at least or exactly or at most 5514, at least or exactly or at most 5515, at least or exactly or at most 5516, at least or exactly or at most 5517, at least or exactly or at most 5518, at least or exactly or at most 5519, at least or exactly or at most 5520, at least or exactly or at most 5521, at least or exactly or at most 5522, at least or exactly or at most 5523, at least or exactly or at most 5524, at least or exactly or at most 5525, at least or exactly or at most 5526, at least or exactly or at most 5527, at least or exactly or at most 5528, at least or exactly or at most 5529, at least or exactly or at most 5530, at least or exactly or at most 5531, at least or exactly or at most 5532, at least or exactly or at most 5533, at least or exactly or at most 5534, at least or exactly or at most 5535, at least or exactly or at most 5536, at least or exactly or at most 5537, at least or exactly or at most 5538, at least or exactly or at most 5539, at least or exactly or at most 5540, at least or exactly or at most 5541, at least or exactly or at most 5542, at least or exactly or at most 5543, at least or exactly or at most 5544, at least or exactly or at most 5545, at least or exactly or at most 5546, at least or exactly or at most 5547, at least or exactly or at most 5548, at least or exactly or at most 5549, at least or exactly or at most 5550, at least or exactly or at most 5551, at least or exactly or at most 5552, at least or exactly or at most 5553, at least or exactly or at most 5554, at least or exactly or at most 5555, at least or exactly or at most 5556, at least or exactly or at most 5557, at least or exactly or at most 5558, at least or exactly or at most 5559, at least or exactly or at most 5560, at least or exactly or at most 5561, at least or exactly or at most 5562, at least or exactly or at most 5563, at least or exactly or at most 5564, at least or exactly or at most 5565, at least or exactly or at most 5566, at least or exactly or at most 5567, at least or exactly or at most 5568, at least or exactly or at most 5569, at least or exactly or at most 5570, at least or exactly or at most 5571, at least or exactly or at most 5572, at least or exactly or at most 5573, at least or exactly or at most 5574, at least or exactly or at most 5575, at least or exactly or at most 5576, at least or exactly or at most 5577,

at least or exactly or at most 5578, at least or exactly or at most 5579, at least or exactly or at most 5580, at least or exactly or at most 5581, at least or exactly or at most 5582, at least or exactly or at most 5583, at least or exactly or at most 5584, at least or exactly or at most 5585, at least or exactly or at most 5586, at least or exactly or at most 5587, at least or exactly or at most 5588, at least or exactly or at most 5589, at least or exactly or at most 5590, at least or exactly or at most 5591, at least or exactly or at most 5592, at least or exactly or at most 5593, at least or exactly or at most 5594, at least or exactly or at most 5595, at least or exactly or at most 5596, at least or exactly or at most 5597, at least or exactly or at most 5598, at least or exactly or at most 5599, at least or exactly or at most 5600, at least or exactly or at most 5601, at least or exactly or at most 5602, at least or exactly or at most 5603, at least or exactly or at most 5604, at least or exactly or at most 5605, at least or exactly or at most 5606, at least or exactly or at most 5607, at least or exactly or at most 5608, at least or exactly or at most 5609, at least or exactly or at most 5610, at least or exactly or at most 5611, at least or exactly or at most 5612, at least or exactly or at most 5613, at least or exactly or at most 5614, at least or exactly or at most 5615, at least or exactly or at most 5616, at least or exactly or at most 5617, at least or exactly or at most 5618, at least or exactly or at most 5619, at least or exactly or at most 5620, at least or exactly or at most 5621, at least or exactly or at most 5622, at least or exactly or at most 5623, at least or exactly or at most 5624, at least or exactly or at most 5625, or at least or exactly or at most 5626 contiguous amino acid residues.

[0098] In some embodiments, the polypeptide of the invention also has a sequence identity with the amino acid sequence of a) defined above of at least 65%, such as at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, and at least 99%. Similarly, the polypeptide of the invention in some embodiments also has a sequence identity with the amino acid sequence of b) defined above of at least 60%, such as at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, and at least 99%.

[0099] In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60 and 62 in any one of SEQ ID NOs: 1-30, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than N-L+1, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b.

[0100] In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73 and 74 in any on of SEQ ID NOs: 2-30, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than N-L+1, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b.

[0101] In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 and 100 in any one of SEQ ID NOs: 3-30, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than N-L+1, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b.

[0102] In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150 and 151 in any one of SEQ ID NOs: 4-30, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than N-L+1, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b.

[0103] In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 152, 153, 154, 155, 156, 157, 158, 159, 160, 171, 172, 173, 174 and 175 in any one of SEQ ID NOs: 5-30, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than N-L+1, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b.

[0104] In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299 and 300 in any one of SEQ ID NOs: 6-30, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the

N-terminal first residue will not be higher numbered than N-L+1, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b.

[0105] In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 301, 302, 303, 304 and 305 in any one of SEQ ID NOs: 7-30, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than N-L+1, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b.

[0106] In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335 and 336 in any one of SEQ ID NOs: 8-30, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than N-L+1, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b.

[0107] In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 337, 338, 339, 340, 341, 342 and 343 in any one of SEQ ID NOs: 9-30, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than N-L+1, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b.

[0108] In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 344, 345, 346, 347 and 348 in any one of SEQ ID NOs: 10-30, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than N-L+1, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b.

[0109] In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415 and 416 in any one of SEQ ID NOs: 11-30, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than N-L+1, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b.

[0110] In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 417, 418, 419, 420, 421, 422 and 423 in any one of SEQ ID NOs: 12-30, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than N-L+1, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b.

[0111] In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to amino acid residue 424 in any one of SEQ ID NOs: 13-30, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than N-L+1, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b.

[0112] In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563 and 564 in SEQ ID NOs: 14-30, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than N-L+1, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b.

[0113] In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574 and 575 in SEQ ID NOs: 15-30, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than N-L+1, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b.

[0114] In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616 and 617 in SEQ ID NOs: 16-30, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than N-L+1, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b.

[0115] In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683 and 684 in SEQ ID NOs: 17-30, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than N-L+1, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b.

[0116] In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737 and 738 in SEQ ID NOs: 18-30, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than N-L+1, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b.

[0117] In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 739, 740, 741, and 742 in SEQ ID NOs: 19-30, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than N-L+1, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b.

[0118] In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779 and 780 in SEQ ID NOs: 20-30, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than N-L+1, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b.

[0119] In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 845, 846 and 847 in SEQ ID NOs: 21-30, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than N-L+1, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b.

[0120] In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 848, 849, 850, 851, 852, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, 873, 874, 875 and 876 in SEQ ID NOs: 22-30, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than N-L+1, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b.

[0121] In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 877, 878, 879, 880, 881, 882, 883, 884, 885, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 896, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910, 911, 912, 913, 914 and 915 in SEQ ID NOs: 23-30, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than N-L+1, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b.

[0122] In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 916, 917, 918, 919, 920, 921, 922, 923, 924, 925, 926, 927, 928, 929, 930, 931, 932, 933, 934, 935, 936, 937, 938, 939, 940, 941, 942, 943, 944, 945, 946, 947, 948, 949, 950, 951, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 965, 966, 967, 968, 969, 970, 971, 972, 973, 974, 975, 976, 977, 978, 979, 980, 981, 982, 983, 984, 985, 986, 987, 988, 989, 990 and 991 in SEQ ID NOs: 24-30, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than N-L+1, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b.

[0123] In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 992, 993, 994, 995, 996, 997, 998, 999, 1000, 1001, 1002, 1003, 1004, 1005, 1006, 1007, 1008, 1009, 1010, 1011, 1012, 1013, 1014, 1015, 1016, 1017, 1018, 1019, 1020, 1021, 1022, 1023, 1024, 1025, 1026, 1027, 1028, 1029, 1030, 1031, 1032, 1033, 1034, 1035, 1036, 1037, 1038, 1039, 1040, 1041, 1042, 1043, 1044, 1045, 1046, 1047, 1048, 1049, 1050, 1051, 1052 and 1053 in SEQ ID NOs: 25-30, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than N-L+1, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b.

[0124] In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 1054, 1055, 1056, 1057, 1058, 1059, 1060, 1061, 1062, 1063, 1064, 1065, 1066, 1067, 1068, 1069, 1070, 1071, 1072, 1073, 1074, 1075, 1076, 1077, 1078, 1079, 1080, 1081, 1082, 1083, 1084, 1085, 1086, 1087, 1088, 1089, 1090, 1091, 1092, 1093, 1094, 1095, 1096, 1097, 1098, 1099, 1100, 1101, 1102, 1103, 1104, 1105, 1106, 1107, 1108, 1109, 1110, 1111, 1112, 1113, 1114, 1115, 1116, 1117, 1118, 1119, 1120, 1121, 1122, 1123, 1124, 1125, 1126, 1127, 1128, 1129, 1130, 1131, 1132, 1133, 1134, 1135, 1136, 1137, 1138, 1139, 1140, 1141, 1142, 1143, 1144, 1145, 1146, 1147, 1148, 1149, 1150, 1151, 1152, 1153, 1154, 1155, 1156, and 1157 in SEQ ID NOs: 26-30, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than N-L+1, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b.

[0125] In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 1158, 1159, 1160, 1161, 1162, 1163, 1164, 1165, 1166, 1167, 1168, 1169, 1170, 1171, 1172, 1173, 1174, 1175, 1176, 1177, 1178, 1179, 1180, 1181, 1182, 1183, 1184, 1185, 1186, 1187, 1188, 1189, 1190, 1191, 1192, 1193, 1194, 1195, 1196, 1197, 1198, 1199, 1200, 1201, 1202, 1203, 1204, 1205, 1206, and 1207 in SEQ ID NOs: 27-30, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than N-L+1, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b.

[0126] In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 1208, 1209, 1210, 1211, 1212, 1213, 1214, 1215, 1216, 1217, 1218, 1219, 1220, 1221, 1222, 1223, 1224, 1225, 1226, 1227, 1228, 1229, 1230, 1231, 1232, 1233, 1234, 1235, 1236, 1237, 1238, 1239, 1240, 1241, 1242, 1243, 1244, 1245, 1246, 1247, 1248, 1249, 1250, 1251, 1252, 1253, 1254, 1255, 1256, 1257, 1258, 1259, 1260, 1261, 1262, 1263, 1264, 1265, 1266, 1267, 1268, 1269, 1270, 1271, 1272, 1273, 1274, 1275, 1276, 1277, 1278, 1279, 1280, 1281, 1282, 1283, 1284, 1285, 1286, 1287, 1288, 1289, 1290, 1291, 1292, 1293, 1294, 1295, 1296, 1297, 1298, 1299, 1300, 1301, 1302, 1303, 1304, 1305, 1306, 1307, 1308, 1309, 1310, 1311, 1312, 1313, 1314, 1315, 1316, 1317, 1318, 1319, 1320, 1321, 1322, 1323, 1324, 1325, 1326, 1327, 1328, 1329, 1330, 1331, 1332, 1333, 1334, 1335, 1336, 1337, 1338, 1339, 1340, 1341, 1342, 1343, 1344, 1345, 1346, 1347, 1348, 1349, 1350, 1351, 1352, 1353, 1354, 1355, 1356, 1357, 1358, 1359, 1360, 1361, 1362, 1363, 1364, 1365, 1366, 1367, 1368, 1369, 1370, 1371, 1372, 1373, 1374, 1375, 1376, 1377, 1378, 1379, 1380, 1381, 1382, 1383, 1384, 1385, 1386, 1387, 1388, 1389, 1390, 1391, 1392, 1393, 1394, 1395, 1396, 1397, 1398, 1399, 1400, 1401, 1402, 1403, 1404, 1405, 1406, 1407, 1408, 1409, 1410, 1411, 1412, 1413, 1414, 1415, 1416, 1417, 1418, 1419, 1420, 1421, 1422, 1423, 1424, 1425, 1426, 1427, 1428, 1429, 1430, 1431, 1432, 1433, 1434, 1435, 1436, 1437, 1438, 1439, 1440, 1441, 1442, 1443, 1444, 1445, 1446, 1447, 1448, 1449, 1450, 1451, 1452, 1453, 1454, 1455, 1456, 1457, 1458, 1459, 1460, 1461, 1462, 1463, 1464, 1465, 1466, 1467, 1468, 1469, 1470, 1471, 1472, 1473, 1474, 1475, 1476, 1477, 1478, 1479, 1480, 1481, 1482, 1483, 1484, 1485, 1486, 1487, 1488, 1489, 1490, 1491, 1492, 1493, 1494, 1495, 1496, 1497, 1498, 1499, 1500, 1501, 1502, 1503, 1504, 1505, 1506, 1507, 1508, 1509, 1510, 1511, 1512, 1513, 1514, 1515, 1516, 1517, 1518, 1519, 1520, 1521, 1522, 1523, 1524, 1525, 1526, 1527, 1528, 1529, 1530, 1531, 1532, 1533, 1534, 1535, 1536, 1537, 1538, 1539, 1540, 1541, 1542, 1543, 1544, 1545, 1546, 1547, 1548, 1549, 1550, 1551, 1552, 1553, 1554, 1555, 1556, 1557, 1558, 1559, 1560, 1561, 1562, 1563, 1564, 1565, 1566, 1567, 1568, 1569, 1570, 1571, 1572, 1573, 1574, 1575, 1576, 1577, 1578, 1579, 1580, 1581, 1582, 1583, 1584, 1585, 1586, 1587, 1588, 1589, 1590, 1591, 1592, 1593, 1594, 1595, 1596, 1597, 1598, 1599, 1600, 1601, 1602, 1603, 1604, 1605, 1606, 1607, 1608, 1609, 1610, 1611, 1612, 1613, 1614, 1615, 1616, 1617, 1618, 1619, 1620, 1621, 1622, 1623, 1624, 1625, 1626, 1627, 1628, 1629, 1630, 1631, 1632, 1633, 1634, 1635, 1636, 1637, 1638, 1639, 1640, 1641, 1642, 1643, 1644, 1645, 1646, 1647, 1648, 1649, 1650, 1651, 1652, 1653, 1654, 1655, 1656, 1657, 1658, 1659, 1660, 1661, 1662, 1663, 1664, 1665, 1666, 1667, 1668, 1669, 1670, 1671, 1672, 1673, 1674, 1675, 1676, 1677, 1678, 1679, 1680, 1681, 1682, 1683, 1684, 1685, 1686, 1687, 1688, 1689, 1690, 1691, 1692, 1693, 1694, 1695, 1696, 1697, 1698, 1699, 1700, 1701, 1702, 1703, 1704, 1705, 1706, 1707, 1708, 1709, 1710, 1711, 1712, 1713, 1714, 1715, 1716, 1717, 1718, 1719, 1720, 1721, 1722, 1723, 1724, 1725, 1726, 1727, 1728, 1729, 1730, 1731, 1732, 1733, 1734, 1735, 1736, 1737, 1738, 1739, 1740, 1741, 1742, 1743, 1744, 1745, 1746, 1747, 1748, 1749, 1750, 1751, 1752, 1753, 1754, 1755, 1756, 1757, 1758, 1759, 1760, 1761, 1762, 1763, 1764, 1765, 1766, 1767, 1768, 1769, 1770, 1771, 1772, 1773, 1774, 1775, 1776, 1777, 1778, 1779, 1780, 1781, 1782, 1783, 1784, 1785, 1786, 1787, 1788, 1789, 1790, 1791, 1792, 1793, 1794, 1795, 1796, 1797, 1798, 1799, 1800, 1801, 1802, 1803, 1804, 1805, 1806, 1807, 1808, 1809, 1810, 1811, 1812, 1813, 1814, 1815, 1816, 1817, 1818, 1819, 1820, 1821, 1822, 1823, 1824, 1825, 1826, 1827, 1828, 1829, 1830, 1831, 1832, 1833, 1834, 1835, 1836, 1837, 1838, 1839, 1840, 1841, 1842, 1843, 1844, 1845, 1846, 1847, 1848, 1849, 1850, 1851, 1852, 1853, 1854, 1855, 1856, 1857, 1858, 1859, 1860, 1861, 1862, 1863, 1864, 1865, 1866, 1867, 1868, 1869, 1870, 1871, 1872, 1873, 1874, 1875, 1876, 1877, 1878, 1879, 1880, 1881, 1882, 1883, 1884, 1885, 1886, 1887, 1888, 1889, 1890, 1891, 1892, 1893, 1894, 1895, 1896, 1897, 1898, 1899, 1900, 1901, 1902, 1903, 1904, 1905, 1906, 1907, 1908, 1909, 1910, 1911, 1912, 1913, 1914, 1915, 1916, 1917, 1918, 1919, 1920, 1921, 1922, 1923, 1924, 1925, 1926, 1927, 1928, 1929, 1930, 1931, 1932, 1933, 1934, 1935, 1936, 1937, 1938, 1939, 1940, 1941, 1942, 1943, 1944, 1945, 1946, 1947, 1948, 1949, 1950, 1951, 1952, 1953, 1954, 1955, 1956, 1957, 1958, 1959, 1960, 1961, 1962, 1963, 1964, 1965, 1966, 1967, 1968, 1969, 1970, 1971, 1972, 1973, 1974, 1975, 1976, 1977, 1978, 1979, 1980, 1981, 1982, 1983, 1984, 1985, 1986, 1987, 1988, 1989, 1990, 1991, 1992, 1993, 1994, 1995, 1996, 1997, 1998, 1999, 2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058, 2059, 2060, 2061, 2062, 2063, 2064, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2072, 2073, 2074, 2075, 2076, 2077, 2078, 2079, 2080, 2081, 2082, 2083, 2084, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092, 2093, 2094, 2095, 2096, 2097, 2098, 2099, 2100, 2101, 2102, 2103, 2104, 2105, 2106, 2107, 2108, 2109, 2110, 2110, 2111, 2112, 2113, 2114, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2122, 2123, 2124, 2125, 2126, 2127, 2128, 2129, 2130, 2131, 2132, 2133, 2134, 2135, 2136, 2137, 2138, 2139, 2140, 2141, 2142, 2143, 2144, 2145, 2146, 2147, 2148, 2149, 2150, 2151, 2152, 2153, 2154, 2155, 2156, 2157, 2158, 2159, 2160, 2171, 2172, 2173, 2174, 2175, 2176, 2177, 2178, 2179, 2180, 2181, 2182, 2183, 2184, 2185, 2186, 2187, 2188, 2189, 2190, 2191, 2192, 2193, 2194, 2195, 2196, 2197, 2198, 2199, 2200, 2201, 2202, 2203, 2204, 2205, 2206, 2207, 2208, 2209, 2210, 2211, 2212, 2213, 2214, 2215, 2216, 2217, 2218, 2219, 2220, 2221, 2222, 2223, 2224, 2225, 2226, 2227, 2228, 2229, 2230, 2231, 2232, 2233, 2234, 2235, 2236, 2237, 2238, 2239, 2240, 2241, 2242, 2243, 2244, 2245, 2246, 2247, 2248, 2249, 2250, 2251, 2252, 2253, 2254, 2255, 2256, 2257, 2258, 2259, 2260, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2279, 2280, 2281, 2282, 2283, 2284, 2285, 2286, 2287, 2288, 2289, 2290, 2291, 2292, 2293, 2294, 2295, 2296, 2297, 2298, 2299, 2300, 2301, 2302, 2303, 2304, 2305, 2306, 2307, 2308, 2309, 2310, 2311, 2312, 2313, 2314, 2315, 2316, 2317, 2318, 2319, 2320, 2321, 2322, 2323, 2324, 2325, 2326, 2327, 2328, 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337, 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351, 2352, 2353, 2354, 2355, 2356, 2357, 2358, 2359, 2360, 2361, 2362, 2363, 2364, 2365, 2366, 2367, 2368, 2369, 2370, 2371, 2372, 2373, 2374, 2375, 2376, 2377, 2378, 2379, 2380, 2381, 2382, 2383, 2384, 2385, 2386, 2387, 2388, 2389, 2390, 2391, 2392, 2393, 2394, 2395, 2396, 2397, 2398, 2399, 2400, 2401, 2402, 2403, 2404, 2405, 2406, 2407, 2408, 2409, 2410, 2411, 2412, 2413, 2414, 2415, 2416, 2417, 2418, 2419, 2420, 2421, 2422, 2423, 2424, 2425, 2426, 2427, 2428, 2429, 2430, 2431, 2432, 2433, 2434, 2435, 2436, 2437, 2438, 2439, 2440, 2441, 2442, 2443, 2444, 2445, 2446, 2447, 2448, 2449, 2450, 2451, 2452, 2453, 2454, 2455, 2456, 2457, 2458, 2459, 2460, 2461, 2462, 2463 and 2464 in SEQ ID NOs: 28-30, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than N-L+1, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b.

[0127] In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 2465, 2466, 2467, 2468, 2469, 2470, 2471, 2472, 2473, 2474, 2475, 2476, 2477, 2478, 2479, 2480, 2481, 2482, 2483, 2484, 2485, 2486, 2487, 2488, 2489, 2490, 2491, 2492, 2493, 2494, 2495, 2496, 2497, 2498, 2499, 2500, 2501, 2502, 2503, 2504, 2505, 2506, 2507, 2508, 2509, 2510, 2511, 2512, 2513, 2514, 2515, 2516, 2517, 2518, 2519, 2520, 2521, 2522, 2523, 2524, 2525, 2526, 2527, 2528, 2529, 2530, 2531, 2532, 2533, 2534, 2535, 2536, 2537, 2538, 2539, 2540, 2541, 2542, 2543, 2544, 2545, 2546, 2547, 2548, 2549, 2550, 2551, 2552, 2553, 2554, 2555, 2556, 2557, 2558, 2559, 2560, 2561, 2562, 2563, 2564, 2565, 2566, 2567, 2568, 2569, 2570, 2571, 2572, 2573, 2574, 2575, 2576, 2577, 2578, 2579, 2580, 2581, 2582, 2583, 2584, 2585, 2586, 2587, 2588, 2589, 2590, 2591, 2592, 2593, 2594, 2595, 2596, 2597, 2598, 2599, 2600, 2601, 2602, 2603, 2604, 2605, 2606, 2607, 2608, 2609, 2610, 2611, 2612, 2613, 2614, 2615, 2616, 2617, 2618, 2619, 2620, 2621, 2622, 2623, 2624, 2625, 2626, 2627, 2628, 2629, 2630, 2631, 2632, 2633, 2634, 2635, 2636, 2637, 2638, 2639, 2640, 2641, 2642, 2643, 2644, 2645, 2646, 2647, 2648, 2649, 2650, 2651, 2652, 2653, 2654, 2655, 2656, 2657, 2658, 2659, 2660, 2661, 2662, 2663, 2664, 2665, 2666, 2667, 2668, 2669, 2670, 2671, 2672, 2673, 2674, 2675, 2676, 2677, 2678, 2679, 2680, 2681, 2682, 2683, 2684, 2685, 2686, 2687, 2688, 2689, 2690, 2691, 2692, 2693, 2694, 2695, 2696, 2697, 2698, 2699, 2700, 2701, 2702, 2703, 2704, 2705, 2706, 2707, 2708, 2709, 2710, 2711, 2712, 2713, 2714, 2715, 2716, 2717, 2718, 2719, 2720, 2721, 2722, 2723, 2724, 2725, 2726, 2727, 2728, 2729, 2730, 2731, 2732, 2733, 2734, 2735, 2736, 2737, 2738, 2739, 2740, 2741, 2742, 2743, 2744, 2745, 2746, 2747, 2748, 2749, 2750, 2751, 2752, 2753, 2754, 2755, 2756, 2757, 2758, 2759, 2760, 2761, 2762, 2763, 2764, 2765, 2766, 2767, 2768, 2769, 2770, 2771, 2772, 2773, 2774, 2775, 2776, 2777, 2778, 2779, 2780, 2781, 2782, 2783, 2784, 2785, 2786, 2787, 2788, 2789, 2790, 2791, 2792, 2793, 2794, 2795, 2796, 2797, 2798, 2799, 2800, 2801, 2802, 2803, 2804, 2805, 2806, 2807, 2808, 2809, 2810, 2811, 2812, 2813, 2814, 2815, 2816, 2817, 2818, 2819, 2820, 2821, 2822, 2823, 2824, 2825, 2826, 2827, 2828, 2829, 2830, 2831, 2832, 2833, 2834, 2835, 2836, 2837, 2838, 2839, 2840, 2841, 2842, 2843, 2844, 2845, 2846, 2847, 2848, 2849, 2850, 2851, 2852, 2853, 2854, 2855, 2856, 2857, 2858, 2859, 2860, 2861, 2862, 2863, 2864, 2865, 2866, 2867, 2868, 2869, 2870, 2871, 2872, 2873, 2874, 2875, 2876, 2877, 2878, 2879, 2880, 2881, 2882, 2883, 2884, 2885, 2886, 2887, 2888, 2889, 2890, 2891, 2892, 2893, 2894, 2895, 2896, 2897, 2898, 2899, 2900, 2901, 2902, 2903, 2904, 2905, 2906, 2907, 2908, 2909, 2910, 2911, 2912, 2913, 2914, 2915, 2916, 2917, 2918, 2919, 2920, 2921, 2922, 2923, 2924, 2925, 2926, 2927, 2928, 2929, 2930, 2931, 2932, 2933, 2934, 2935, 2936, 2937, 2938, 2939, 2940, 2941, 2942, 2943, 2944, 2945, 2946, 2947, 2948, 2949, 2950, 2951, 2952, 2953, 2954, 2955, 2956, 2957, 2958, 2959, 2960, 2961, 2962, 2963, 2964, 2965, 2966, 2967, 2968, 2969, 2970, 2971, 2972, 2973, 2974, 2975, 2976, 2977, 2978, 2979, 2980, 2981, 2982, 2983, 2984, 2985, 2986, 2987, 2988, 2989, 2990, 2991, 2992, 2993, 2994, 2995, 2996, 2997, 2998, 2999, 3000, 3001, 3002, 3003, 3004, 3005, 3006, 3007, 3008, 3009, 3010, 3011, 3012, 3013, 3014, 3015, 3016, 3017, 3018, 3019, 3020, 3021, 3022, 3023, 3024, 3025, 3026, 3027, 3028, 3029, 3030, 3031, 3032, 3033, 3034, 3035, 3036, 3037, 3038, 3039, 3040, 3042, 3043, 3044, 3045, 3046, 3047, 3048, 3049, 3050, 3051, 3052, 3053, 3054, 3055, 3056, 3057, 3058, 3059, 3060, 3061, 3062, 3063, 3064, 3065, 3066, 3067, 3068, 3069, 3070, 3071, 3072, 3073, 3074, 3075, 3076, 3077, 3078, 3079, 3080, 3081, 3082, 3083, 3084, 3085, 3086, 3087, 3088, 3089, 3090, 3091, 3092, 3093, 3094, 3095, 3096, 3097, 3098, 3099, 3100, 3101, 3102, 3103, 3104, 3105, 3106, 3107, 3108, 3109, 3110, 3110, 3111, 3112, 3113, 3114, 3115, 3116, 3117, 3118, 3119, 3120, 3121, 3122, 3123, 3124, 3125, 3126, 3127, 3128, 3129, 3130, 3131, 3132, 3133, 3134, 3135, 3136, 3137, 3138, 3139, 3140, 3141, 3142, 3143, 3144, 3145, 3146, 3147, 3148, 3149, 3150, 3151, 3152, 3153, 3154, 3155, 3156, 3157, 3158, 3159, 3160, 3171, 3172, 3173, 3174, 3175, 3176, 3177, 3178, 3179, 3180, 3181, 3182, 3183, 3184, 3185, 3186, 3187, 3188, 3189, 3190, 3191, 3192, 3193, 3194, 3195, 3196, 3197, 3198, 3199, 3200, 3201, 3202, 3203, 3204, 3205, 3206, 3207, 3208, 3209, 3210, 3211, 3212, 3213, 3214, 3215, 3216, 3217, 3218, 3219, 3220, 3221, 3222, 3223, 3224, 3225, 3226, 3227, 3228, 3229, 3230, 3231, 3232, 3233, 3234, 3235, 3236, 3237, 3238, 3239, 3240, 3241, 3242, 3243, 3244, 3245, 3246, 3247, 3248, 3249, 3250, 3251, 3252, 3253, 3254, 3255, 3256, 3257, 3258, 3259, 3260, 3271, 3272, 3273, 3274, 3275, 3276, 3277, 3278, 3279, 3280, 3281, 3282, 3283, 3284, 3285, 3286, 3287, 3288, 3289, 3290, 3291, 3292, 3293, 3294, 3295, 3296, 3297, 3298, 3299, 3300, 3301, 3302, 3303, 3304, 3305, 3306, 3307, 3308, 3309, 3310, 3311, 3312, 3313, 3314, 3315, 3316, 3317, 3318, 3319, 3320, 3321, 3322, 3323, 3324, 3325, 3326, 3327, 3328, 3329, 3330, 3331, 3332, 3333, 3334, 3335, 3336, 3337, 3338, 3339, 3340, 3341, 3342, 3343, 3344, 3345, 3346, 3347, 3348, 3349, 3350, 3351, 3352, 3353, 3354, 3355, 3356, 3357, 3358, 3359, 3360, 3361, 3362, 3363, 3364, 3365, 3366, 3367, 3368, 3369, 3370, 3371, 3372, 3373, 3374, 3375, 3376, 3377, 3378, 3379, 3380, 3381, 3382, 3383, 3384, 3385, 3386, 3387, 3388, 3389, 3390, 3391, 3392, 3393, 3394, 3395, 3396, 3397, 3398, 3399, 3400, 3401, 3402, 3403, 3404, 3405, 3406, 3407, 3408, 3409, 3410, 3411, 3412, 3413, 3414, 3415, 3416, 3417, 3418, 3419, 3420, 3421, 3422, 3423, 3424, 3425, 3426, 3427, 3428, 3429, 3430, 3431, 3432, 3433, 3434, 3435, 3436, 3437, 3438, 3439, 3440, 3441, 3442, 3443, 3444, 3445, 3446, 3447, 3448, 3449, 3450, 3451, 3452, 3453, 3454, 3455, 3456, 3457, 3458, 3459, 3460, 3461, 3462, 3463, 3464, 3465, 3466, 3467, 3468, 3469, 3470, 3471, 3472, 3473, 3474, 3475, 3476, 3477, 3478, 3479, 3480, 3481, 3482, 3483, 3484, 3485, 3486, 3487, 3488, 3489, 3490, 3491, 3492, 3493, 3494, 3495, 3496, 3497, 3498, 3499, 3500, 3501, 3502, 3503, 3504, 3505, 3506, 3507, 3508, 3509, 3510, 3511, 3512, 3513, 3514, 3515, 3516, 3517, 3518, 3519, 3520, 3521, 3522, 3523, 3524, 3525, 3526, 3527, 3528, 3529, 3530 and 3531 in SEQ ID NOs: 29-30, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than N-L+1, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b.

[0128] In the embodiments defined by option b) above, the polypeptide of the invention is also one that has at least 5 contiguous amino acid residues defined for option b) above and also has its N-terminal amino acid residue corresponding to any one of amino acid residues 3532, 3533, 3534, 3535, 3536, 3537, 3538, 3539, 3540, 3541, 3542, 3543, 3544, 3545, 3546, 3547, 3548, 3549, 3550, 3551, 3552, 3553, 3554, 3555, 3556, 3557, 3558, 3559, 3560, 3561, 3562, 3563, 3564, 3565, 3566, 3567, 3568, 3569, 3570, 3571, 3572, 3573, 3574, 3575, 3576, 3577, 3578, 3579, 3580, 3581, 3582, 3583, 3584, 3585, 3586, 3587, 3588, 3589, 3590, 3591, 3592, 3593, 3594, 3595, 3596, 3597, 3598, 3599, 3600, 3601, 3602, 3603, 3604, 3605, 3606, 3607, 3608, 3609, 3610, 3611, 3612, 3613, 3614, 3615, 3616, 3617, 3618, 3619, 3620, 3621, 3622, 3623, 3624, 3625, 3626, 3627, 3628, 3629, 3630, 3631, 3632, 3633, 3634, 3635, 3636, 3637, 3638, 3639, 3640, 3641, 3642, 3643, 3644, 3645, 3646, 3647, 3648, 3649, 3650, 3651, 3652, 3653, 3654, 3655, 3656, 3657, 3658, 3659, 3660, 3661, 3662, 3663, 3664, 3665, 3666, 3667, 3668, 3669, 3670, 3671, 3672, 3673, 3674, 3675, 3676, 3677, 3678, 3679, 3680, 3681, 3682, 3683, 3684, 3685, 3686, 3687, 3688, 3689, 3690, 3691, 3692, 3693, 3694, 3695, 3696, 3697, 3698, 3699, 3700, 3701, 3702, 3703, 3704, 3705, 3706, 3707, 3708, 3709, 3710, 3711, 3712, 3713, 3714, 3715, 3716, 3717, 3718, 3719, 3720, 3721, 3722, 3723, 3724, 3725, 3726, 3727, 3728, 3729, 3730, 3731, 3732, 3733, 3734, 3735, 3736, 3737, 3738, 3739, 3740, 3741, 3742, 3743, 3744, 3745, 3746, 3747, 3748, 3749, 3750, 3751, 3752, 3753, 3754, 3755, 3756, 3757, 3758, 3759, 3760, 3761, 3762, 3763, 3764, 3765, 3766, 3767, 3768, 3769, 3770, 3771, 3772, 3773, 3774, 3775, 3776, 3777, 3778, 3779, 3780, 3781, 3782, 3783, 3784, 3785, 3786, 3787, 3788, 3789, 3790, 3791, 3792, 3793, 3794, 3795, 3796, 3797, 3798, 3799, 3800, 3801, 3802, 3803, 3804, 3805, 3806, 3807, 3808, 3809, 3810, 3811, 3812, 3813, 3814, 3815, 3816, 3817, 3818, 3819, 3820, 3821, 3822, 3823, 3824, 3825, 3826, 3827, 3828, 3829, 3830, 3831, 3832, 3833, 3834, 3835, 3836, 3837, 3838, 3839, 3840, 3841, 3842, 3843, 3844, 3845, 3846, 3847, 3848, 3849, 3850, 3851, 3852, 3853, 3854, 3855, 3856, 3857, 3858, 3859, 3860, 3861, 3862, 3863, 3864, 3865, 3866, 3867, 3868, 3869, 3870, 3871, 3872, 3873, 3874, 3875, 3876, 3877, 3878, 3879, 3880, 3881, 3882, 3883, 3884, 3885, 3886, 3887, 3888, 3889, 3890, 3891, 3892, 3893, 3894, 3895, 3896, 3897, 3898, 3899, 3900, 3901, 3902, 3903, 3904, 3905, 3906, 3907, 3908, 3909, 3910, 3911, 3912, 3913, 3914, 3915, 3916, 3917, 3918, 3919, 3920, 3921, 3922, 3923, 3924, 3925, 3926, 3927, 3928, 3929, 3930, 3931, 3932, 3933, 3934, 3935, 3936, 3937, 3938, 3939, 3940, 3941, 3942, 3943, 3944, 3945, 3946, 3947, 3948, 3949, 3950, 3951, 3952, 3953, 3954, 3955, 3956, 3957, 3958, 3959, 3960, 3961, 3962, 3963, 3964, 3965, 3966, 3967, 3968, 3969, 3970, 3971, 3972, 3973, 3974, 3975, 3976, 3977, 3978, 3979, 3980, 3981, 3982, 3983, 3984, 3985, 3986, 3987, 3988, 3989, 3990, 3991, 3992, 3993, 3994, 3995, 3996, 3997, 3998, 3999, 4000, 4001, 4002, 4003, 4004, 4005, 4006, 4007, 4008, 4009, 4010, 4011, 4012, 4013, 4014, 4015, 4016, 4017, 4018, 4019, 4020, 4021, 4022, 4023, 4024, 4025, 4026, 4027, 4028, 4029, 4030, 4031, 4032, 4033, 4034, 4035, 4036, 4037, 4038, 4039, 4040, 4042, 4043, 4044, 4045, 4046, 4047, 4048, 4049, 4050, 4051, 4052, 4053, 4054, 4055, 4056, 4057, 4058, 4059, 4060, 4061, 4062, 4063, 4064, 4065, 4066, 4067, 4068, 4069, 4070, 4071, 4072, 4073, 4074, 4075, 4076, 4077, 4078, 4079, 4080, 4081, 4082, 4083, 4084, 4085, 4086, 4087, 4088, 4089, 4090, 4091, 4092, 4093, 4094, 4095, 4096, 4097, 4098, 4099, 4100, 4101, 4102, 4103, 4104, 4105, 4106, 4107, 4108, 4109, 4110, 4110, 4111, 4112, 4113, 4114, 4115, 4116, 4117, 4118, 4119, 4120, 4121, 4122, 4123, 4124, 4125, 4126, 4127, 4128, 4129, 4130, 4131, 4132, 4133, 4134, 4135, 4136, 4137, 4138, 4139, 4140, 4141, 4142, 4143, 4144, 4145, 4146, 4147, 4148, 4149, 4150, 4151, 4152, 4153, 4154, 4155, 4156, 4157, 4158, 4159, 4160, 4171, 4172, 4173, 4174, 4175, 4176, 4177, 4178, 4179, 4180, 4181, 4182, 4183, 4184, 4185, 4186, 4187, 4188, 4189, 4190, 4191, 4192, 4193, 4194, 4195, 4196, 4197, 4198, 4199, 4200, 4201, 4202, 4203, 4204, 4205, 4206, 4207, 4208, 4209, 4210, 4211, 4212, 4213, 4214, 4215, 4216, 4217, 4218, 4219, 4220, 4221, 4222, 4223, 4224, 4225, 4226, 4227, 4228, 4229, 4230, 4231, 4232, 4233, 4234, 4235, 4236, 4237, 4238, 4239, 4240, 4241, 4242, 4243, 4244, 4245, 4246, 4247, 4248, 4249, 4250, 4251, 4252, 4253, 4254, 4255, 4256, 4257, 4258, 4259, 4260, 4271, 4272, 4273, 4274, 4275, 4276, 4277, 4278, 4279, 4280, 4281, 4282, 4283, 4284, 4285, 4286, 4287, 4288, 4289, 4290, 4291, 4292, 4293, 4294, 4295, 4296, 4297, 4298, 4299, 4300, 4301, 4302, 4303, 4304, 4305, 4306, 4307, 4308, 4309, 4310, 4311, 4312, 4313, 4314, 4315, 4316, 4317, 4318, 4319, 4320, 4321, 4322, 4323, 4324, 4325, 4326, 4327, 4328, 4329, 4330, 4331, 4332, 4333, 4334, 4335, 4336, 4337, 4338, 4339, 4340, 4341, 4342, 4343, 4344, 4345, 4346, 4347, 4348, 4349, 4350, 4351, 4352, 4353, 4354, 4355, 4356, 4357, 4358, 4359, 4360, 4361, 4362, 4363, 4364, 4365, 4366, 4367, 4368, 4369, 4370, 4371, 4372, 4373, 4374, 4375, 4376, 4377, 4378, 4379, 4380, 4381, 4382, 4383, 4384, 4385, 4386, 4387, 4388, 4389, 4390, 4391, 4392, 4393, 4394, 4395, 4396, 4397, 4398, 4399, 4400, 4401, 4402, 4403, 4404, 4405, 4406, 4407, 4408, 4409, 4410, 4411, 4412, 4413, 4414, 4415, 4416, 4417, 4418, 4419, 4420, 4421, 4422, 4423, 4424, 4425, 4426, 4427, 4428, 4429, 4430, 4431, 4432, 4433, 4434, 4435, 4436, 4437, 4438, 4439, 4440, 4441, 4442, 4443, 4444, 4445, 4446, 4447, 4448, 4449, 4450, 4451, 4452, 4453, 4454, 4455, 4456, 4457, 4458, 4459, 4460, 4461, 4462, 4463, 4464, 4465, 4466, 4467, 4468, 4469, 4470, 4471, 4472, 4473, 4474, 4475, 4476, 4477, 4478, 4479, 4480, 4481, 4482, 4483, 4484, 4485, 4486, 4487, 4488, 4489, 4490, 4491, 4492, 4493, 4494, 4495, 4496, 4497, 4498, 4499, 4500, 4501, 4502, 4503, 4504, 4505, 4506, 4507, 4508, 4509, 4510, 4511, 4512, 4513, 4514, 4515, 4516, 4517, 4518, 4519, 4520, 4521, 4522, 4523, 4524, 4525, 4526, 4527, 4528, 4529, 4530, 4531, 4532, 4533, 4534, 4535, 4536, 4537, 4538, 4539, 4540, 4541, 4542, 4543, 4544, 4545, 4546, 4547, 4548, 4549, 4550, 4551, 4552, 4553, 4554, 4555, 4556, 4557, 4558, 4559, 4560, 4561, 4562, 4563, 4564, 4565, 4566, 4567, 4568, 4569, 4570, 4571, 4572, 4573, 4574, 4575, 4576, 4577, 4578, 4579, 4580, 4581, 4582, 4583, 4584, 4585, 4586, 4587, 4588, 4589, 4590, 4591, 4592, 4593, 4594, 4595, 4596, 4597, 4598, 4599, 4600, 4601, 4602, 4603, 4604, 4605, 4606, 4607, 4608, 4609, 4610, 4611, 4612, 4613, 4614, 4615, 4616, 4617, 4618, 4619, 4620, 4621, 4622, 4623, 4624, 4625, 4626, 4627, 4628, 4629, 4630, 4631, 4632, 4633, 4634, 4635, 4636, 4637, 4638, 4639, 4640, 4641, 4642, 4643, 4644, 4645, 4646, 4647, 4648, 4649, 4650, 4651, 4652, 4653, 4654, 4655, 4656, 4657, 4658, 4659, 4660, 4661, 4662, 4663, 4664, 4665, 4666, 4667, 4668, 4669, 4670, 4671, 4672, 4673, 4674, 4675, 4676, 4677, 4678, 4679, 4680, 4681, 4682, 4683, 4684, 4685, 4686, 4687, 4688, 4689, 4690, 4691, 4692, 4693, 4694, 4695, 4696, 4697, 4698, 4699, 4700, 4701, 4702, 4703, 4704, 4705, 4706, 4707, 4708, 4709, 4710, 4711, 4712, 4713, 4714, 4715, 4716, 4717, 4718, 4719, 4720, 4721, 4722, 4723, 4724, 4725, 4726, 4727, 4728, 4729, 4730, 4731, 4732, 4733, 4734, 4735, 4736, 4737, 4738, 4739, 4740, 4741, 4742, 4743, 4744, 4745, 4746, 4747, 4748, 4749, 4750, 4751, 4752, 4753, 4754, 4755, 4756, 4757, 4758, 4759, 4760, 4761, 4762, 4763, 4764, 4765, 4766, 4767, 4768, 4769, 4770, 4771, 4772, 4773, 4774, 4775, 4776, 4777, 4778, 4779, 4780, 4781, 4782, 4783, 4784, 4785, 4786, 4787, 4788, 4789, 4790, 4791, 4792, 4793, 4794, 4795, 4796, 4797, 4798, 4799, 4800, 4801, 4802, 4803, 4804, 4805, 4806, 4807, 4808, 4809, 4810, 4811, 4812, 4813, 4814, 4815, 4816, 4817, 4818, 4819, 4820, 4821, 4822, 4823, 4824, 4825, 4826, 4827, 4828, 4829, 4830, 4831, 4832, 4833, 4834, 4835, 4836, 4837, 4838, 4839, 4840, 4841, 4842, 4843, 4844, 4845, 4846, 4847, 4848, 4849, 4850, 4851, 4852, 4853, 4854, 4855, 4856, 4857, 4858, 4859, 4860, 4861, 4862, 4863, 4864, 4865, 4866, 4867, 4868, 4869, 4870, 4871, 4872, 4873, 4874, 4875, 4876, 4877, 4878, 4879, 4880, 4881, 4882, 4883, 4884, 4885, 4886, 4887, 4888, 4889, 4890, 4891, 4892, 4893, 4894, 4895, 4896, 4897, 4898, 4899, 4900, 4901, 4902, 4903, 4904, 4905, 4906, 4907, 4908, 4909, 4910, 4911, 4912, 4913, 4914, 4915, 4916, 4917, 4918, 4919, 4920, 4921, 4922, 4923, 4924, 4925, 4926, 4927, 4928, 4929, 4930, 4931, 4932, 4933, 4934, 4935, 4936, 4937, 4938, 4939, 4940, 4941, 4942, 4943, 4944, 4945, 4946, 4947, 4948, 4949, 4950, 4951, 4952, 4953, 4954, 4955, 4956, 4957, 4958, 4959, 4960, 4961, 4962, 4963, 4964, 4965, 4966, 4967, 4968, 4969, 4970, 4971, 4972, 4973, 4974, 4975, 4976, 4977, 4978, 4979, 4980, 4981, 4982, 4983, 4984, 4985, 4986, 4987, 4988, 4989, 4990, 4991, 4992, 4993, 4994, 4995, 4996, 4997, 4998, 4999, 5000, 5001, 5002, 5003, 5004, 5005, 5006, 5007, 5008, 5009, 5010, 5011, 5012, 5013, 5014, 5015, 5016, 5017, 5018, 5019, 5020, 5021, 5022, 5023, 5024, 5025, 5026, 5027, 5028, 5029, 5030, 5031, 5032, 5033, 5034, 5035, 5036, 5037, 5038, 5039, 5040, 5042, 5043, 5044, 5045, 5046, 5047, 5048, 5049, 5050, 5051, 5052, 5053, 5054, 5055, 5056, 5057, 5058, 5059, 5060, 5061, 5062, 5063, 5064, 5065, 5066, 5067, 5068, 5069, 5070, 5071, 5072, 5073, 5074, 5075, 5076, 5077, 5078, 5079, 5080, 5081, 5082, 5083, 5084, 5085, 5086, 5087, 5088, 5089, 5090, 5091, 5092, 5093, 5094, 5095, 5096, 5097, 5098, 5099, 5100, 5101, 5102, 5103, 5104, 5105, 5106, 5107, 5108, 5109, 5110, 5110, 5111, 5112, 5113, 5114, 5115, 5116, 5117, 5118, 5119, 5120, 5121, 5122, 5123, 5124, 5125, 5126, 5127, 5128, 5129, 5130, 5131, 5132, 5133, 5134, 5135, 5136, 5137, 5138, 5139, 5140, 5141, 5142, 5143, 5144, 5145, 5146, 5147, 5148, 5149, 5150, 5151, 5152, 5153, 5154, 5155, 5156, 5157, 5158, 5159, 5160, 5171, 5172, 5173, 5174, 5175, 5176, 5177, 5178, 5179, 5180, 5181, 5182, 5183, 5184, 5185, 5186, 5187, 5188, 5189, 5190, 5191, 5192, 5193, 5194, 5195, 5196, 5197, 5198, 5199, 5200, 5201, 5202, 5203, 5204, 5205, 5206, 5207, 5208, 5209, 5210, 5211, 5212, 5213, 5214, 5215, 5216, 5217, 5218, 5219, 5220, 5221, 5222, 5223, 5224, 5225, 5226, 5227, 5228, 5229, 5230, 5231, 5232, 5233, 5234, 5235, 5236, 5237, 5238, 5239, 5240, 5241, 5242, 5243, 5244, 5245, 5246, 5247, 5248, 5249, 5250, 5251, 5252, 5253, 5254, 5255, 5256, 5257, 5258, 5259, 5260, 5271, 5272, 5273, 5274, 5275, 5276, 5277, 5278, 5279, 5280, 5281, 5282, 5283, 5284, 5285, 5286, 5287, 5288, 5289, 5290, 5291, 5292, 5293, 5294, 5295, 5296, 5297, 5298, 5299, 5300, 5301, 5302, 5303, 5304, 5305, 5306, 5307, 5308, 5309, 5310, 5311, 5312, 5313, 5314, 5315, 5316, 5317, 5318, 5319, 5320, 5321, 5322, 5323, 5324, 5325, 5326, 5327, 5328, 5329, 5330, 5331, 5332, 5333, 5334, 5335, 5336, 5337, 5338, 5339, 5340, 5341, 5342, 5343, 5344, 5345, 5346, 5347, 5348, 5349, 5350, 5351, 5352, 5353, 5354, 5355, 5356, 5357, 5358, 5359, 5360, 5361, 5362, 5363, 5364, 5365, 5366, 5367, 5368, 5369, 5370, 5371, 5372, 5373, 5374, 5375, 5376, 5377, 5378, 5379, 5380, 5381, 5382, 5383, 5384, 5385, 5386, 5387, 5388, 5389, 5390, 5391, 5392, 5393, 5394, 5395, 5396, 5397, 5398, 5399, 5400, 5401, 5402, 5403, 5404, 5405, 5406, 5407, 5408, 5409, 5410, 5411, 5412, 5413, 5414, 5415, 5416, 5417, 5418, 5419, 5420, 5421, 5422, 5423, 5424, 5425, 5426, 5427, 5428, 5429, 5430, 5431, 5432, 5433, 5434, 5435, 5436, 5437, 5438, 5439, 5440, 5441, 5442, 5443, 5444, 5445, 5446, 5447, 5448, 5449, 5450, 5451, 5452, 5453, 5454, 5455, 5456, 5457, 5458, 5459, 5460, 5461, 5462, 5463, 5464, 5465, 5466, 5467, 5468, 5469, 5470, 5471, 5472, 5473, 5474, 5475, 5476, 5477, 5478, 5479, 5480, 5481, 5482, 5483, 5484, 5485, 5486, 5487, 5488, 5489, 5490, 5491, 5492, 5493, 5494, 5495, 5496, 5497, 5498, 5499, 5500, 5501, 5502, 5503, 5504, 5505, 5506, 5507, 5508, 5509, 5510, 5511, 5512, 5513, 5514, 5515, 5516, 5517, 5518, 5519, 5520, 5521, 5522, 5523, 5524, 5525, 5526, 5527, 5528, 5529, 5530, 5531, 5532, 5533, 5534, 5535, 5536, 5537, 5538, 5539, 5540, 5541, 5542, 5543, 5544, 5545, 5546, 5547, 5548, 5549, 5550, 5551, 5552, 5553, 5554, 5555, 5556, 5557, 5558, 5559, 5560, 5561, 5562, 5563, 5564, 5565, 5566, 5567, 5568, 5569, 5570, 5571, 5572, 5573, 5574, 5575, 5576, 5577, 5578, 5579, 5580, 5581, 5582, 5583, 5584, 5585, 5586, 5587, 5588, 5589, 5590, 5591, 5592, 5593, 5594, 5595, 5596, 5597, 5598, 5599, 5600, 5601, 5602, 5603, 5604, 5605, 5606, 5607, 5608, 5609, 5610, 5611, 5612, 5613, 5614, 5615, 5616, 5617, 5618, 5619, 5620, 5621, 5622 and 5623 in SEQ ID NO: 30, if the length of the at least 5 amino acid residues so permit—if the length of the at least 5 amino acids are higher than 5, the N-terminal first residue will not be higher numbered than N-L+1, where N is the number of amino acid residues of the reference sequence and L is the number of amino acids defined for option b.

[0129] The polypeptide of the invention is in certain embodiments also fused or conjugated to an immunogenic carrier molecule; or, phrased otherwise, the polypeptide of the invention also includes such an immunogenic carrier molecule in addition to the material derived from SEQ ID NOs. 1-30. The immunogenic carrier molecule is a typically polypeptide that induces T-helper lymphocyte responses in a majority of humans, such as immunogenic carrier proteins selected from the group consisting of keyhole limpet hemocyanino or a fragment thereof, tetanus toxoid or a fragment thereof, dipththeria toxoid or a fragment thereof. Other suitable carrier molecules are discussed infra.

[0130] In preferred embodiments, the polypeptide of the invention detailed above is capable of inducing an adaptive immune response against the polypeptide in a mammal, in particular in a human being. Preferably, the adaptive immune response is a protective adaptive immune response against infection with *Pseudomonas aeruginosa*. The polypeptide may in these cases induce a humeral and/or a cellular immune response.

[0131] A particularly preferred polypeptide of the invention is derived from SEQ ID NO: 17 and is otherwise as defined above.

Epitopes

[0132] SEQ ID NOs: 1-30 include antigenic determinants (epitopes) that are as such recognized by antibodies and/or when bound to MHC molecules by T-cell receptors. For the purposes of the present invention, B-cell epitopes (i.e. antibody binding epitopes) are of particular relevance.

[0133] It is relatively uncomplicated to identify linear B-cell epitopes—one very simple approach entails that antibodies raised agains *Pseudomonas aeruginosa* or *Pseudomonas aeruginosa* derived proteins disclosed herein are tested for binding to overlapping oligomeric peptides derived from any one of SEQ ID NO: 1-30. Thereby, the regions of the *Pseudomonas aeruginosa* polypeptide which are responsible for or contribute to binding to the antibodies can be identified.

[0134] Alternatively, or additionally, one can produce mutated versions of the polypeptides of the invention, e.g. version where each single non-alanine residue in SEQ ID NOs.: 1-30 are point mutated to alanine—this method also assists in identifying complex assembled B-cell epitopes; this is the case when binding of the same antibody is modified by exchanging amino acids in different areas of the full-length polypeptide.

[0135] Also, in silico methods for B-cell epitope prediction can be employed: useful state-of-the-art systems for β-turn prediction is provided in Petersen B et al. (November 2010), Plos One 5(11): e15079; prediction of linear B-cell epitopes, cf: Larsen J E P et al. (April 2006), Immunome Research, 2:2; predictionof solvent exposed amino acids: Petersen B et al (July 2009), BMC Structural Biology, 9:51.

The Nucleic Acid Fragments of the Invention

[0136] The nucleic acid fragment of the invention referred to above is preferably is a DNA fragment (such as SEQ ID NOs: 31-60) or an RNA fragment (such as SEQ ID NOs 61-90).

[0137] The nucleic acid fragment of the invention typically consists of at least 11, such as at least 12, at least 13, at least 14, at least 15, at least 16, at least 17 at least 18, at least 19, at least 20, at least 21, at least 22, at least 23, at least 24, at least 25, at least 26, at least 27, at least 28, at least 29, at least 30, at least 31, at least 32, at least 33, at least 34, at least 35, at least 36, at least 37, at least 38, at least 39, at least 40, at least 41, at least 42, at least 43, at least 44, at least 45, at least 46, at least 47, at least 48, at least 49, at least 50, at least 51, at least 52, at least 53, at least 54, at least 55, at least 56, at least 57, at least 58, at least 59, at least 60, at least 61, at least 62, at least 63, at least 64, at least 65, at least 66, at least 67, at least 68, at least 69, at least 70, at least 71, at least 72, at least 73, at least 74, at least 75, at least 76, at least 77, at least 78, at least 79, at least 80, at least 81, at least 82, at least 83, at least 84, at least 85, at least 86, at least 87, at least 88, at least 89, at least 90, at least 91, at least 92, at least 93, at least 94, at least 95, at least 96, at least 97, at least 98, at least 99, at least 100, at least 101, at least 102, at least 103, at least 104, at least 105, at least 106, at least 107, at least 108, at least 109, at least 110, at least 111, at least 112, at least 113, at least 114, at least 115, at least 116, at least 117, at least 118, at least 119, at least 120, at least 121, at least 122, at least 123, at least 124, at least 125, at least 126, at least 127, at least 128, at least 129, at least 130, at least 131, at least 132, at least 133, at least 134, at least 135, at least 136, at least 137, at least 138, at least 139, at least 140, at least 141, at least 142, at least 143, at least 144, at least 145, at least 146, at least 147, at least 148, at least 149, at least 150, at least 151, at least 152, at least 153, at least 154, at least 155, at least 156, at least 157, at least 158, at least 159, at least 160, at least 171, at least 172, at least 173, at least 174, at least 175, at least 176, at least 177, at least 178, at least 179, at least 180, at least 181, at least 182, at least 183, at least 184, at least 185, at least 186, at least 187, at least 188, at least 189, at least 190, at least 191, at least 192, at least 193, at least 194, at least 195, at least 196, at least 197, at least 198, at least 199, at least 200 and at least 201 consecutive nucleotides in any one of SEQ ID NOs: 31-90. Longer fragments are contemplated, i.e. fragments having at least 200, at least 300 at least 400, at least 500, at least 600, at least 700, at least 800, at least 900, at least 1000, at least 1500, at least 2000, at least 2500, at least 3000, at least 3500, and at least 4000 nucleotides from those of SEQ ID NOs: 31-90 that encompass fragments of such lengths.

[0138] The nucleic acid fragment of the invention discussed above typically has a sequence identity with the nucleotide sequence defined for i) or ii) above, which is at least 65%, such as at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, and at least 99%.

[0139] The nucleic acid fragment of the invention discussed above may also have a sequence identity with the nucleotide sequence defined for iii) above, which is at least 65%, such as at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, and at least 99%.

The Vectors of the Invention

[0140] Vectors of the invention fall into several categories discussed infra. One preferred vector of the invention comprises in operable linkage and in the 5'-3' direction, an expression control region comprising an enhancer/promoter for driving expression of the nucleic acid fragment defined for option i) above, optionally a signal peptide coding sequence, a nucleotide sequence defined for option i), and optionally a terminator. Hence, such a vector constitutes an expression vector useful for effecting production in cells of the polypeptide of the invention. Since the polypeptides of the invention are bacterial of orgin, recombinant production is conveniently effected in bacterial host cells, so here it is preferred that the expression control region drives expression in prokaryotic cell such as a bacterium, e.g. in *E coli*. However, if the vector is to drive expression in mammalian cell (as would be the case for a DNA vaccine vector), the expression control region should be adapted to this particular use.

[0141] At any rate, certain vectors of the invention are capable of autonomous replication.

[0142] Also, the vector of the invention may be one that is capable of being integrated into the genome of a host cell—this is particularly useful if the vector is use in the production of stably transformed cells, where the progeny will also include the genetic information introduced via the vector. Alternatively, vectors incapable of being integrated into the genome of a mammalian host cell are useful in e.g. DNA vaccination.

[0143] Typically, the vector of the invention is selected from the group consisting of a virus, such as a attenuated virus (which may in itself be useful as a vaccine agent), a bacteriophage, a plasmid, a minichromosome, and a cosmid.

[0144] A more detailed discussion of vectors of the invention is provided in the following:

[0145] Polypeptides of the invention may be encoded by a nucleic acid molecule comprised in a vector. A nucleic acid sequence can be "heterologous," which means that it is in a context foreign to the cell in which the vector is being introduced, which includes a sequence homologous to a sequence in the cell but in a position within the host cell where it is ordinarily not found. Vectors include naked DNAs, RNAs, plasmids, cosmids, viruses (bacteriophage, animal viruses, and plant viruses), and artificial chromosomes (e.g., YACs). One of skill in the art would be well equipped to construct a vector through standard recombinant techniques (for example Sambrook et al, 2001; Ausubel et al, 1996, both incorporated herein by reference). In addition to encoding the polypeptides of this invention, a vector of the present invention may encode polypeptide sequences such as a tag or immunogenicity enhancing peptide (e.g. an immunogenic carrier or a fusion partner that stimulates the immune system, such as a cytokine or active fragment thereof). Useful vectors encoding such fusion proteins include pIN vectors (Inouye et al, 1985), vectors encoding a stretch of histidines, and pGEX vectors, for use in generating glutathione S-transferase (GST) soluble fusion proteins for later purification and separation or cleavage.

[0146] Vectors of the invention may be used in a host cell to produce a polypeptide of the invention that may subsequently be purified for administration to a subject or the vector may be purified for direct administration to a subject for expression of the protein in the subject (as is the case when administering a nucleic acid vaccine).

[0147] Expression vectors can contain a variety of "control sequences," which refer to nucleic acid sequences necessary for the transcription and possibly translation of an operably linked coding sequence in a particular host organism. In addition to control sequences that govern transcription and translation, vectors and expression vectors may contain nucleic acid sequences that serve other functions as well and are described infra.

1. Promoters and Enhancers

[0148] A "promoter" is a control sequence. The promoter is typically a region of a nucleic acid sequence at which initiation and rate of transcription are controlled. It may contain genetic elements at which regulatory proteins and molecules may bind such as RNA polymerase and other transcription factors. The phrases "operatively positioned," "operatively linked," "under control," and "under transcriptional control" mean that a promoter is in a correct functional location and/or orientation in relation to a nucleic acid sequence to control transcriptional initiation and expression of that sequence. A promoter may or may not be used in conjunction with an "enhancer," which refers to a cis-acting regulatory sequence involved in the transcriptional activation of a nucleic acid sequence.

[0149] A promoter may be one naturally associated with a gene or sequence, as may be obtained by isolating the 5' non-coding sequences located upstream of the coding segment or exon. Such a promoter can be referred to as "endogenous." Similarly, an enhancer may be one naturally associated with a nucleic acid sequence, located either downstream or upstream of that sequence. Alternatively, certain advantages will be gained by positioning the coding nucleic acid segment under the control of a recombinant or heterologous promoter, which refers to a promoter that is not normally associated with a nucleic acid sequence in its natural environment. A recombinant or heterologous enhancer refers also to an enhancer not normally associated with a nucleic acid sequence in its natural state. Such promoters or enhancers may include promoters or enhancers of other genes, and promoters or enhancers isolated from any other prokaryotic, viral, or eukaryotic cell, and promoters or enhancers not "naturally occurring," i.e., containing different elements of different transcriptional regulatory regions, and/or mutations that alter expression. In addition to producing nucleic acid sequences of promoters and enhancers synthetically, sequences may be produced using recombinant cloning and/or nucleic acid amplification technology, including PCR™, in connection with the compositions disclosed herein (see U.S. Pat. No. 4,683,202, U.S. Pat. No. 5,928,906, each incorporated herein by reference).

[0150] Naturally, it may be important to employ a promoter and/or enhancer that effectively direct(s) the expression of the DNA segment in the cell type or organism chosen for expression. Those of skill in the art of molecular biology generally know the use of promoters, enhancers, and cell type combinations for protein expression (see Sambrook et al, 2001, incorporated herein by reference). The promoters employed may be constitutive, tissue-specific, or inducible and in certain embodiments may direct high level expression of the introduced DNA segment under specified conditions, such as large-scale production of recombinant proteins or peptides.

[0151] Examples of inducible elements, which are regions of a nucleic acid sequence that can be activated in response to a specific stimulus, include but are not limited to Immunoglobulin Heavy Chain, Immunoglobulin Light Chain, T Cell Receptor, HLA DQa and/or DQβ, β-Interferon, Interleukin-2, Interleukin-2 Receptor, MHC Class II 5, MHC Class II HLA-DRa, β-Actin, Muscle Creatine Kinase (MCK), Prealbumin (Transthyretin), Elastase I, Metallothionein (MTII), Collagenase, Albumin, α-Fetoprotein, γ-Globin, β-Globin, c-fos, c-HA-ras, Insulin, Neural Cell Adhesion Molecule (NCAM), al-Antitrypain, H2B (TH2B) Histone, Mouse and/or Type I Collagen, Glucose-Regulated Proteins (GRP94 and GRP78), Rat Growth Hormone, Human Serum Amyloid A (SAA), Troponin I (TN I), Platelet-Derived Growth Factor (PDGF), Duchenne Muscular Dystrophy, SV40, Polyoma, Retroviruses, Papilloma Virus, Hepatitis B Virus, Human Immunodeficiency Virus, Cytomegalovirus (CMV) IE, and Gibbon Ape Leukemia Virus.

[0152] Inducible Elements include MT II—Phorbol Ester (TFA)/Heavy metals; MMTV (mouse mammary tumor virus)—Glucocorticoids; β-Interferon—poly(rl)x/poly(rc); Adenovirus 5 E2—EIA; Collagenase—Phorbol Ester (TPA); Stromelysin—Phorbol Ester (TPA); SV40—Phorbol Ester (TPA); Murine MX Gene—Interferon, Newcastle Disease Virus; GRP78 Gene—A23187; α-2-Macroglobulin—IL-6; Vimentin—Serum; MHC Class I Gene H-2κb—Interferon; HSP70—E1A/SV40 Large T Antigen; Proliferin—Phorbol Ester/TPA; Tumor Necrosis Factor—PMA; and Thyroid Stimulating Hormonea Gene—Thyroid Hormone.

[0153] Also contemplated as useful in the present invention are the dectin-1 and dectin-2 promoters. Additionally any promoter/enhancer combination (as per the Eukaryotic Promoter Data Base EPDB) could also be used to drive expression of structural genes encoding oligosaccharide processing enzymes, protein folding accessory proteins, selectable marker proteins or a heterologous protein of interest.

[0154] The particular promoter that is employed to control the expression of peptide or protein encoding polynucleotide of the invention is not believed to be critical, so long as it is capable of expressing the polynucleotide in a targeted cell, preferably a bacterial cell. Where a human cell is targeted, it is preferable to position the polynucleotide coding region adjacent to and under the control of a promoter that is capable of being expressed in a human cell. Generally speaking, such a promoter might include either a bacterial, human or viral promoter.

[0155] In various embodiments, the human cytomegalovirus (CMV) immediate early gene promoter, the SV40 early promoter, and the Rous sarcoma virus long terminal repeat can be used to obtain high level expression of a related polynucleotide to this invention. The use of other viral or mammalian cellular or bacterial phage promoters, which are well known in the art, to achieve expression of polynucleotides is contemplated as well.

[0156] In embodiments in which a vector is administered to a subject for expression of the protein, it is contemplated that a desirable promoter for use with the vector is one that is not down-regulated by cytokines or one that is strong enough that even if down-regulated, it produces an effective amount of the protein/polypeptide of the current invention in a subject to elicit an immune response. Non-limiting examples of these are CMV IE and RSV LTR. In other embodiments, a promoter that is up-regulated in the presence of cytokines is employed. The MHC I promoter increases expression in the presence of IFN-γ.

[0157] Tissue specific promoters can be used, particularly if expression is in cells in which expression of an antigen is desirable, such as dendritic cells or macrophages. The mammalian MHC I and MHC II promoters are examples of such tissue-specific promoters. 2. Initiation Signals and Internal Ribosome Binding Sites (IRES)

[0158] A specific initiation signal also may be required for efficient translation of coding sequences. These signals include the ATG initiation codon or adjacent sequences. Exogenous translational control signals, including the ATG initiation codon, may need to be provided. One of ordinary skill in the art would readily be capable of determining this and providing the necessary signals. It is well known that the initiation codon must be "in-frame" with the reading frame of the desired coding sequence to ensure translation of the entire insert. The exogenous translational control signals and initiation codons can be either natural or synthetic and may be operable in bacteria or mammalian cells. The efficiency of expression may be enhanced by the inclusion of appropriate transcription enhancer elements.

[0159] In certain embodiments of the invention, the use of internal ribosome entry sites (IRES) elements are used to create multigene, or polycistronic, messages. IRES elements are able to bypass the ribosome scanning model of 5' methylated Cap dependent translation and begin translation at internal sites. IRES elements from two members of the picornavirus family (polio and encephalomyocarditis) have been described, as well an IRES from a mammalian message. IRES elements can be linked to heterologous open reading frames. Multiple open reading frames can be transcribed together, each separated by an IRES, creating polycistronic messages. By virtue of the IRES element, each open reading frame is accessible to ribosomes for efficient translation. Multiple genes can be efficiently expressed using a single promoter/enhancer to transcribe a single message (see U.S. Pat. Nos. 5,925,565 and 5,935,819, herein incorporated by reference).

2. Multiple Cloning Sites

[0160] Vectors can include a multiple cloning site (MCS), which is a nucleic acid region that contains multiple restriction enzyme sites, any of which can be used in conjunction with standard recombinant technology to digest the vector. (See Carbonelli et al, 1999, Levenson et al, 1998, and Cocea, 1997, incorporated herein by reference.) Frequently, a vector is linearized or fragmented using a restriction enzyme that cuts within the MCS to enable exogenous sequences to be ligated to the vector. Techniques involving restriction enzymes and ligation reactions are well known to those of skill in the art of recombinant technology.

3. Splicing Sites

[0161] Most transcribed eukaryotic RNA molecules will undergo RNA splicing to remove introns from the primary transcripts. If relevant in the context of vectors of the present invention, vectors containing genomic eukaryotic sequences may require donor and/or acceptor splicing sites to ensure proper processing of the transcript for protein expression. (See Chandler et al, 1997, incorporated herein by reference.)

4. Termination Signals

[0162] The vectors or constructs of the present invention will generally comprise at least one termination signal. A "termination signal" or "terminator" is comprised of the DNA sequences involved in specific termination of an RNA transcript by an RNA polymerase. Thus, in certain embodiments a termination signal that ends the production of an RNA transcript is contemplated. A terminator may be necessary in vivo to achieve desirable message levels.

[0163] In eukaryotic systems, the terminator region may also comprise specific DNA sequences that permit site-specific cleavage of the new transcript so as to expose a polyadenylation site. This signals a specialized endogenous polymerase to add a stretch of about 200 A residues (poly A) to the 3' end of the transcript. RNA molecules modified with this polyA tail appear to more stable and are translated more efficiently. Thus, in other embodiments involving eukaryotes, it is preferred that that terminator comprises a signal for the cleavage of the RNA, and it is more preferred that the terminator signal promotes polyadenylation of the message.

[0164] Terminators contemplated for use in the invention include any known terminator of transcription described herein or known to one of ordinary skill in the art, including but not limited to, for example, the bovine growth hormone terminator or viral termination sequences, such as the SV40 terminator. In certain embodiments, the termination signal may be a lack of transcribable or translatable sequence, such as due to a sequence truncation.

5. Polyadenylation Signals

[0165] In expression, particularly eukaryotic expression (as is relevant in nucleic acid vaccination), one will typically include a polyadenylation signal to effect proper polyadenylation of the transcript. The nature of the polyadenylation signal is not believed to be crucial to the successful practice of the invention, and/or any such sequence may be employed. Preferred embodiments include the SV40 polyadenylation signal and/or the bovine growth hormone polyadenylation signal, convenient and/or known to function well in various target cells. Polyadenylation may increase the stability of the transcript or may facilitate cytoplasmic transport.

6. Origins of Replication

[0166] In order to propagate a vector in a host cell, it may contain one or more origins of replication sites (often termed "ori"), which is a specific nucleic acid sequence at which replication is initiated. Alternatively an autonomously replicating sequence (ARS) can be employed if the host cell is yeast.

7. Selectable and Screenable Markers

[0167] In certain embodiments of the invention, cells containing a nucleic acid construct of the present invention may be identified in vitro or in vivo by encoding a screenable or selectable marker in the expression vector. When transcribed and translated, a marker confers an identifiable change to the cell permitting easy identification of cells containing the expression vector. Generally, a selectable marker is one that confers a property that allows for selection. A positive selectable marker is one in which the presence of the marker allows for its selection, while a negative selectable marker is one in which its presence prevents its selection. An example of a positive selectable marker is a drug resistance marker.

[0168] Usually the inclusion of a drug selection marker aids in the cloning and identification of transformants, for example, markers that confer resistance to neomycin, puromycin, hygromycin, DHFR, GPT, zeocin or histidinol are useful selectable markers. In addition to markers conferring a phenotype that allows for the discrimination of transformants based on the implementation of conditions, other types of markers including screenable markers such as GFP for colorimetric analysis. Alternatively, screenable enzymes such as herpes simplex virus thymidine kinase (tk) or chloramphenicol acetyltransferase (CAT) may be utilized. One of skill in the art would also know how to employ immunologic markers that can be used in conjunction with FACS analysis. The marker used is not believed to be important, so long as it is capable of being expressed simultaneously with the nucleic acid encoding a protein of the invention. Further examples of selectable and screenable markers are well known to one of skill in the art.

The Transformed Cells of the Invention

[0169] Transformed cells of the invention are useful as organisms for producing the polypeptide of the invention, but also as simple "containers" of nucleic acids and vectors of the invention.

[0170] Certain transformed cells of the invention are capable of replicating the nucleic acid fragment defined for option i) of the second aspect of the invention. Preferred transformed cells of the invention are capable of expressing the nucleic acid fragment defined for option i).

[0171] For recombinant production it is convenient, but not a prerequisite that the transformed cell according is prokaryotic, such as a bacterium, but generally both prokaryotic cells and eukaryotic cells may be used.

[0172] Suitable prokaryotic cells are bacterial cells selected from the group consisting of *Escherichia* (such as *E. coli*.), *Bacillus* [e.g. *Bacillus subtilis*], *Salmonella*, and *Mycobacterium* [preferably non-pathogenic, e.g. *M. bovis* BCG].

[0173] Eukaryotic cells can be in the form of yeasts (such as *Saccharomyces cerevisiae*) and protozoans. Alternatively, the transformed eukaryotic cells are derived from a multicellular organism such as a fungus, an insect cell, a plant cell, or a mammalian cell.

[0174] For production purposes, it is advantageous that the transformed cell of the invention is is stably transformed by having the nucleic acid defined above for option i) stably integrated into its genome, and in certain embodiments it is also preferred that the transformed cell secretes or carries on its surface the polypeptide of the invention, since this facilitates recovery of the polypeptides produced. A particular version of this embodiment is one where the transformed cell is a bacterium and secretion of the polypeptide of the invention is into the periplasmic space.

[0175] An interesting production system is the use of plants. For instance, proteins can be produced at low cost in plants using an *Agrobacterium* transfection system to genetically modify plants to express genes that encode the protein of interest. One commercially available platform are those provided by iBio CMO LLC (8800 HSC Pkwy, Bryan, Tex. 77807, USA) and iBio, Inc (9 Innovatoin Way, Suite 100, Newark, Del. 19711, USA) and disclosed in e.g. EP 2 853 599, EP 1 769 068, and EP 2 192 172. Hence, in such systems the vector is an *Agrobacterium* vector or other vector suitable for transfection of plants.

[0176] As noted above, stably transformed cells are preferred—these i.a. allows that cell lines comprised of transformed cells as defined herein may be established—such cell lines are partilucarly preferred aspects of the invention.

[0177] Further details on cells and cell lines are presented in the following:

[0178] Suitable cells for recombinant nucleic acid expression of the nucleic acid fragments of the present invention are prokaryotes and eukaryotes. Examples of prokaryotic cells include *E. coli*; members of the *Staphylococcus* genus, such as *S. epidermidis*; members of the *Lactobacillus* genus, such as *L. plantarum*; members of the *Lactococcus* genus, such as *L. lactis*; members of the *Bacillus* genus, such as *B. subtilis*; members of the *Corynebacterium* genus such as *C. glutamicum*; and members of the *Pseudomonas* genus such as Ps. *fluorescens*. Examples of eukaryotic cells include mammalian cells; insect cells; yeast cells such as members of the *Saccharomyces* genus (e.g. *S. cerevisiae*), members of the *Pichia* genus (e.g. *P. pastoris*), members of the *Hansenula* genus (e.g. *H. polymorpha*), members of the *Kluyveromyces* genus (e.g. *K. lactis* or *K. fragilis*) and members of the *Schizosaccharomyces* genus (e.g. *S. pombe*).

[0179] Techniques for recombinant gene production, introduction into a cell, and recombinant gene expression are well known in the art. Examples of such techniques are provided in references such as Ausubel, Current Protocols in Molecular Biology, John Wiley, 1987-2002, and Sambrook et al., Molecular Cloning, A Laboratory Manual, 2 nd Edition, Cold Spring Harbor Laboratory Press, 1989.

[0180] As used herein, the terms "cell," "cell line," and "cell culture" may be used interchangeably. All of these terms also include their progeny, which is any and all subsequent generations. It is understood that all progeny may not be identical due to deliberate or inadvertent mutations. In the context of expressing a heterologous nucleic acid sequence, "host cell" refers to a prokaryotic or eukaryotic cell, and it includes any transformable organism that is capable of replicating a vector or expressing a heterologous gene encoded by a vector. A host cell can, and has been, used as a recipient for vectors or viruses. A host cell may be "transfected" or "transformed," which refers to a process by which exogenous nucleic acid, such as a recombinant protein-encoding sequence, is transferred or introduced into the host cell. A transformed cell includes the primary subject cell and its progeny.

[0181] Host cells may be derived from prokaryotes or eukaryotes, including bacteria, yeast cells, insect cells, and mammalian cells for replication of the vector or expression of part or all of the nucleic acid sequence(s). Numerous cell lines and cultures are available for use as a host cell, and they can be obtained through the American Type Culture Collection (ATCC), which is an organization that serves as an archive for living cultures and genetic materials (www.atcc.org) or from other depository institutions such as Deutsche Sammlung vor Micrroorganismen and Zellkulturen (DSM). An appropriate host can be determined by one of skill in the art based on the vector backbone and the desired result. A plasmid or cosmid, for example, can be introduced into a prokaryote host cell for replication of many vectors or expression of encoded proteins. Bacterial cells used as host cells for vector replication and/or expression include *Staphylococcus* strains, DH5a, JMI 09, and KC8, as well as a number of commercially available bacterial hosts such as SURE® Competent Cells and SOLOP ACK™ Gold Cells (STRATAGENE®, La Jolla, Calif.). Alternatively, bacterial cells such as *E. coli* LE392 could be used as host cells for phage viruses. Appropriate yeast cells include *Saccharomyces cerevisiae, Saccharomyces pombe*, and *Pichia pastoris.*

[0182] Examples of eukaryotic host cells for replication and/or expression of a vector include HeLa, NIH3T3, Jurkat, 293, Cos, CHO, Saos, and PC12. Many host cells from various cell types and organisms are available and would be known to one of skill in the art. Similarly, a viral vector may be used in conjunction with either a eukaryotic or prokaryotic host cell, particularly one that is permissive for replication or expression of the vector.

[0183] Some vectors may employ control sequences that allow it to be replicated and/or expressed in both prokaryotic and eukaryotic cells. One of skill in the art would further understand the conditions under which to incubate all of the above described host cells to maintain them and to permit replication of a vector. Also understood and known are techniques and conditions that would allow large-scale production of vectors, as well as production of the nucleic acids encoded by vectors and their cognate polypeptides, proteins, or peptides.

Expression Systems

[0184] Numerous expression systems exist that comprise at least a part or all of the compositions discussed above. Prokaryote- and/or eukaryote-based systems can be employed for use with the present invention to produce nucleic acid sequences, or their cognate polypeptides, proteins and peptides. Many such systems are commercially and widely available.

[0185] The insect cell/baculovirus system can produce a high level of protein expression of a heterologous nucleic acid segment, such as described in U.S. Pat. Nos. 5,871,986, 4,879,236, both herein incorporated by reference, and which can be bought, for example, under the name MAXBAC® 2.0 from INVITROGEN® and BACPACK™ Baculovirus expression system from CLONTECH®

[0186] In addition to the disclosed expression systems of the invention, other examples of expression systems include STRATAGENE®'s COMPLETE CONTROL™ Inducible Mammalian Expression System, which involves a synthetic ecdysone-inducible receptor, or its pET Expression System, an *E. coli* expression system. Another example of an inducible expression system is available from INVITROGEN®, which carries the T-REX™ (tetracycline-regulated expression) System, an inducible mammalian expression system that uses the full-length CMV promoter. INVITROGEN® also provides a yeast expression system called the *Pichia methanolica* Expression System, which is designed for high-level production of recombinant proteins in the methylotrophic yeast *Pichia methanolica*. One of skill in the art would know how to express a vector, such as an expression construct, to produce a nucleic acid sequence or its cognate polypeptide, protein, or peptide.

Amplification of Nucleic Acids

[0187] Nucleic acids used as a template for amplification may be isolated from cells, tissues or other samples according to standard methodologies (Sambrook et al, 2001). In certain embodiments, analysis is performed on whole cell or tissue homogenates or biological fluid samples without substantial purification of the template nucleic acid. The nucleic acid may be genomic DNA or fractionated or whole cell RNA. Where RNA is used, it may be desired to first convert the RNA to a complementary DNA.

[0188] The term "primer," as used herein, is meant to encompass any nucleic acid that is capable of priming the synthesis of a nascent nucleic acid in a template-dependent process. Typically, primers are oligonucleotides from ten to twenty and/or thirty base pairs in length, but longer sequences can be employed. Primers may be provided in double-stranded and/or single-stranded form, although the single-stranded form is preferred.

[0189] Pairs of primers designed to selectively hybridize to nucleic acids corresponding to sequences of genes identified herein are contacted with the template nucleic acid under conditions that permit selective hybridization. Depending upon the desired application, high stringency hybridization conditions may be selected that will only allow hybridization to sequences that are completely complementary to the primers. In other embodiments, hybridization may occur under reduced stringency to allow for amplification of nucleic acids containing one or more mismatches with the primer sequences. Once hybridized, the template-primer complex is contacted with one or more enzymes that facilitate template-dependent nucleic acid synthesis. Multiple rounds of amplification, also referred to as "cycles," are conducted until a sufficient amount of amplification product is produced.

[0190] The amplification product may be detected or quantified. In certain applications, the detection may be performed by visual means. Alternatively, the detection may involve indirect identification of the product via chemiluminescence, radioactive scintigraphy of incorporated radiolabel or fluorescent label or even via a system using electrical and/or thermal impulse signals (Bellus, 1994).

[0191] A number of template dependent processes are available to amplify the oligonucleotide sequences present in a given template sample. One of the best known amplification methods is the polymerase chain reaction (referred to as PCR™) which is described in detail in U.S. Pat. Nos. 4,683,195, 4,683,202 and 4,800,159, and in Innis et al., 1988, each of which is incorporated herein by reference in their entirety.

[0192] Alternative methods for amplification of target nucleic acid sequences that may be used in the practice of the present invention are disclosed in U.S. Pat. Nos. 5,843,650, 5,846,709, 5,846,783, 5,849,546, 5,849,497, 5,849,547, 5,858,652, 5,866,366, 5,916,776, 5,922,574, 5,928,905, 5,928,906, 5,932,451, 5,935,825, 5,939,291 and 5,942,391, GB Application No. 2 202 328, and in PCT Application No. PCT/US89/01025, each of which is incorporated herein by reference in its entirety.

Methods of Gene Transfer

[0193] Suitable methods for nucleic acid delivery to effect expression of compositions of the present invention are believed to include virtually any method by which a nucleic acid (e.g., DNA, including viral and nonviral vectors) can be introduced into a cell, a tissue or an organism, as described herein or as would be known to one of ordinary skill in the art. Such methods include, but are not limited to, direct delivery of DNA such as by injection (U.S. Pat. Nos. 5,994,624, 5,981,274, 5,945,100, 5,780,448, 5,736,524, 5,702,932, 5,656,610, 5,589,466 and 5,580,859), including microinjection (U.S. Pat. No. 5,789,215); by electroporation (U.S. Pat. No. 5,384,253); by calcium phosphate precipitation; by using DEAE dextran followed by polyethylene glycol; by direct sonic loading; by liposome mediated transfection; by microprojectile bombardment (PCT Application Nos. WO 94/09699 and 95/06128; U.S. Pat. Nos. 5,610,042; 5,322,783 5,563,055, 5,550,318, 5,538,877 and 5,538,880); by agitation with silicon carbide fibers (U.S. Pat. Nos. 5,302,523 and 5,464,765); by *Agrobacterium* mediated transformation (U.S. Pat. Nos. 5,591,616 and 5,563,055); or by PEG mediated transformation of protoplasts (U.S. Pat. Nos. 4,684,611 and 4,952,500); by desiccation/inhibition mediated DNA uptake. Through the application of techniques such as these, organelle(s), cell(s), tissue(s) or organism(s) may be stably or transiently transformed. See also "Fish Vaccination", 2014, edited by Gudding R., Lillehaug A, and Evensen Ø, published by Wiley Blackwell, ISBN 978-0-470-67455-0, chapter 5, which deals specifically with DNA vaccination of fish.

The Antibodies of the Invention—and their Production/Isolation

[0194] Antibodies directed against the proteins of the invention are useful for affinity chromatography, immunoassays, and for distinguishing/identifying *Pseudomonas* proteins as well as for passive immunisation and therapy.

[0195] Antibodies to the proteins of the invention, both polyclonal and monoclonal, may be prepared by conventional methods. In general, the protein is first used to immunize a suitable animal, preferably a mouse, rat, rabbit or goat. Rabbits and goats are preferred for the preparation of polyclonal sera due to the volume of serum obtainable, and the availability of labeled anti-rabbit and anti-goat antibodies. Immunization is generally performed by mixing or emulsifying the protein in saline, preferably in an adjuvant such as Freund's complete adjuvant, and injecting the mixture or emulsion parenterally (generally subcutaneously or intramuscularly). A dose of 10-200 μg/injection is typically sufficient. Immunization is generally boosted 2-6 weeks later with one or more injections of the protein in saline, preferably using Freund's incomplete adjuvant. One may alternatively generate antibodies by in vitro immunization using methods known in the art, which for the purposes of this invention is considered equivalent to in vivo immunization. Polyclonal antiserum is obtained by bleeding the immunized animal into a glass or plastic container, incubating the blood at 25 C for one hour, followed by incubating at 4 C for 2-18 hours. The serum is recovered by centrifugation (eg. 1,000 g for 10 minutes). About 20-50 ml per bleed may be obtained from rabbits.

[0196] Monoclonal antibodies are prepared using the standard method of Kohler & Milstein [Nature (1975) 256: 495-96], or a modification thereof. Typically, a mouse or rat is immunized as described above. However, rather than bleeding the animal to extract serum, the spleen (and optionally several large lymph nodes) is removed and dissociated into single cells. If desired, the spleen cells may be screened (after removal of nonspecifically adherent cells) by applying a cell suspension to a plate or well coated with the protein antigen. B-cells expressing membrane-bound immunoglobulin specific for the antigen bind to the plate, and are not rinsed away with the rest of the suspension. Resulting B-cells, or all dissociated spleen cells, are then induced to fuse with myeloma cells to form hybridomas, and are cultured in a selective I aedium (elg. hypexanthine, aminopterin, thymidine medium, "HAT"). The resulting hybridomas are plated by limiting dilution, and are assayed for production of antibodies, which bind specifically to the immunizing antigen (and which do not bind to unrelated antigens). The selected MAb-secreting hybridomas are then cultured either in vitro (eg. in tissue culture bottles or hollow fiber reactors), or in vivo (as ascites in mice).

[0197] If desired, the antibodies (whether polyclonal or monoclonal) may be labeled using conventional techniques. Suitable labels include fluorophores, chromophores, radioactive atoms (particularly 32p and 1251), electron-dense reagents, enzymes, and ligands having specific binding partners. Enzymes are typically detected by their activity. For example, horseradish peroxidase is usually detected by its ability to convert 3,3', 5,5'-tetramethylbenzidine (TMB) to a blue pigment, quantifiable with a spectrophotometer. "Specific binding partner" refers to a protein capable of binding a ligand molecule with high specificity, as for example in the case of an antigen and a monoclonal antibody specific therefor. Other specific binding partners include biotin and avidin or streptavidin, IgG and protein A, and the numerous receptor-ligand couples known in the art. It should be understood that the above description is not meant to categorize the various labels into distinct classes, as the same label may serve in several different modes. For example, 1151 may serve as a radioactive label or as an electron-dense reagent. HRP may serve as enzyme or as antigen for a MAb. Further, one may combine various labels for desired effect. For example, MAbs and avidin also require labels in the practice of this invention: thus, one might label a MAb with biotin, and detect its presence with avidin labeled with, 1251, or with an anti-biotin MAb labeled with HRP. Other permutations and possibilities will be readily apparent to those of ordinary skill in the art, and are considered as equivalents within the scope of the instant invention.

[0198] According to the invention, the isolated monoclonal antibody or antibody analogue is preferably a monoclonal antibody selected from a multi-domain antibody such as a murine antibody, a chimeric antibody such as a humanized antibody, a fully human antibody, and single-domain antibody of a llama or a camel, or which is an antibody analogue selected from a fragment of an antibody such as an Fab or an $F(ab')_2$, an scFV; cf. also the definition of the term "antibody" presented above.

Compositions of the Invention; Vaccines

[0199] Pharmaceutical compositions, in particular vaccines, according to the invention may either be prophylactic (ie. to prevent infection) or therapeutic (ie, to treat disease after infection).

[0200] In some embodiments of the invention, the pharmaceutical compositions such as vaccines include merely one single antigen, immunogen, polypeptide, protein, nucleic acid or vector of the invention, but in other embodiments, the pharmaceutical compositions comprise "cocktails" of the antigens or of the immunogens or of the polypeptides or of the protein or of the nucleic acids or of the vectors of the invention.

[0201] In particularly interesting embodiments, the pharmaceutical composition is an MVA vector mentioned herein, which encodes and can effect expression of at least 2 nucleic acid fragments of the invention.

[0202] An embodiment of a pharmaceutical composition of the invention comprises exactly Y or at least Y distinct (i.e. having non-identical primary structure) polypeptides of the invention described above, where each of said Y or at least Y distinct polypeptides comprises an immunogenic amino acid sequence present in or derived from any one of SEQ ID NOs: 1-30 and wherein said Y or at least Y distinct polypeptides together comprise immunogenic amino acid sequences present in or derived from Y or at least Y of SEQ ID NOs. 1-30, wherein Y is an integer selected from 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, and 30.

[0203] Another embodiment of a pharmaceutical composition of the invention comprises a peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from SEQ ID NO: 1 in combination with at least one *P. aeruginosa* peptide/polypeptide, in particular with at least one peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from any one of SEQ ID NOs: 2-30. Another embodiment of a pharmaceutical composition of the invention comprises a peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from SEQ ID NO: 2 in combination with at least one *P. aeruginosa* peptide/polypeptide, in particular with at least one peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from any one of SEQ ID NOs: 1, and 3-30. Another embodiment of a pharmaceutical composition of the invention comprises a peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from SEQ ID NO: 3 in combination with at least one *P. aeruginosa* peptide/polypeptide, in particular with at least one peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from any one of SEQ ID NOs: 1, 2, and 4-30. Another embodiment of a pharmaceutical composition of the invention comprises a peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from SEQ ID NO: 4 in combination with at least one *P. aeruginosa* peptide/polypeptide, in particular with at least one peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from any one of SEQ ID NOs: 1-3, and 5-30. Another embodiment of a pharmaceutical composition of the invention comprises a peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from SEQ ID NO: 5 in combination with at least one *P. aeruginosa* peptide/polypeptide, in particular with at least one peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from any one of SEQ ID NOs: 1-4, and 6-30. Another embodiment of a pharmaceutical composition of the invention comprises a peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from SEQ ID NO: 6 in combination with at least one *P. aeruginosa* peptide/polypeptide, in particular with at least one peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from any one of SEQ ID NOs: 1-5, and 7-30. Another embodiment of a pharmaceutical composition of the invention comprises a peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from SEQ ID NO: 7 in combination with at least one *P. aeruginosa* peptide/polypeptide, in particular with at least one peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from any one of SEQ ID NOs: 1-6, and 8-30. Another embodiment of a pharmaceutical composition of the invention comprises a peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from SEQ ID NO: 8 in combination with at least one *P. aeruginosa* peptide/polypeptide, in particular with at least one peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from any one of SEQ ID NOs: 1-7, and 9-30. Another embodiment of a pharmaceutical composition of the invention comprises a peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from SEQ ID NO: 9 in combination with at least one *P. aeruginosa* peptide/polypeptide, in particular with at least one peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from any one of SEQ ID NOs: 1-8, and 10-30. Another embodiment of a pharmaceutical composition of the invention comprises a peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from SEQ ID NO: 10 in combination with at least one *P. aeruginosa* peptide/polypeptide, in particular with at least one peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from any one of SEQ ID NOs: 1-9, and 11-30. Another embodiment of a pharmaceutical composition of the invention comprises a peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from SEQ ID NO: 11 in combination with at least one *P. aeruginosa* peptide/polypeptide, in particular with at least one peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from any one of SEQ ID NOs: 1-10, and 12-30. Another embodiment of a pharmaceutical composition of the invention comprises a peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from SEQ ID NO: 12 in combination with at least one *P. aeruginosa* peptide/polypeptide, in particular with at least one peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from any one of SEQ ID NOs: 1-11, and 13-30. Another embodiment of a pharmaceutical composition of the invention comprises a peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from SEQ ID NO: 13 in combination with at least one *P. aeruginosa* peptide/polypeptide, in particular with at least one peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from any one of SEQ ID NOs: 1-12, and 14-30. Another embodiment of a pharmaceutical composition of the invention comprises a peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from SEQ ID NO: 14 in combination with at least one *P. aeruginosa* peptide/polypeptide, in particular with at least one peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from any one of SEQ ID NOs: 1-13, and 15-30. Another embodiment of a pharmaceutical composition of the invention comprises a peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from SEQ ID NO: 15 in combination with at least one *P. aeruginosa* peptide/polypeptide, in particular with at least one peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from any one of SEQ ID NOs: 1-14, and 16-30. Another embodiment of a pharmaceutical composition of the invention comprises a peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from SEQ ID NO: 16 in combination with at least one *P. aeruginosa* peptide/polypeptide, in particular with at least one peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from any one of SEQ ID NOs: 1-15, and 17-30. Another embodiment of a pharmaceutical composition of the invention comprises a peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from SEQ ID NO: 17 in combination with at least one *P. aeruginosa* peptide/polypeptide, in particular with at least one peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from any one of SEQ ID NOs: 1-16, and 18-30. Another embodiment of a pharmaceutical composition of the invention comprises a peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from SEQ ID NO: 18 in combination with at least one *P. aeruginosa* peptide/polypeptide, in particular with at least one peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from any one of SEQ ID NOs: 1-17, and 19-30. Another embodiment of a pharmaceutical composition of the invention comprises a peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from SEQ ID NO: 19 in combination with at least one *P. aeruginosa* peptide/polypeptide, in particular with at least one peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from any one of SEQ ID NOs: 1-18, and 20-30. Another embodiment of a pharmaceutical composition of the invention comprises a peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from SEQ ID NO: 20 in combination with at least one *P. aeruginosa* peptide/polypeptide, in particular with at least one peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from any one of SEQ ID NOs: 1-19, and 21-30. Another embodiment of a pharmaceutical composition of the invention comprises a peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from SEQ ID NO: 21 in combination with at least one *P. aeruginosa* peptide/polypeptide, in particular with at least one peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from any one of SEQ ID NOs: 1-20, and 22-30. Another embodiment of a pharmaceutical composition of the invention comprises a peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from SEQ ID NO: 22 in combination with at least one *P. aeruginosa* peptide/polypeptide, in particular with at least one peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from any one of SEQ ID NOs: 1-21, and 23-30. Another embodiment of a pharmaceutical composition of the invention comprises a peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from SEQ ID NO: 23 in combination with at least one *P. aeruginosa* peptide/polypeptide, in particular with at least one peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from any one of SEQ ID NOs: 1-22, and 24-30. Another embodiment of a pharmaceutical composition of the invention comprises a peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from SEQ ID NO: 24 in combination with at least one *P. aeruginosa* peptide/polypeptide, in particular with at least one peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from any one of SEQ ID NOs: 1-23, and 25-30. Another embodiment of a pharmaceutical composition of the invention comprises a peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from SEQ ID NO: 25 in combination with at least one *P. aeruginosa* peptide/polypeptide, in particular with at least one peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from any one of SEQ ID NOs: 1-24, and 26-30. Another embodiment of a pharmaceutical composition of the invention comprises a peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from SEQ ID NO: 26 in combination with at least one *P. aeruginosa* peptide/polypeptide, in particular with at least one peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from any one of SEQ ID NOs: 1-25, and 27-30. Another embodiment of a pharmaceutical composition of the invention comprises a peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from SEQ ID NO: 27 in combination with at least one *P. aeruginosa* peptide/polypeptide, in particular with at least one peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from any one of SEQ ID NOs: 1-26, and 28-30. Another embodiment of a pharmaceutical composition of the invention comprises a peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from SEQ ID NO: 28 in combination with at least one *P. aeruginosa* peptide/polypeptide, in particular with at least one peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from any one of SEQ ID NOs: 1-27, 29, and 30. Another embodiment of a pharmaceutical composition of the invention comprises a peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from SEQ ID NO: 29 in combination with at least one *P. aeruginosa* peptide/polypeptide, in particular with at least one peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from any one of SEQ ID NOs: 1-28, and 30. Another embodiment of a pharmaceutical composition of the invention comprises a peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from SEQ ID NO: 30 in combination with at least one *P. aeruginosa* peptide/polypeptide, in particular with at least one peptide/polypeptide comprising or consisting of an immunogenic amino acid sequence present in or derived from any one of SEQ ID NOs: 1-29.

[0204] These embodiments entail combinations of peptides/polypeptides which are admixed with each other. Alternatively, the same combinations of peptides/polypeptides can be constructed as fusion polypeptides. Another alternative entails compositions where the immunogens are nucleic acids encoding the peptide combinations or, preferably, encoding such fusion polypeptides.

[0205] Another embodiment of the pharmaceutical composition of the invention comprises Z or at least Z distinct nucleic acid molecules each encoding a polypeptide of the invention, where each of said Z or at least Z distinct nucleic acid molecules encodes an immunogenic amino acid sequence present in or derived from any one of SEQ ID NOs: 1-30 and wherein said at Z or least Z distinct nucleic acid molecules together encode immunogenic amino acid sequences present in or derived from at Z or least Z of SEQ ID NOs. 1-30, wherein Z is an integer selected from 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, and 30. Also, such a pharmaceutical composition may include nucleic acid that encode several immunogenic amino acid sequences disclosed herein, either as separate encoded species or as peptides fused to each other.

[0206] Vaccines of the invention typically comprise immunising antigen(s), immunogen(s), polypeptide(s), protein(s) or nucleic acid(s), usually in combination with “pharmaceutically acceptable carriers”, which include any carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition or targeting the protein/pathogen. Suitable carriers are typically large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, lipid aggregates (such as oil droplets or liposomes), and inactive virus particles.

[0207] Such carriers are well known to those of ordinary skill in the art. Additionally, these carriers may function as immunostimulating agents (“adjuvants”). Furthermore, the antigen or immunogen may be conjugated to a bacterial toxoid, such as a toxoid from diphtheria, tetanus, cholera, *H. pylori*, etc. pathogen, cf. the description of immunogenic carriers supra.

[0208] The pharmaceutical compositions of the invention thus typically contain an immunological adjuvant, which is commonly an aluminium based adjuvant or one of the other adjuvants described in the following:

[0209] Preferred adjuvants to enhance effectiveness of the composition include, but are not limited to: (1) aluminum salts (alum), such as aluminum hydroxide, aluminum phosphate, aluminum sulfate, etc; (2) oil-in-water emulsion formulations (with or without other specific immunostimulating agents such as muramyl peptides (see below) or bacterial cell wall components), such as for example (a) MF59 (WO 90/14837; Chapter 10 in Vaccine design: the subunit and adjuvant approach, eds. Powell & Newman, Plenum Press 1995), containing 5% Squalene, 0.5% Tween 80, and 0.5% Span 85 (optionally containing various amounts of MTP-PE (see below), although not required) formulated into submicron particles using a microfluidizer such as Model 110Y microfluidizer (Microfluidics, Newton, Mass.), (b) SAF, containing 10% Squalane, 0.4% Tween 80, 5% pluronic-blocked polymer L121, and thr-MDP (see below) either microfluidized into a submicron emulsion or vortexed to generate a larger particle size emulsion, and (c) Ribi adjuvant system (RAS), (Ribi Immunochem, Hamilton, Mont.) containing 2% Squalene, 0.2% Tween 80, and one or more bacterial cell wall components from the group consisting of monophosphoryl lipid A (MPL), trehalose dimycolate (TDM), and cell wall skeleton (CWS), preferably MPL+CWS (Detox™); (3) saponin adjuvants such as Stimulon™ (Cambridge Bioscience, Worcester, Mass.) may be used or particles generated therefrom such as ISCOMs (immunostimulating complexes); (4) Complete Freund’s Adjuvant (CFA) and Incomplete Freund’s Adjuvant (IFA); (5) cytokines, such as interleukins (eg. IL-1, IL-2, IL-4, IL-5, IL-6, IL-7, IL-12, etc.), interferons (eg. gamma interferon), macrophage colony stimulating factor (M-CSF), tumor necrosis factor (TNF), etc.; and (6) other substances that act as immunostimulating agents to enhance the effectiveness of the composition. Alum and MF59™ adjuvants are preferred.

[0210] As mentioned above, muramyl peptides include, but are not limited to, N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP), N-acetyl-normuramyl-L-alanyl-D-isoglutamine (nor-MDP), N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2"-2'-dipalmitoyl-sn-glycero-3-hydroxyphosphoryloxy)-ethylamine (MTP-PE), etc.

[0211] The immunogenic compositions (eg. the immunising antigen or immunogen or polypeptide or protein or nucleic acid, pharmaceutically acceptable carrier, and adjuvant) typically will contain diluents, such as water, saline, glycerol, ethanol, etc. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present in such vehicles.

[0212] Typically, the immunogenic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. The preparation also may be emulsified or encapsulated in liposomes for enhanced adjuvant effect, as discussed above under pharmaceutically acceptable carriers.

[0213] Immunogenic compositions used as vaccines comprise an immunologically effective amount of the antigenic or immunogenic polypeptides, as well as any other of the above-mentioned components, as needed. By “immunollogically effective amount”, it is meant that the administration of that amount to an individual, either in a single dose or as part of a series, is effective for treatment or prevention. This amount varies depending upon the health and physical condition of the individual to be treated, the taxonomic group of individual to be treated (eg. nonhuman primate, primate, etc.), the capacity of the individual’s immune system to synthesize antibodies or generally mount an immune response, the degree of protection desired, the formulation of the vaccine, the treating doctor’s assessment of the medical situation, and other relevant factors. It is expected that the amount will fall in a relatively broad range that can be determined through routine trials. However, for the purposes of protein vaccination, the amount administered per immunization is typically in the range between 0.5 μg and 500 mg (however, often not higher than 5,000 μg), and very often in the range between 10 and 200 μg.

[0214] The immunogenic compositions are conventionally administered parenterally, eg, by injection, either subcutaneously, intramuscularly, or transdermally/transcutaneously (eg. WO98/20734). Additional formulations suitable for other modes of administration include oral, pulmonary and nasal formulations, suppositories, and transdermal applications. In the case of nucleic acid vaccination and antibody treatment, also the intravenous or intraarterial routes may be applicable.

[0215] Dosage treatment may be a single dose schedule or a multiple dose schedule. The vaccine may be administered in conjunction with other immunoregulatory agents.

[0216] As an alternative to protein-based vaccines, DNA vaccination (also termed nucleic acid vaccination or gene vaccination) may be used [eg. Robinson & Torres (1997) Seminars in ImIllunol 9: 271-283; Donnelly et al. (1997) Avnu Rev Innnunol 15: 617-648; later herein].

Treatment Methods of the Invention

[0217] The method of the sixth aspect of the invention generally relates to induction of immunity and as such also entails method that relate to treatment, prophylaxis and amelioration of disease.

[0218] When immunization methods entail that a polypeptide of the invention or a composition comprising such a polypeptide is administered the animal (e.g. the human) typically receives between 0.5 and 5,000 μg of the polypeptide of the invention per administration.

[0219] In preferred embodiments of the sixth aspect, the immunization scheme includes that the animal (e.g. the human) receives a priming administration and one or more booster administrations.

[0220] Preferred embodiments of the 6^{th} aspect of the invention comprise that the administration is for the purpose of inducing protective immunity against *Pseudomonas aeruginosa*. In this embodiment it is particularly preferred that the protective immunity is effective in reducing the risk of attracting infection with *Pseudomonas aeruginosa* or is effective in treating or ameliorating infection with *Pseudomonas aeruginosa*.

[0221] As mentioned herein, the preferred vaccines of the invention induce humoral immunity, so it is preferred that the administration is for the purpose of inducing antibodies specific for *Pseudomonas aeruginosa* and wherein said antibodies or B-lymphocytes producing said antibodies are subsequently recovered from the animal.

[0222] But, as also mentioned the method of the 6^{th} aspect may also be useful in antibody production, so in other embodiments the administration is for the purpose of inducing antibodies specific for *Pseudomonas aeruginosa* and wherein B-lymphocytes producing said antibodies are subsequently recovered from the animal and used for preparation of monoclonal antibodies.

[0223] Pharmaceutical compositions can as mentioned above comprise polypeptides, antibodies, or nucleic acids of the invention. The pharmaceutical compositions will comprise a therapeutically effective amount thereof.

[0224] The term "therapeutically effective amount" or "prophylactically effective amount" as used herein refers to an amount of a therapeutic agent to treat, ameliorate, or prevent a desired disease or condition, or to exhibit a detectable therapeutic or preventative effect. The effect can be detected by, for example, chemical markers or antigen levels. Therapeutic effects also include reduction in physical symptoms, such as decreased body temperature. The precise effective amount for a subject will depend upon the subject's size and health, the nature and extent of the condition, and the therapeutics or combination of therapeutics selected for administration. Thus, it is not useful to specify an exact effective amount in advance.

[0225] Reference is however made to the ranges for dosages of immunologically effective amounts of polypeptides, cf. above.

[0226] However, the effective amount for a given situation can be determined by routine experimentation and is within the judgement of the clinician.

[0227] For purposes of the present invention, an effective dose will be from about 0.01 mg/kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

[0228] A pharmaceutical composition can also contain a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" refers to a carrier for administration of a therapeutic agent, such as antibodies or a polypeptide, genes, and other therapeutic agents. The term refers to any pharmaceutical carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition, and which may be administered without undue toxicity. Suitable carriers may be large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

[0229] Pharmaceutically acceptable salts can be used therein, for example, mineral acid salts such as hydrochlorides, hydrobromides, phosphates, sulfates, and the like; and the salts of organic acids such as acetates, propionates, malonates, benzoates, and the like. A thorough discussion of pharmaceutically acceptable excipients is available in Remington's Pharmaceutical Sciences (Mack Pub. Co., N. J. 1991).

[0230] Pharmaceutically acceptable carriers in therapeutic compositions may contain liquids such as water, saline, glycerol and ethanol. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present in such vehicles. Typically, the therapeutic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. Liposomes are included within the definition of a pharmaceutically acceptable carrier.

[0231] As is apparent from the claim, the invention also relates to related embodiments to the treatment and prophylaxis disclosed herein: the invention also includes embodiments where

- **[0232]** the polypeptide of the invention is for use as a pharmaceutical, in particular for use as a pharmaceutical in the treatment, prophylaxis or amelioration of infection with *Pseudomonas aeruginosa;*
- **[0233]** the nucleic acid fragment of the invention or the vector of the invention is for use as a pharmaceutical, in particular for use as a pharmaceutical in the treatment, prophylaxis or amelioration of infection with *Pseudomonas aeruginosa;*
- **[0234]** the transformed cell of the invention is for use as a pharmaceutical, in particular for use as a pharmaceutical in the treatment, prophylaxis or amelioration of infection with *Pseudomonas aeruginosa.*
- **[0235]** the antibody, antibody fragment or antibody analogue of the invention is for use as a pharmaceutical, in particular for use as a pharmaceutical in the treatment, prophylaxis or amelioration of infection with *Pseudomonas aeruginosa.*

Example 1

[0236] The protective effect of PA1302-31-851, PA0931-29-742, PA2070-29-880, PA2070-173-880, PA2976-1-480, PA3901-33-784 and PA0041-34-550 in a murine model of pneumonia

[0237] The purpose of the experiment was to test the potentially protective effect of a combination of seven antigensof the invention in a well-characterized animal model of *Pseudomonas aeruginosa*-induced pneumonia. The primary parameter of comparison for this model is lung bacteriology, and secondly clinical symptoms, body temperature and weight loss.

Materials and Methods

Materials

[0238] NMRI mice, female (Janvier, France)

[0239] PA1302-31-851 (in 4 M urea; produced at University of Southern Denmark)

[0240] PA0931-29-742 (in 4 M urea; produced at University of Southern Denmark)

[0241] PA2070-29-880 (in 4 M urea; produced at University of Southern Denmark)

[0242] PA2070-173-880 (in 4 M urea; produced at University of Southern Denmark)

[0243] PA2976-1-480 (in 2 M urea; produced at University of Southern Denmark)

[0244] PA3901-33-784 (in 2 M urea; produced at University of Southern Denmark)

[0245] PA0041-34-550 (in 2 M urea; produced at University of Southern Denmark)

[0246] Aluminum hydroxide (Alhydrogel 2.0%; Brenntag, cat. no. 21645-51-2)

[0247] Freund's incomplete adjuvant (Sigma, cat. no. F5506-10X10ML)

[0248] Isoflurane

[0249] *Pseudomonas aeruginosa* PA01 Iglewski

[0250] Luria broth agar plates

[0251] Luria broth medium

[0252] Seaweed alginate (Pronatal LF 10/60 FT sample; FMC Biopolymer)

[0253] Ketamine (50 mg/ml)

[0254] Xylazine (20 mg/ml)

[0255] Pentobarbital

[0256] Microtainer tubes with serum separator additive (BD, #365967)

[0257] *Pseudomonas* isolation agar (Sigma-Aldrich, #17208-500G)

Immunization

[0258] A group of 21 female NMRI mice were immunized with seven recombinant proteins in combination with adjuvant. The 7-valent combination vaccine consisted of PA1302-31-851, PA0931-29-742, PA2070-29-880, PA2070-173-880, PA2976-1-480, PA3901-33-784 and PA0041-34-550. A second group made up the negative control group, which was immunized only with adjuvant. The amount of adjuvant used for immunization of the control group was the same as the amount used when immunizing the vaccine group. Each mouse was immunized subcutaneously three times at approximately two week intervals (Table 1). At all three immunizations the mice in the vaccine group received 15 μg of each protein. For the first immunization the proteins were mixed with aluminum hydroxide ($Al(OH)_3$) and Freund's incomplete adjuvant, whereas only $Al(OH)_3$ was used for the subsequent immunizations. Due to restrictions on injection volume in mice the seven protein antigens were split into two separate volumes; three proteins, in combination with adjuvant, were injected on the left side of the mouse and the other four proteins were injected on the right side. This immunization routine was the same in all three rounds of immunization.

TABLE 1

Time line of experiment. The two groups of mice were immunized simultaneously at approximately two week intervals. The length of the challenge was four days.

	Immunization number			Challenge	
	1	2	3	Start	End
Date	06.17.15	06.29.15	07.10.15	07.26.15	07.30.15
Days before challenge start	39	27	16	0	+4

Temperature Transponders

[0259] Four days before inoculation temperature transponders (BMDS, cat. no. IPTT-300) were inserted into each mouse. The mice were briefly anaesthetised by inhalation of isoflurane, and a temperature transponder inserted underneath the skin on the lower back or side of the mouse.

[0260] Using a compatible wireless scanner (BMDS Smart Probe; BMDS, cat. no. DAS-7007s) body temperature could be registered when placing the scanner close to the transponders underneath the skin of the mouse.

Preparation of Bacterial Inoculum

[0261] A small amount of *Pseudomonas aeruginosa* PA01 Iglewski was extracted from a freeze stock (stored at −80° C.) and streaked out on a Luria broth agar plate. The plate was place at 37° C. over night. The following day a single colony was used to inoculate 100 ml sterile Luria broth medium. The culture was left to incubate at 37° C., with constant shaking, for 18 hours. After the 18 hours of incubation 50 ml of the bacterial culture was centrifuged at 5000×g for 10 minutes at 20° C. The pellet was resuspended in 5 ml Luria broth medium. The bacterial suspension was mixed with seaweed alginate in a ratio of 0.5 ml bacterial suspension to 12 ml seaweed alginate, and small alginate beads were created as described in Bjarnsholt et al. (2014). The number of colony forming units (CFU) per ml alginate bead solution was determined by dissolving the alginate beads in saline.

Challenge Setup

[0262] The mice were housed at the Biocenter at the University of Copenhagen. The animals were kept in an environment characterized by a 12 hours light-dark cycle and temperature and humidity control. They had access to food and water ad libitum. The experimental procedures were carried out in accordance with the guidelines of the Danish National Animal Ethics Committee (license number 2013-15-2934-00857).

[0263] Before inoculation the mice were anaesthetized with an intraperitoneal injection of ketamine (100 mg/kg) and xylazine (10 mg/kg). Once sedated each mouse was inoculated intranasally with 1.0×10^7 CFU of *Pseudomonas aeruginosa* PA01 Iglewski embedded in seaweed alginate beads. To ensure that the mice did not die from dehydration during the four day challenge, the mice received 1 ml of physiological saline subcutaneously once a day.

[0264] The mice were assessed daily to register symptoms and development of disease over the course of the four day challenge. To ensure a consistent evaluation of all animals each animal was scored individually following the scale of clinical symptoms given in table 2. Before the start of the challenge, the mouse cages were "blinded", leaving the scientist involved unaware of which treatment had been given to which animals. This ensured an unbiased scoring of the animals' clinical symptoms.

TABLE 2

Scale of clinical symptoms. The mice were individually assessed on their physical appearance and behavior, specifically registering details of fur, posture, movement, eyes and breathing for each animal. The sum of the scores was used in the overall evaluation of animal welfare, and in relation to humane endpoints.

Fur	0-well groomed
	1-slightly ruffled
	2-very ruffled
Posture	0-normal
	1-slightly hunched back
	2-hunched back
Movement	0-normal
	1-decreased activity
	2-completely immobile
Eyes	0-normal
	1-semi-closed
	2-closed
Breathing	0-normal
	1-affected/forced breathing

Humane Endpoints.

[0265] Animals were euthanized if the sum of clinical scores reached 9, using the scale given in table 2, or if the body temperature was below 30° C.

Organ Extraction and Bacteriology

[0266] Following registration of weight, temperature and clinical symptoms on day four after inoculation, the mice were euthanized by intraperitoneal injection of pentobarbital. Subsequently, the lungs were extracted aseptically, and placed in a tubes containing 4 ml sterile saline. Blood was collected after cardiac puncture and transferred to Microtainer tubes, in order to save serum for later ELISA analysis.

[0267] The lungs were homogenized, serially diluted and 100 μl of each dilution was plated on *Pseudomonas* Isolation agar-plates. The plates were incubated at 37° C. over night, and the number of colony forming units was quantified the following day.

Results

Clinical Symptoms

[0268] The animals were scored daily to register disease progression. The results of the clinical scoring are given in FIG. **1**.

Temperature and Weight Loss

[0269] Body weight and body temperature were registered daily, as part of the overall assessment of animal welfare. The results of the registration of weight and temperature are given in FIGS. **2** and **3**, respectively. Note that there was a general issue of malfunctioning temperature transponders, especially in the group immunized with the 7-valent combination vaccine, hence the low number of data points.

Bacteriology

[0270] Results are shown in FIG. **4**.

Antibody Titer

[0271] After challenge completion blood was collected from the mice. The serum was used for subsequent analysis of antibody titer, using ELISA. The antibody titer to the seven antigens were analysed for eight of the vaccinated mice. FIG. **5** shows the mean antibody response to the seven protein antigens—each curve is the mean of eight separate ELISA curves.

Conclusions

[0272] The results indicate that the 7-valent combination vaccine protects mice from *Pseudomonas aeruginosa* PA01 Iglewski-induced pneumonia. The mice immunized with the combination vaccine had a significantly lower lung CFU compared to the negative controls. Similarly the clinical symptoms were significantly lower for mice immunized with the combination vaccine, hence these animals appeared less ill to an unbiased observer. Moreover, the animals immunized with the combination vaccine had a significantly smaller weight loss over the four days following inoculation, which is another indicator of a greater well-being. There was no significant difference in body temperature, when comparing the data from the two groups. It should, however, be noted that a great number of the animals in the vaccine group had been equipped with temperature transponders that were malfunctioning, hence the small number of data points. Analysis of the serum samples show that the mice immunized with the 7-valent combination vaccine had a relatively high antibody response to five of the seven protein antigens.

Example 2

[0273] Confirmation of the protective effect of PA1302-31-851, PA0931-29-742, PA2070-29-880, PA2070-173-880, PA2976-1-480, PA3901-33-784 and PA0041-34-550 in a murine model of pneumonia ER_ 0040

[0274] The purpose of the experiment was to verify the results of claim **1**, i.e. that a 7-valent combination vaccine protected mice against a *Pseudomonas aeruginosa*-induced pneumonia. The primary parameter of comparison for this model is lung bacteriology, and secondly clinical symptoms, body temperature and weight loss.

Materials and Methods

Materials

[0275] NMRI mice, female (Janvier, France)

[0276] PA1302-31-851 (in 4 M urea; produced at University of Southern Denmark)

[0277] PA0931-29-742 (in 4 M urea; produced at University of Southern Denmark)

[0278] PA2070-29-880 (in 4 M urea; produced at University of Southern Denmark)

[0279] PA2070-173-880 (in 4 M urea; produced at University of Southern Denmark)

[0280] PA2976-1-480 (in 2 M urea; produced at University of Southern Denmark)

[0281] PA3901-33-784 (in 2 M urea; produced at University of Southern Denmark)

[0282] PA0041-34-550 (in 2 M urea; produced at University of Southern Denmark)

[0283] Aluminum hydroxide (Alhydrogel 2.0%; Brenntag, cat. no. 21645-51-2)

[0284] Freund's incomplete adjuvant (Sigma, cat. no. F5506-10X10ML)

[0285] Isoflurane

[0286] *Pseudomonas aeruginosa* PA01 Iglewski

[0287] Luria broth agar plates

[0288] Luria broth medium

[0289] Seaweed alginate (Pronatal LF 10/60 FT sample; FMC Biopolymer)

[0290] Ketamine (50 mg/ml)

[0291] Xylazine (20 mg/ml)

[0292] Pentobarbital

[0293] Microtainer tubes with serum separator additive (BD, #365967)

[0294] *Pseudomonas* isolation agar (Sigma-Aldrich, #17208-500G)

Immunization

[0295] A group of 32 female NMRI mice were immunized with seven recombinant proteins in combination with adjuvant. The 7-valent combination vaccine consisted of PA1302-31-851, PA0931-29-742, PA2070-29-880, PA2070-173-880, PA2976-1-480, PA3901-33-784 and PA0041-34-550.

[0296] A second group made up the negative control group, which was immunized only with adjuvant. The amount of adjuvant used for immunization of the control group was the same as the amount used when immunizing the vaccine group. Each mouse was immunized subcutaneously three times at approximately two week intervals (Table 3). At all three immunizations the mice in the vaccine group received 15 μg of each protein. For the first immunization the proteins were mixed with aluminum hydroxide ($Al(OH)_3$) and Freund's incomplete adjuvant, whereas only $Al(OH)_3$ was used for the subsequent immunizations (see appendix 5). Due to restrictions on injection volume in mice the seven protein antigens were split into two separate volumes; three proteins, in combination with adjuvant, were injected on the left side of the mouse and the other four proteins were injected on the right side. This immunization routine was the same at all three rounds of immunization.

TABLE 3

Time line of experiment. The two groups of mice were immunized simultaneously at approximately two week intervals. The length of the challenge was four days.

	Immunization number			Challenge	
	1	2	3	Start	End
Date	11.26.15	12.11.15	12.26.15	01.09.16	01.14.16
Days before challenge start	44	29	14	0	+4

Temperature Transponders

[0297] Four days before inoculation temperature transponders (BMDS, cat. no. IPTT-300) were inserted into each mouse. The mice were briefly anaesthetised by inhalation of isoflurane, and a temperature transponder inserted underneath the skin on the lower back or side of the mouse.

[0298] Using a compatible wireless scanner (BMDS Smart Probe; BMDS, cat. no. DAS-7007s) body temperature could be registered when placing the scanner close to the transponders underneath the skin of the mouse.

Preparation of Bacterial Inoculum

[0299] A small amount of *Pseudomonas aeruginosa* PA01 Iglewski was extracted from a freeze stock (stored at −80° C.) and streaked out on a Luria broth agar plate. The plate was place at 37° C. over night. The following day a single colony was used to inoculate 100 ml sterile Luria broth medium. The culture was left to incubate at 37° C., with constant shaking, for 18 hours. After the 18 hours of incubation 50 ml of the bacterial culture was centrifuged at 5000×g for 10 minutes at 20° C. The pellet was resuspended in 5 ml Luria broth medium. The bacterial suspension was mixed with seaweed alginate in a ratio of 0.5 ml bacterial suspension to 12 ml seaweed alginate, and small alginate beads were created as described in Bjarnsholt et al (2014). The number of colony forming units (CFU) per ml alginate bead solution was determined by dissolving the alginate beads in saline.

Challenge Setup

[0300] The mice were housed at the Biocenter at the University of Copenhagen. The animals were kept in an environment characterized by a 12 hours light-dark cycle and temperature and humidity control. They had access to food and water ad libitum. The experimental procedures were carried out in accordance with the guidelines of the Danish National Animal Ethics Committee (license number 2013-15-2934-00857).

[0301] Before inoculation the mice were anaesthetized with an intraperitoneal injection of ketamine (100 mg/kg) and xylazine (10 mg/kg). Once sedated each mouse was inoculated intranasally with 1.0×10^7 CFU of *Pseudomonas aeruginosa* PA01 Iglewski embedded in seaweed alginate beads. To ensure that the mice did not die from dehydration during the four day challenge, the mice received 1 ml of physiological saline subcutaneously once a day.

[0302] The mice were assessed daily to register symptoms and development of disease over the course of the four day challenge. To ensure a consistent evaluation of all animals each animal was scored individually following the scale of clinical symptoms given in table 2 in Example 1. Before the start of the challenge, the mouse cages were "blinded", leaving the scientist involved unaware of which treatment had been given to which animals. This ensured an unbiased scoring of the animals' clinical symptoms.

Humane Endpoints.

[0303] Animals were euthanized if the sum of clinical scores reached 9, using the scale given in table 2, or if the body temperature was below 30° C.

Organ Extraction and Bacteriology

[0304] Following registration of weight, temperature and clinical symptoms on day four after inoculation, the mice were euthanized by intraperitoneal injection of pentobarbital. Subsequently, the lungs were extracted aseptically, and placed in a tubes containing 4 ml sterile saline. Blood was collected after cardiac puncture and transferred to Microtainer tubes, in order to save serum for later ELISA analysis.

[0305] The lungs were homogenized, serially diluted and 100 μl of each dilution was plated on *Pseudomonas* Isolation agar-plates. The plates were incubated at 37° C. over night, and the number of colony forming units was quantified the following day.

Results

Clinical Symptoms

[0306] The animals were scored daily to register disease progression. The results of the clinical scoring are given in FIG. **6**.

Temperature and Weight Loss

[0307] Body weight and body temperature were registered daily, as part of the overall assessment of animal welfare. The results of the registration of weight and temperature are given in FIGS. **7** and **8**, respectively.

Bacteriology

[0308] Results are shown in FIG. **9**, and the pooled results with those of Example 1 are shown in FIG. **10**.

Antibody Titer

[0309] After challenge completion blood was collected from the mice. The serum was used for subsequent analysis of antibody titer, using ELISA. The antibody titer to the seven antigens were analysed for all of the surviving vaccinated mice, i.e. 26 mice. FIG. **6** shows the mean antibody response to the seven protein antigens—each curve is the mean of 26 separate ELISA curves.

Conclusions

[0310] Generally the results indicate that the 7-valent combination vaccine protects mice from *Pseudomonas aeruginosa* PA01 Iglewski-induced pneumonia—results also found in Example 1. Analysis of the primary parameter of comparison—the lung bacteriology—did not suggest a protective effect of treatment with the 7-valent vaccine, as there was no significant difference in lung CFU when comparing the two groups. Only when the CFU results from both Examples 1 and 2 were analysed together, did a significant effect of the protein vaccine appear. The other parameters of interest collectively suggest that the protein-immunized mice had a better recovery from infection. The vaccinated group had significantly lower clinical scores in addition to a significantly higher body temperature and a significantly lower weight loss. Analysis of the serum samples show that the mice immunized with the 7-valent combination vaccine had a relatively high antibody response to five of the seven protein antigens.

Biologic Sequence Information

[0311] The full-length, native polypeptides of the invention have the following designations used herein:

SEQ ID NO:	Polypeptide name
1	PA1034
2	PA1592
3	PA3284
4	PA4107
5	PA0912
6	PA0070
7	PA5060
8	PA1954
9	PA0971
10	PA5253
11	PA0724
12	PA1441
13	PA5133
14	PA3716
15	PA4016
16	PA1805
17	PA3729
18	PA0931
19	PA2688
20	PA3901
21	PA1302
22	PA2070
23	PA3115
24	PA3535
25	PA2976
26	PA4554
27	PA4282
28	PA1874
29	PA0041
30	PA2462

[0312] A number of the polypeptides of the invention are fragments of the full-length, native polypeptides. Such fragments as follows: PAXXXX-Y-Z, where XXXX is the number in the polypeptide name, X is the number of the N-terminal amino acid residue in the fragment and Z is the number of the C-terminal amino acid residue. For instance, PA2070-29-880 is the polypeptide having the amino acid sequence SEQ ID NO: 22, residues 29-880.

[0313] The polypeptides of the present invention have the following amino acid sequences:

SEQ ID NO: 1
MSQEPHVHGPNCNHDHDHHHDHGHGHVHGPHCNHSHEPVRNPLKAVGRND
PCPCGSEKKFKKCHGA

SEQ ID NO: 2
MKKTVTLALLLAASLGLAACDKKEEDKAAAPAAPATETQPSAPATPPAEP
SAPAPSSDTPATPQTPAPTPEQPQQNQQ

SEQ ID NO: 3
MKKISLASSVVGAALLGVASVGAHAAQNPFAVQELSSGYSVAAAEKAKEG
SCGEAKCGADKGKREASKAGHEGSCGADRKAKEGSCGGEKKAGEGNCGAD
KKKS

SEQ ID NO: 4
MSVFDSRQKTSASLLGAVLVGGMLLGGSAFAVEPLGQGLQVAAASAGEGK

CGEGKCGSGGSAKTPAKAGAEGKCGEGKCGDASFARTDTDHDGKVSRAEF

LAVAKDRAGEFDSIDSDHDGFISEAEAYEHLRKTYEANGKPMPAGLFSKL

EQGQH

SEQ ID NO: 5
MRSLSLLLLLSLASTCEAAAVFRCEDASGHVSFTQLGCPAGQAGETVVAD

NPPPGGRSVTPMAETKTKKASIGRKSVPLAVIGEREDRCGRRLDEKERRK

AIVEQRIMAGMTRSDVERALGKPDRVSGNNAEVRYQYKADKRRGARSVSF

DQEGCVKGREGTGWSESIPGAKAGPSSYR

SEQ ID NO: 6
MSQPSENRLITSARYALCLLTASGVLLSGCASSGVGSVAQTTRAEYYPSC

YEPVSHLRSTDNAVRNSAITGAITGGLLGGLAGGLASDENRGRNAALAAA

GGALAGGAAGYYMEKQKQISDDRARIGSYGTDVDRSTVEINRSVAYAKSA

QSCYQSQFKALLDGRKNKSINEAEGRKRLAEIVSGLQETNALLVAANGRA

GENISNYTQAYEKDLQQVGVPRAEVTKVAEAENRASTTKGGSKPKTGSNP

KVPKEAVATEQTIRKAQDAQSEGNKVASQGQGMIREVCNSPDMGDWAPPS

CAKA

SEQ ID NO: 7
MAGKKKSEKESSWIGEIEKYSRQIWLAGLGAYSKVSKDGSKLFETLVKDG

EKAEKEAKSDVDAQVGAAKASARSAKSKVDEVRDRALGKWSELEEAFDKR

LNSAISRLGVPSRNEVKELHSKVDTLTKQIEKLTGVSVKPAAKAAAKPAA

KPAAKPAAKTAAAKPAAKPAAKAAAKPAAKPAAKKTAAKTAAAKPAAKPA

AKPTAKAAAKPATKPAAKAAAKPAAKPAAAKPAAKPAAKPAAATAAKPAA

KPAAKPAAKKPAAKKPAAKPAAAKPAAPAASSSAPAAPAATPAASAPAAN

APATPSSQG

SEQ ID NO: 8
MKATMVLTPLALAMAAVLSVSAYAGNEGGWHPPKPNPQSNNKGGATALVV

DTQQNYNNKVSNFGTLNNASVSGSIKDASGNVGVNVAAGDNNQQANAAAL

ASADASFVFGTATASTSVLQSGYGNTLNNYSNPNTASLSNSANNVSGNLG

VNVAAGNFNQQKNDLAAAVSNGQYSTAGSAASQTSTGNTTVNSANYAYGG

TYVSLKLNADGSYKGTSDQIGDVYLDTWEGQTHPGGSNTGHIDVDSQAQG

-continued

AKDLNHDGGAFAFKEKGDVDLKGTVSGFIPAIVGFKTPVTNNASLSNSLQ

NVSGNVGVNIAAGGGNQQSNSLSIAAGCSSCPAGGESLGF

SEQ ID NO: 9
MKQQFERSPSESYFWPVVLAVVLHVLIFAMLFVSWAFAPELPPSKPIVQA

TLYQLKSKSQATTOTNQKIAGEAKKTASKQYEVEQLEQKKLEQQKLEQQK

LEQQQVAAAKAAEQKKADEARKAEAQKAAEAKKADEAKKAAEAKAAEQKK

QADIAKKRAEDEAKKKAAEDAKKKAAEDAKKKAAEEAKKKAAAEAAKKKA

AVEAAKKKAAAAAAAARKAAEDKKARALAELLSDTTERQQALADEVGSEV

TGSLDDLIVNLVSQQWRRPPSARNGMSVEVLIEMLPDGTITNASVSRSSG

DKPFDSSAVAAVRNVGRIPEMQQLPRATFDSLYRQRRIIFKPEDLSL

SEQ ID NO: 10
MSANKKPVTTPLHLLQQLSHSLVEHLEGACKQALVDSEKLLAKLEKQRGK

AQEKLHKARTKLQDAAKAGKTKAQAKARETISDLEEALDTLKARQADTRT

YIVGLKRDVQESLKLAQGVGKVKEAAGKALESRKAKPATKPAAKAAAKPA

VKTVAAKPAAKPAAKPAAKPAAKPAAKTAAAKPAAKPTAKPAAKPAAKPA

AKTAAAKPAAKPAAKPVAKPAAKPAAKTAAAKPAAKPAAKPVAKPTAKPA

AKTAAAKPAAKPAAKPAAKPAAKPVAKSAAAKPAAKPAAKPAAKPAAKPA

AKPVAAKPAATKPATAPAAKPAATPSAPAAASSAASATPAAGSNGAAPTS

AS

SEQ ID NO: 11
MWGLTMKFASLILMLLFATVARAEDYYWKIQSLPERFSSPSAACAAWAKA

TGRPGEFTFTGSMKARDQTSFWCEFTNNETGKTAAGYGPAGRYGDSCPEG

TEYDKATGVCKSPPQECKEGELFPAKGPDSPVVTSGGRNYVGDGGAPTAC

YQSCEYGGNPSPASCYLVKGSTTTGFCNYILKGTGQNCGADSYTFSQTGD

SLNPPDTPNTDPSDPNDPGCPPGWSWSGTTCVKAPTDPTDPTDPTTPGSD

GGGDGNGGGNNNGGGNDGGTGNGGDGSGGGDGNGGGDGSGDGDGSGTGGD

GNGTCDPAKENCSTGPEGPGGELKEPTPGTWDDAIATWEKKVEDAKQELK

TKVKANVDQMKGAFDLNLAEGGGQLPCESMTIWGKSYSLCISDYAGQLSS

LRVALLLMAALIAALILLKD

SEQ ID NO: 12
MAVAPGVLLPPTPDVKPKAAAPKSQQKTPEPSNDKTSSFSDMYAKETAKK

PAERADGPAKGSRDKPRDAGKDAAEAQPTDAVRQPAVAEDGKPLPADGQA

KADGEDKVETPVDPLQLLGLGGAVPLLDENTQATLLPPAVPTASSAPASL

TEASSDPTLVKLNGVPAVNMALEQGAQDAAQTAKGGPAKSADPRQANLGD

ALAGLTSDSLTKAVDGKALEAQLQQTAEPAVASAASESLLESKAEPRGEP

FAAKLNGLTQAMAQQALTNRPVNGTVPGQPVAMQQNGWSEAVVDRVMWMS

SQNLKSAEIQLDPAELGRLDVRIHMTADQTQVTFASPNAGVRDALESQMH

RLRDMFSQQGMNQLDVNVSDQSLARGWQGQQQGEGGSARGRGLAGEASGD

EETLAGVSEIRSRPGASAARGLVDYYA

SEQ ID NO: 13
MLRLLPLLLSLACLAPAFADERADTQRQLEQTQKDIGELKKLLDGIQQEK

SGVQKQLKSTETEMGDLEKQIKALQDELDKSEAELKRLDGEKKKLQDARI

-continued

EQQRLLAIQARAAYQSGREEYLKLLLNQEHPEKFSRTLTYYDYINKARLE

QLASFNETLRQLANVEQDISAQKAEQLSKQGELDSRREALAATRKERQQA

LAKLNSDYRERDQKLKSRQQDQAELAKVLRTIEETLARQAREAAAAAERE

RQRALAAERERARQQQAAPGRVTSPPREPAPGPLVSSTGAVYGGAFGSAR

GKLPWPVNGRVVARFGSQRGDDPRAKWDGVLISASAGSTVRAVHGGRVVF

ADWLRGAGLLVILDHGGGYLSLYGHNQSLLKDAGDTVKAGDPIATVGTSG

GQSSPAVYFAIRFIQGRPADPTTWCRAQG

SEQ ID NO: 14

MQRLSRIGRNTLAVSVSTLLLSACNQGDDAPKPAAVAPQPAAPSMAALSI

PLCLNGQCAVIDQDAKLLVPFDNDYDNIVASAYQGTLMAAREERWNLIQA

KDGKVLRDDIGEALSLLTPNLYGFVRDGKYGVVDGQGKEVQAPRFDDIYP

NSANEFIIYEIDGKRGILDAKGKQLTEALYDTTLVNGSVAEHGGLISAER

GEEKWIINLATGEQKAVAYESLGDLHDGVMSASVIGKGSQLVDAKGDVVG

DGKSYDYLGTPANGLVAFREKYDSPCGYLDYQGKVAIAAQFAGCGAFGKQ

GGLAQQRMEDGSSGKYGLIDRSGAWKVQPQYDSADSAGLTALGYTVDVPG

LAAVGVSTGLFSADFGIFNLDEGSEWVKPGYAQIGALGNDLFVVAKKGGP

QKTVSFMGSESQVPVVGLMDRSGKMLLEPDELISIQSAYDGRFLEGLDGM

DNAAHTVLLDRQGRTLVPALWQKLEVNPQQGYILGYEVSGTGDEATETLR

ALYDLNGKPRFTVATTDCGAEQLLDGNGKAIWPQDPTPYCQSDDEQDDEG

EPEQEPAPVEESEETSES

SEQ ID NO: 15

MLRPARSLSLCSALVILLAACGEGEPLLPADARLPDGARYRGELVDGRLE

GQGRLDYDNGAWYAGRFEHGLLHGHGTWQGADGSRYSGGFAAGLFDGQGR

LAMADGSVYQGGFRQGLFDGEGSLEQQGTRYRGGFRKGLYSGQGTLDGSD

GSRYQGSFRQGRLEGEGSFSDSQGNQYAGTFRDGQLNGKGRWSGPDGDRY

VGQFKDNQFHGQGRYESASGDVWIGRFSEGALNGPGELLGADGSRYRGGF

QFWRFHGQGLLEQLDGTRYEGGFAAGAYAGQGTLDRADGSREQGLWADGK

RIRDAAGKALPDTLEVGLLAQGRLLDEELRKIPASTPASELYALSLGGDG

RQGVFLREADYAGDLLGQRFAARGVIRLVNHRDHFGDRPLATRESLSRAV

RTLAERSGPEDLVFIYLTSHGSSDHQLALDMPGLNLGDLPAAELAELLAP

LRQRDKVLVVSACYSGGFIPPLKDERTLILTAARADRVSFGCSDDADFTY

FGRALLANALNRTDDLSKAFELAKEEVRQREKEEGFEASEPQAWLPERVL

AHWRTLRGQQAERALASREGKTGEGAAGK

SEQ ID NO: 16

MLQNIRDNSQGWIAKTIIGVIIVLLSLTGFDAIIRATDHSNVAAKVNGDD

ISLNEVQQAVDMQRRQLLQRLGKDFDPSMLDDKLLKEAALKGLIERTLLL

QAAKDDKFAFSDQALDQLILQTPEFQVDGKFNADRFDQVIRQMNYSRMQF

RQMLGQEMLIGQLRAGLAGTGFVTDNELQSFARLEKQTRDFATLAIKADA

SKSSVSDDEVKAFYEGHKSEFMTPEQVVVEYVELKKSSFFDQVKVKQEDL

EALYQKEIANLSEQRDAAHILIEVNDKVGDEQAKAKIDEIKARLAKGEDF

-continued

AALAKEFSQDIGSAATGGDLGYAGRGVYDPAFEEALYALKQGEVSAPVKT

PYGYHLIKLLGVQAPEVPSLESLKPKLEDELKKQMVEQRFVEATKDLESS

AYEAADLSQPAQEMGLKVQTSQPFGRSGGDGIAANRQIVQTAFSAEVLEE

AANSGAIELDPDTVVVLRVKEHNKPKEQPLEQVAANIRERLAAEKAAEEA

QKRGEALIAELREGRTSSAAGESWKVVEAASRGHEGVDPKLLQAVFRMQR

PEAKDKPSFSGVTLANGDYVVIRLNGVSEPEEAISDDEKAMYRRFLASRS

GQADFAAFRRQLQDKAEVEKY

SEQ ID NO: 17

MDMTSLMPLLLGVGLVVLLVVGLLALFKAFYIKVPQGTALIVNDMSSTPK

VHFTGALVYPVIHLKEFMRISLITLEVDRRGKDGLICRDNMRADITVAFY

LRVNETQDDVLKVAKAIGVDRASDRSAVNELFNAKFSEALKTVGKQFDFV

QLFENRQDFRDRIIEVIGNDLNGYVLEDVAIDYLEQTAKNSLDPSNILDA

EGIRKITELTATQNVITNELERNEELAIKKKNVETREAALALERQQADAE

ARQKREIETIRAREEAETARVKEEERLKAEQARIQAQQEIDVRTENHQRE

VEVAQQNRQRAVVIEVEKVTRAKDLEIVAREREVELQKIEKEKALEEQRK

NIANVIRERVAVEKTVAQEEERIKEVREVSEAERVKQVILLQAQAEAEQE

LVRQVKQAEADEARSKHKAVEINTMAQAELEAASKQAEAKKRLAEGIEAE

RAAPGLADARVLEVTAAAKEKDGLAAARVRAEQUAEARGDEERGLADARV

LEAQAAAKEKDGLAEAKVLAEKLGAQARGEEQLGAAKAKATKDQGSAEAE

VLLQRLNAEAEGLGKKFGALDALSDSARQHEEFRMQLEKSFEEAMAAIAA

NKDIAKDQAEVLATALGKANIEIVGGEGDFFNSFAKSLSVGKAIEGVVGK

SPVVQDVLARLLNGRGAAAAVMPERKSGHENEPAAEV

SEQ ID NO: 18

MYPQFRRGHLAAAVLFASSSLLGGQALAEDERLEELDERAESVVQLGDEV

VLGTAEQELKQAPGVSIITAEDIRKRPPVNDLSEIIRTMPGVNLTGNSSS

GQRGNNRQIDIRGMGPENTLILVDGKPVSSRNSVRYGWRGERDTRGDSNW

VPPEEVERIEVLRGPAAARYGSGAAGGVVNIITKRPTDRLRGSMTVFTNI

PESSKDGATRRANFSLSGPLTEALSFRAYGSANKTDSDDTDINLGHTVNP

SRTVAGREGVRNRDLSGMLSWQVTPDQVVDFEAGFSRQGNIYAGDTQNNN

GTANTQGLADDGAETNRMYRENYAITHNGTWSGTSRFVAQYDSTRNNRLE

EGLAGSVEGQIGADRSFSASKLENYRLSGELNLPLHALFEQVLTVGAEWN

KETLNDPSSLKQGFVGSDSLPGTPAAGSRSPKSKAEIRALYVEDNIELRP

GTMLTPGLRLDDHSDFGLNWSPSLNASQTLGEYFTVKAGIARAFKAPNLY

QSNPNYLLYTRGNGCPIQTSSGGCYLVGNENLDAETSVNKELGIEFRRDG

WVAGLTYFRNDYKNKIVAPLDVMGQTGTGNNILQWSNAKKAVVEGLEGNL

LVPLHEDLSWSTNLTYMWSKDKDTGNPLSVIPEYTLNSTLDWQASERLST

QLTSTIYGRQEPPKHGTSRNTPVVSRKEVGTYGIWGVSAGYTFSENLSVR

GGVSNLFDKRLYRQGNSFDAGAATYNEPGRAYYVSMTTSF

SEQ ID NO: 19

MSSRALPAVPFLLLSSCLLANAVHAAGQGDGSVIELGEQTVVATAQEETK

QAPGVSIITAEDIAKRPPSNDLSQIIRTMPGVNLTGNSSSGQRGNNRQID

-continued

IRGMGPENTLILVDGKPVSSRNSVRYGWRGERDSRGDTNWVPADQVERIE

VIRGPAAARYGNGAAGGVVNIITKQAGAETHGNLSVYSNFPQHKAEGASE

RMSFGLNGPLTENLSYRVYGNIAKTDSDDWDINAGHESNRTGKQAGTLPA

GREGVRNKDIDGLLSWRLTPEQTLEFEAGFSRQGNIYTGDTQNTNSNNYV

KQMLGHETNRMYRETYSVTHRGEWDFGSSLAYLQYEKTRNSRINEGLAGG

TEGIFDPNNAGFYTATLRDLTAHGEVNLPLHLGYEQTLTLGSEWTEQKLD

DPSSNTQNTEEGGSIPGLAGKNRSSSSSARIFSLFAEDNIELMPGTMLTP

GLRWDHHDIVGDNWSPSLNLSHALTERVTLKAGIARAYKAPNLYQLNPDY

LLYSRGQGCYGQSTSCYLRGNDGLKAETSVNKELGIEYSHDGLVAGLTYF

RNDYKNKIESGLSPVDHASGGKGDYANAAIYQWENVPKAVVEGLEGTLTL

PLADGLKWSNNLTYMLQSKNKETGDVLSVTPRYTLNSMLDWQATDDLSLQ

ATVTWYGKQKPKKYDYHGDRVTGSANDQLSPYAIAGLGGTYRLSKNLSLG

AGVDNLFDKRLFRAGNAQGVVGIDGAGAATYNEPGRTFYTSLTASF

SEQ ID NO: 20

MSPSRALSPLSRALLLACLGGPVLVSAGSACAAEIRTDARQYYRLPAEPL

EQALNHLGRQAGVLIAFSPEQTAARRSQALDGEYTLEEALAALLVGSGLE

ARARGDGAYTLEALPVEDPANLQALTVVGDWLADASAADVFEHPGARDVV

RREQFQAQGAASTREVLERIPGVSAPLNNGTGSHDLALNFGIRGLNPRLA

SRSTVLMDGIPVPFAPYGQPQLSLAPVSIGNMDAVDVVRGGGAVRYGPQN

VGGIVNFVTRAIPEDFATKLDVHSELSPSSSQDGLKTTHNVLIGGTGANG

LGGALLYSGTRGGDWREHSDTRIDDLILKGRFQPSDEHTFSAMTQYYDGE

ADMPGGLGTAAYHDDPYQSTRPYDKFWGRRTLASASYEYTPNASQKLNVT

GFFTKTLRSGYLDQGRNLTLSPREYWVRGLETRFSQGFELGESRHEVGIG

HRYVNEASHELRYWTRADSGQLPSTGSRNDRDTRGSTEANAFYIDDRIDI

GNWTITPGIRYEKIDSEQKNLLKNSKDSGRYNASLPALNVIYHLTPSWNL

YANTEGSFGTVQYSQMGKAVRSGDIEPEKARTWELGSRYDDGILRAELGA

FLINFDNQYESNQQTDSVTARGKTRHKGIEAAIAYDLADLDPLLSGFDVY

ASYAYVDASIREDGPNKGNQVPFSSKHKGTLGANYRTGAWSYNLDGSFQT

SQYADNANTESESADGSTGRIAGWMVWSARGTYDFGPQLNDLKLGLGVKN

LFDRRYYTRSFDDNNKGLYVGQPRTLYVQASVGF

SEQ ID NO: 21

MTLPFTRAAWRPLCSAAVLGAALWAAGASAAERRFDLPAQPLAASLSRLA

QQAQVQVLFDESLLRGLRAPALSGSYGVREALERLLVGSELELVEAGGGY

VVRRRQVDAYSDNALQLDAQTIVGNGREVDASNVGRSTLTRRDIERQQAD

NIPSLLQTLPGVTMGGSPKPGGQTTNIWGLGDAEDVPYTLDGAQKSGFER

YQQGTVFIEPEMIKRIEVEKGPHSVFTGNGGFGGTVHMETKDAPDLLREG

RDVGAMLKYGYHSNDQQKIYSGAVFGRSEDRRVDALLYLNGRDGRDMKLA

DNLPLSPTDYPINPKRLPNSAQDEKTGLFKLNLHPTEEHDLGFTYLRSKS

SRWTPFSASSYPTPPSQWTIDRYGYELGLTRLLAHRDTTDTTWTGKYNYH

PLDNPWIDLQLSYSDARTEQLDRREDTAFYQLATGGKRMRTEYQDKVLEL

-continued

RNTSRFDTGALQHELTLGAALHKHKRDILMHMPGKTYETPRYNYGWLQPA

FMPAGKQDTQSFYIQDAITYGSLTVTPSMRFDSVRNDGQANLAPIYDNPK

LGHDYRAQTYSGWSPRLSVFWTATPNLAFFADYTETWRAPVIDEQYEVQN

SSTIGGSSRDLDAERIHAIRGGSVINLPDLLVAGDSLQIRTTLFQNRIKD

EIFRTRSVGCRQQSIDNGSIGGSCGDMLPLSNYRNLPGLTIKGFEIESFY

DSQRLFGSLSYSWMTGKHDGAYSNPWGPNVWARDIPPPKWVAMLGLKVPE

WDAKLGWQGEFVRKTDRLPSDRYSGGMGTGSGDIYWDHAANDSYDTHRLF

AEWVPAKLGLKDTRIDFTVDNLFNRSYRQPLGGDLVYSQGRNAKISVTQF

F

SEQ ID NO: 22

MHRSLHTDAPLGAALLLALQLAPGSAAAAEEQAPVDPPTVQLQRIEVTGS

AIRRVDAETAVPISVLRAEELRQQGVTSTEELIGRLSGNQGVYNSSRSVG

SATGGASFADLRGIGANKTLVLLNGRRLANNAIDGSAVDLNTIPFAAIDR

VEVLRDGASALYGTDAIGGVINFITRKSLNEGRFDSGYASPTHDGGGNQR

NVSASWGFGELEEDRFNVFAVANYDKQERLGAKDRGYTYNYQPGRGLDYS

SGTAFPGNWSQGANASNPLAAGGCKGADLIPRNGICRQSLWRYLDLVPET

EKTSVFSRATGKLADEHNVSLEYFWSRSDNATQVGPGTLTGLQIDPGTAF

YPGNGITPGPGGFVLDPSRPVEVNWRQSVLGPRLQSSQNTGQRLLLGFDG

QFAGWDYDIGASYNQNKVVDHIHSGYVDDRAAALGIANGTLNPFGPQTDA

GLAYLGSHALSGDFRTSVGRVKGLDARASREIGDWFGAGPAALALGGEFR

KEAFHQDIQDFAGNVQSLGVDPAATVSGERNLKAQYAELNVPVLDSLELS

AAIRHDKYSDFGSTSNPKYSFRFQPFRQLVLRGAYSEGFRAPSLYELYNP

TFTTYTSANYDDPRLCAGGQPSQGGIANRDCAQQFYNATGGNTDLRPETA

RNVTLGLVYQPLRDLSVGLDFWWIRIANQIAEFPEAAIFADPQAYAGRIV

RKADGSIDHVVTGLANLGKVKTSGVDLSLDYRFPASRYGQFGLDLQGTYV

SRYDFQQQIGGQYLDNVGDFQGVGVIARWKHVANATWSRDAWQATLSNRY

TSGYNDYDRASHGKVGSWNLWDLAGSYRLSHALGLTLGVKNLFDREPPFS

NQTYTFQSGYDPRYTDPYGRILFGRLSYSF

SEQ ID NO: 23

MVRLRTLVRAIAAASVLTSGMAHGLGLGEITLKSALNGLDAEIELLEVRD

LGSGEVIPSLASPEEFSKAGVDRLYYLTDLKFTPVVKPNGKSVIRVTSSK

PVQEPYLNFLVQVLWPNGRLLREYTVLLDPPLYSPQAAASAPQAPVSAPR

ATGAPRAPQAPAPVRTTAPAGSDTYRTVSNDTLWEIAQRNRTDRVSVPQA

MLAFQELNPGAFVDGNINRLKSGQVLRIPTEQQMLERSPREALSQVQAQN

QSWRGSRNPAAGSAGAQLDATQRNAAGSAPSKVDATDNLRLVSGEGKASK

GADKGGKGDSKAIADTLAVTKESLDSTRRENEELQSRMQDLQSQLDKLQK

LIQLKDAQLAKLQGQLGAEGQGAAQPNAALPDASQPNAAAQAPAQPGTPA

AAAPTPAPAGEAPAAPAQPPVAPPPAPAAEKPPAPAVPAPAPVQAAEQPA

PSFLDELLANPLWLAVIGGSALLALLVLLMILSRRNAQKEKEEAQAFAAD

TGEEQEDALDLGKDGFDDLTLDEPEPQVAAVAPQVEKTTAQTSDALGEAD

-continued

IYIAYGRFNQAAELLQNAIYDEPQRTDLRLKLMEVYAEMGDREGFARQNE

LREIGGAQPQVEQLKSRYPAMVAVAAVAGLAGAKLAQDELDSFSLDDLSL

DDSGHAAKPDAAGQDLDDAFDLSLDDLGGDDVQADLKSDSGALDDLTLDS

DLDLAASTPADKPVDDLDFGLDFAELAETPSQPKHDDLGDFSLDLDAPED

KLSDDDFLLSLNDEVPAAAPADNEFTLDTEAAEEPALSLPDDFDLSLADE

PTEPAAPEKGEDSFAAQLDEVSAQLDELASNLDEPKSATPSFSAEDAAVA

SALDGDADDDFDFLSGADEAATKLDLARAYIDMGDSEGARDILDEVLAEG

NDSQQAEARELLERLA

SEQ ID NO: 24

MTDDHSFRPRPTSLSAALLLGAWIAQPATAAYVEAGRPGDPASWRSAEYQ

QDWGLERMRADQAYAAGIDGQGVKIGEMDSGFDPSHPDTPASRYQPVTAS

GTYVDGTPFSVSGAMNGNNDSHGTHVGGTLGASRDGVGMHGVAYAAQVYV

ANTNQNDSFLFGPTPDPNYFKAAYQALADAGVRAINNSWGSQPKVSYETL

DGLHAAYAQHYGRSTWLDAAAGVSRQGVINVFSAGNSGYANASVRSALPY

FQPDLEGHWLAVSGLDQQNGQRYNRCGIAKYWCITTPGRLINSTMPGGGY

ANKSGTSMAAPHATGALALVMQRYPLNNEQALQVLLTTATQLDGTPTGAP

TDTVGWGVPDLGRAMHGPGQLLGRFEANLPAGLRDEWSNPISDSALLQRQ

AEDAAEHAAWQRTLKDKGWENGLPAGASQQERTDYAIGMARDQAAAQRQY

QGSLVKAGAGSLVLSGDSTYRGPTLVDGGLLSVDGSLLSAVEVNAGGTLG

GSGRIGGLLARSGGTVAAGNSIGTLEVAGDLRFESGSTYAVELSESASDR

IVASGKASIAGGNVTLAMENSPDLLSQSQVESLVGRRYDILDAAGGIDGR

FDAVLPNYLFLGGTLDYAANAIRLDIGRNGTTLASVAQTPNQAAVAGAVE

TLGAGNPVYESLLLSENAATAQRAFQQLSGEIYPALAGLLLNDSRYLRDS

VGERLRQTSDGEAGGEAPEGWFKALGSWGKSADGSHGSEGYRHSVGGFLL

GVDSQVASDTRLGLVAGYSNSSLNMDSSLQSSASIDSYHLGAYLGRQLQQ

WRLSLGAAHAWHRAEVKRDLQYGAVAGKQKAKLDAQSSQLFAEAAYALGW

RSLELEPFAGLAYVHVASDDFRERGSAAALEGGDDNLDAAFTTLGLRAKR

HFELDAGRRLALSGTLGWRHNLSDTTPQRHLAFASGSQPFSVESVALSRD

AALLGVDASLAVNREVSVRLGYNGLLGSREKDHGVGLAVDWRF

SEQ ID NO: 25

MKRMLINATQPEELRVALVDGQRLFDLDIESGAREQKKANIYKGRITRVE

PSLEAAFVDFGAERHGFLPLKEISREYFKKSPEGRINIKEVLSEGQEVIV

QVEKEERGNKGAALTTFISLAGRYLVLMPNNPRAGGISRRIEGEERNELR

EALNGLNAPADMGLIVRTAGLGRSTEELQWDLDYLLQLWSAIKEASGERG

APFLIYQESNVIIRAIRDYLRQDIGEVLIDSIDAQEEALNFIRQVMPQYA

SKVKLYQDSVPLFNRFQIESQIETAFQREVKLPSGGSIVIDPTEALVSID

INSARATKGGDIEETALQTNLEAAEEIARQLRLRDIGGLIVIDFIDMTPA

KNQRAVEERVREALEADRARVQVGRISRFGLLEMSRQRLRPSLGETSGIV

CPRCNGQGIIRDVESLSLAILRLIEEEALKDRTAEVRARVPFQVAAFLLN

EKRNAITKIELRTRARIFILPDDHLETPHFEVQRLRDDSPELVAGQTSYE

-continued

MATVEHEEAQPVSSTRTLVRQEAAVKTVAPQQPAPQHTEAPVEPAKPMPE

PSLFQGLVKSLVGLFAGKDQPAAKPAETSKPAAERQTRQDERRNGRQQNR

RRDGRDGNRRDEERKPREERAERQPREERAERPNREERSERRREERAERP

AREERQPREGREERAERTPREERQPREGREGREERSERRREERAERPARE

ERQPREGREERAERPAREERQPREDRQARDAAALEAEALPNDESLEQDEQ

DDTDGERPRRRSRGQRRRSNRRERQREVSGELEGSEATDNAAAPLNTVAA

AAAAGIAVASEAVEANVEQAPATTSEAASETTASDETDASTSEAVETQGA

DSEANTGETADIEAPVTVSVVRDEADQSTLLVAQATEEAPFASESVESRE

DAESAVQPATEAAEEVAAPVPVEVAAPSEPAATEEPTPAIAAVPANATGR

ALNDPREKRRLQREAERLAREAAAAAEAAAQAAPAVEEIPAVASEEASAQ

EEPAAPQAEEITQADVPSQADEAQEAVQAEPEASGEGAADTEHAKKTEES

ETSRPHA

SEQ ID NO: 26

MKSVLHQIGKTSLAAALSGAVLLSAQTTHAAALSVSQQPLMLIQGVAPNM

LVTLDDSGSMAFAYAPDSISGYGNYTFFASNSFNPMYFDPNTQYKLPKKL

TLVNGQVQIQDYPAPNFSSAWRNGFTRSGSINLSNSYKVTIEYGRGYDKE

STIKADAAYYYDFTGSSSCNRTNQACYTRRYVSTEQRQNFANWYSFYRTR

ALATQTAANLAFYSLPENARVSWQLLNDSNCNQMGSGSSSGNCFSNYLRD

FTGQHRVNFFNWLEKLSVNGGTPLRQAMTRAGEFLKKTGVNGPYAYRPGT

QTAPEYSCRGSYHILMTDGLWNNDSANVGNADSTARNLPDGKSYSSQTPY

RDGTFDTLADQAFHYWATDARPDIDDNIKPYIPYPDQANPSAEYWNPRND

PATWQHMVTYTLGLGLTTSLTSPRWEGSTFSGGYNDIVAGNLSWPRASNN

DSNNVYDLWHAAVNSRGEFFSADSPDQLVAAFQDILNRISGKDLPASRPA

ISSSLQEDDTGDKLTRFAYQTSFASDKNWAGDLTRYSLTTQDKATVQTKL

WSAQSILDAMPNGGAGRKIMMAGSGTSGLKEFTWGSLSADQQRQLNRDPD

RNDVADTKGQDRVAFLRGDRRKENSDNFRTRNSILGDIINSSPATVGKAQ

YLTYLAQPIEPSGNYSTFAEAQKTRAPRVYVGANDGMLHGFDTDGNETFA

FIPSAVFEKLHKLTARGYQGGAHQFYVDGSPVVADAFFGGAWHTVLIGSL

RAGGKGLFALDVTDPANIKLLWEIGVDQEPDLGYSFPKPTVARLHNGKWA

VVTGNGYSSLNDKAALLIIDLETGAITRKLEVTGRTGVPNGLSSPRLADN

NSDGVADYAYAGDLQGNLWRFDLIAGKVNQDDPFSRANDGPAVASSFRVS

FGGQPLYSAVDSAGAAQAITAAPSLVRHPTRKGYIVIFGTGKYFENADAR

ADTSRAQTLYGIWDQQTKGEAAGSTPRLTRGNLQQQTLDLQADSTFASTA

RTIRIASQNPVNWLNNDGSTKQSGWYLDFMVNGTLKGEMLIEDMIAIGQV

VLLQTITPNDDPCADGASNWTYGLDPYTGGRTSFTVFDLARQGVVDSKSD

YSYNKQNVAVSGTEQKGLGGLTLSTNEQGNPEVCSSGECLTVNPGPNTRG

RQNWRPIEGKN

SEQ ID NO: 27

MKILAIRLKNLASLAGEQEIDFTREPLSSAGLFAITGPTGAGKSTVLDAL

CLALFGSTPRLESTSASSKVPDGRNELSSNDERNLLRRGCASGYAEVDFV

-continued

GIDGHRYRARWETRRSRDKADGALQKSQQSLQDLETQQMLAANKKSEFRE

QLEQKLGLNFAQFTRAVLLAQSEFSAFLKASDNDRGALLEKLTDTGLYSQ

LSKAAYQRASQADEQRKQLEQRLEGSLPLAEQARAGLEAALESHAQARLQ

EQQALQRLEGQQQWFTEEQRLLQSCEHAQGQLAEARQAWDALATERETLQ

WLERLAPVRGLIERLKQLEQELRHSEQQQRQRTEQQAAGTERLQGLQARL

QEARERQAQADNHLRQAQAPLREAFQLESEARRLERTLAERQELHRQSNQ

RHAQQSDAARQLDMEQQRHVAEQAQLQAALRDSQALAALGDAWVTHQGQL

ATFVQRRQRALESQAQLPELEKSLAHAGEPLERLQAQWTALHGSEPDDLA

ARLVELRRQTDSLERQQALHKEWQQVLDQRAGLARRLGELDQRMVEQEQA

LLDLKRQGSQCAEEVKAAEQALQVTRELLQRQRLARSASVEQLRAGLVDG

EACPVCGSQEHPYHHSEQLLAALGEHDDQEQVRAEQSLERLRQTLVGLRE

GYSSQRERLNQSRQEQQELTGQLAALDRQLDQWTLPEELRLLQPSAQLEW

LAQRLDDLAGQRQQCQRDFDRLIARQRQTQQLQQELRAAETILQQRQQAL

TEQRQRYEHLQQQVEEDSQQLRPLLSDEHWQRWQADPLRTFQALGESIEQ

RRQQQARLQQIEQRLQELKQRCDESSWQLKQSDEQRNEARQAEERAQAEL

AELNGRLGAHLGQHACAQDWQLSLEHAAQAAQSAVETLQAPLDSLREEQL

RLAEALEHLQQQRQRQQDEFQRLQADWQAWRERQDNLDDSRLDALLGLSE

EQATQWREQLQRLQEEITRQQTLEAERQAQLLQHRRQRPETDREALEDNL

RQQRERLAASEQAYLETYSQLQADNQRREQSQALLAELERARAEFRRWGR

LNELIGSSSGDKFRRIAQGYNLDLLVQHSNVQLRQLARRYRLQRGGSELG

LLVVDTEMGDELRSVYSLSGGETFLISLALALGLASMASSKLRIESLFID

EGFGSLDPESLQLAMDALDNLQAQGRKVAVISHVQEMHERIPVQVRVQRE

GNGMSSLKVVG

SEQ ID NO: 28

MSIQAKVTPIDQSISSAAAVEVPENGILKLSQSSNVALDVAPESVAGYSK

SGSDLIVQLKTGESVRIANFYAEGQPSSQLFLADKDKLVAVDLPPVAADG

PLMAGYIPQESLAGFESLTGAGVLGGMSAGTALLVGAAAIGAGVAISNSS

GGGGGGGSSVPPDTTPPKAASGLKIAPDGSSISGQAEAGASVGIDTNGDG

KPDLTVIADANGNFTAPLNPPLTNGQTVTVVVTDPAGNASPPAQVTAPDT

TAPAPATDVQVAPDGSSVTGKAEPGSTVGVDTDGDGQPDTTVVVGPGGSF

EVPLNPPLTNGETVTVIVTDPAGNNSTPVTVEAPDTTAPAPATDVQVAPD

GSSVTGNAEPGATVGVDTDGDGQPDTTVVVGPGGSFEVPLNPPLTNGETV

TVIVTDPAGNSSTPVTAEAPDFPDAPQVNASNGSVLSGTAEAGVTIVITD

GNGNPIGQTSADANGNWSFPGSQLPDGTVVNVVARDAAGNSSPATSITVD

GVAPNAPVVEPSNGSELSGTAEPGSSVTLTDGNGNPIGQTTADANGNWSF

TPSTPLPDGTVVNVVARDAAGNSSPPASVTVDAVAPATPTVDPSNGTTLS

GAEPGSSVTLTDGNGNPIGQVTADGSGNWTFTPSTPLPNGTVVNATATDP

SGNASSPASVTVDAVAPATPVVNPSNGTTLSGTAEPGATVTLTDGNGNPI

GQVTADGSGNWSFTPTTPLPNGTVVNATATDASGNTSAGSSVTVDSVAPA

-continued

TPVINPSNGTTLSGTAEPGSSVTLTDGNGNPIGQVTADGSGNWSFTPSTP

LADGTVVNATATDPAGNTSGQGSTTVDGVAPTTPTVNLSNGSSLSGTAEP

GSTVILTDGNGNPIAEVTADGSGNWTYTPSTPIANGTVVNVVAQDAAGNS

SPGASVTVDSQAPAAPVVNPSNGTTLSGTAEPGATVTLTDGNGNPIGQVT

ADGSGNWSFTPGTPLANGTVVNATASDPTGNTSAPASTTVDSVAPAAPVV

NPSNGAEISGTAEPGATVTLTDGSGNPIGQVTADGSGNWSFTPSTPLADG

TVVNATATDPAGNTGGQGSTTVDAIAPATPTVNLSNGSSLSGTAEPGSTV

ILTDGNGNPIAEVTADGSGNWTYTPSTPIANGTVVNVVAQDASGNSSPPA

TVTVDSSAPPAPVINPSNGVVISGTAEAGATVTLTDAGGNPIGQVTADGS

GNWSFTPGTPLANGTVIVATATDPTGNTGPQAATTVDAVAPPAPVIDPSN

GTTISGTAEAGAKVILTDGNGNPIGETTADGSGNWSFTPGTPLANGTVVN

AVAQDPAGNTGPQGSTTVDAVAPNTPVVNPSNGNLLNGTAEPGSTVTLTD

GNGNPIGQTTADGSGNWSFTPGSQLPNGTVVNVTASDAAGNTSLPATTTV

DSSLPSIPQVDPSNGSVISGTADAGNTIIITDGNGNPIGQVTADGSGNWS

FTPGIPLPDGTVVNVVARSPSNVDSAPAVITVDGVAPAAPVIDPSNGTEI

SGTAEAGATVILTDGGGNPIGQATADGSGNWTFTPSTPLANGTVINAVAQ

DPAGNTSGPASVTVDAIAPPAPVINPSNGVVISGTAEAGATVILTDGNGN

PIGQVTADGSGNWSFTPGTPLANGSVINALAQDAAGNNSSPTSATVDSLA

PAAPVIDPSNGSVIAGTAEAGATVILTDGNGNPIGQVTADGSGNWSFTPG

TPLSNGTVVNAVAQDAAGNTSGPVSTTVDAVAPATPVIDPSNGVELSGTA

EPGVRVILTDGNGNPIGQTLADGSGNWSFTPGTPLANGTVVNAVAQDPAG

NTSGPASTTVDTVAPATPVINPSNGSVITGTAEVGAKVILTDGNGNPIGE

TTADGSGNWTFTPGTPLANGTVINAVAEDAAGNASGPASTTVDSVAPSAP

LLSISADGALLTGTAEPNSQVRIVVNGDTANPITVTVDGAGNFSLPFAPP

LITGELIAGVAVDAAGNVSGPATINAPDLAPPTISVPEAADTWINAAEIG

DGIQVDVTVRPTMQVGQVVTVKFAGQNGYEAEVSHTLTAGDIAAGNLTLT

LTPPGGMGPFPEGASTVTADINGGTASTPVPFTIDTIPPATPVLSLVGNI

LTISAEPGTELTVTVDVGGVTATATVTADNSGLASLNLLTDLDIDFSWDQ

LLNAQVSVVGRDPAGNPSNTASIGVGTSIEQPVTIGNFGLDVSLNPLNPR

FGFSGTTEPDSSVVIRVITPALNVELLPIQADSSGNFSLNLLSPTILTQL

GLNITDILNLGSQ1SFNLVSTDSNGNDSAAYGITLTPNGLSLNIGQIDVN

GTSGDDVLSGANGSSEHINGGDGSDLIFNVGTGDHVVAGNGNDTIQITAT

DFVSIDGGAGFDTLVLANGIDLDYNAVGVGTLSNLERIDLGKGDSGSVLT

LTAAEVDAITDANNTLQITGENNDTLNVVGAVNTGTTQLINGITYDVYTF

GSTTLLIEDNTVQVVV

SEQ ID NO: 29

MDIRSPLNQCIALSLAGILFLNPIVAAAAGLALDKAAGGNTGLGQAGNGV

PIVNIATPNDAGLSNNHFRDYNVGANGLILNNATGKTQGTQLGGIILGNP

NLKGQAAQVILNQVTGGNRSTLAGYTEVAGQSARVIVANPHGITCQGCGF

INTPRATLTTGKPIMDGQRLERFQVDGGDIVVEGAELNVGNLEQFDLITR

-continued

SAKLNAKLYAKNLNIVTGRNDVQADSLQATPRAADGSEKPQLAIDSSALG

GMYAGAIRLVGTEQGVGVRLAGDMAASGGDIRIDASGKLSLAQASSQGDL

KIAAQAVELNGKTYAGGSAEIRSAEELVNRQSLAARERIVLEAAHIDNAG

VIEAGVEPDERRNARGDLELRSGTLRNAGSLVASRALEAKASQALDNQGG

SLKGATVRVDAGHLDNRGGKLLAEGELRVEASSLDNRQDGLLQSRDRAVV

KTRGDLDNRGGQVIGLNDLEVGAATLDNGQQGLLGSQQSTRVSAQALVNR

GDGEVSGKRVEARVGSLDNRGGKLIGDDLLVVASGAIDNRLGLFSAANRL

DLRARSLDNSGKGTLSSRGGLEVSLGGLLDNRDEGNLLSQGAQRVTVGQL

DNRAGGLLSSRSELNVHGASLDNRGGVLVADAGLSATGGAFDNRDGGSAS

GKAGVRVEVASLRNDQGGKLLSDGRLDLAANAVGNAGGRIAAKGDLQATL

GSLAQQGGELVSEKTLKVAADTLDNSQSGLIAANGGIAIEARQVDNRAGE

ISSTSKVAVNAREQLDNRGGKVIGDSGLRLTVQRLLNQAKGVLAGRDGLS

LDGGELFNGDGGRLDSQNSLSVSLGGVLDNQGGALVSEGSLTARAARLDN

RGGTFSSAGALALTSQAALDNQGGRLLSDAGVTLQGASLDNSRSGVISAK

GAVDIRTGVLDNSRNGGIGSNAGITLVAARLDNGQQGRVSAKGLLDANLK

GLDQRGGGVLISETGVTLDLNGGTLVNRDGGLIATPGALLLRQLGAVDNG

AGGEISSDRAFTLAAASLDNRGGRLIGAANLTLRIAQALDNSLAGVISGA

AGLDIAAARLDNSAKGTLASRAGIDLRVDGALDNHAEGTVSGARLTLASA

SLDNSGKGLLSGNAGLSVATGALDNAEGGQLISQGVLDVSSADLDNRGGA

LSGKQSLRLSAANLDNRGGLLTSDGELELTAGRVDSADGGEISARGDLRL

TVERLVQRQGRLVGERGVSLDLRGGDLDNQGGLISARGPLSIERLSVLDN

RQGGEISSQQGFELLARRIDNGQQGRIISAGKLRLDADALGNAGAGLLSG

WQGLTVTGGSLDNSAGGTLSSKDGELAISLGGALDNHGQGALVSKGAQRI

DAASLDNAQGIVSGESDVTLSIAGKLDNGQGGLVSAQRALSFERDDTLLN

NAGGRINGGSLLLKGASLDNSDGQLISQGRLDAILGGALVNTGAARLASG

GDLLLRSASVDNRGGKLVSQGLLEISAGSLDNSASGTLASQAGMSLRLGG

GALRNQQDGLIFSQAGALDVQAGSLDNRQGTLQAQGDNRLRIGGALDNQG

GRLDSRAGNLDLQSGSLDNGAGGVLNSAKGWLKLVTGLFDNSAGVTQAQS

LEIRAGQGVRNQQGHLSALGGDNRIVTADFDNQGGGLYASGLLSLDGQRF

LNQGAAAGQGGKVGAGRIDFSLAGALANRFGQLESESELHLRAAAIDNSG

GSLRALGRSGSTRLVAGGLNNAYGVLESANQDLDLQLGSLANAGGRILHT

GNGTFGLDSGQVIRAGGELTTNGLLDIRASEWTNSSVLQAGRLNLDIGTF

RQTAEGKLLAVQSFTGRGGDWSNDGLLASDGSFRLDLSGGYRGNGRATSL

GDFALNAASLDLGNAASLAGGANVTLGAGNLLVNRGRITAAGDLVASAAS

LNNYGTLGGGGNLRLNAPALLNERGLLFSGADMTLRAGDITNLYGDVYSL

GRLDIARDDAGNRAASLRNLSGVIESGKDFSLRASLIENRRAVLESKSGL

YTAKMEQTACIEGVNAGDCSGKRNAIWTITQRDKTEVTASSAMGQLLAGG

DFAIDGGTLNNLSSLIGSGGNLTANLEVLDNQGLETGELETIRVLRTARG

GDIGGIDQKSRNFTNLYWYQSANFDPARAGEIPAALNAILSDWSFEYEFP

-continued

SKGPTPISSGDQSYAAVIQAAGDVTVNASTRIDNGVTRPGYTFVGSGRQV

GDSAVGGSGVSVVVPLTSQLPPDLARRQVNPVTLPGFSLPQGDNGLFRLS

SRFAEDGNGSAALGAGADRTQGGSGVSVGQQGAGNAAGTWQGQGVRVDGL

AGAANVQGQGGSTLGGSLPGVARVQGVPGNATPSASKYLIETNPALTELK

QFLNSDYLLSGLGMNPDDSKKRLGDGLYEQRLIRDAVVARTGQRYIDGLS

SDEALFRYLMDNAIAYKDQLHLQLGVGLSAEQMAALTHDIVWLEEVEVNG

EKVLAPVVYLAQAEGRLAPNGALIQGRDVKLVSGGDLHNVGTLRARNDLS

ATADNLDNSGLIEAGKRLDLLAGDSIRNRQGGVIAGRDSLTALTGDVINE

RSVTRYDSALDGRTWERSFADSAARVEAANSLNVQAGRDIANLGGVLQSR

GDLSLDAGRDVTVAAVEDRQGQTRWSTSRLQSVTQLGAEVSAGRDLNVSA

GRDLTAVASTLEARRDIALSAGRDVTLAAAANEEHAYSKTRKVTYQEDKV

AQQGTRVDAGGDLAINAGQDLRLIASQASAGDEAYLVAGDKLELLAANDS

NYYLYDKKKKGDFGRKETRRDEVTDVKAVGSQISSGGDLTLLSGGDQTYQ

GAKLESGNDLAIVSGGAVTFEAVKDLHQESHEKSKGDLAWNSAKGKGQTD

ETLRQTQIVAQGNLAIKAVEGLKIDLKHIDQKTVSQTIDAMVQADPQLAW

LKEAEQRGDVDWRMVQEVHDSWKYSNSGMGPATQIAVAIAAAAIGGMAAA

GALSGAGVGASSFAMGAGVGAAGSLSGTAAVSLINNKGDLGKVLKDSFSS

DSLKQIAIASLTGGLTAEYFDGILQTKTDPLTGKVTVDLSSLSGVGRFAA

NQAMQNATSTVLSQALGQGGSLNEALKSALYNSFAAAGFNFVGDIGQEYS

LKPGDPSMVTMHALMGGLAAQVSGGDFATGAAAAGANEALVAKLDQAFKS

LSPENREAMVTMGSQLVGVLAAAVRDPDVTGKALESAAWVAKNSTQYNFL

NHQDVADLDNALQKCKSQGNCRQVEEEFKARSDENRRRLNGCVAVGNCAE

IRAEIDAGSTALNELVARQETANPGGSDSDIAYGFLMGRNVVDWTTAGQL

HLEQTANLWWNGNPQWQKEVGAYLDQTGFNPFGIGVPAMGGAAGKVTAKA

LMNALKAGELPKGEVAPGKANLPTIGALADAEAGMPYTHPVKLAAKATGT

AGKIKIEAGAIPDANEVRAGQGLSGLGYDVTHQTTASAKGIQGQRTADLH

VDGLGSIDVYTPKNLDPTKIVRAIEKKSNQAGGVLVQADLPSTDMSSIAA

RMWGKTNAQSIKTIFFQKPDGSLVRFDRPAGGG

SEQ ID NO: 30

MDIRSPLNQCIALSLAGILFLNPIVAAAAGLALDKAAGGNTGLGQAGNGV

PIVNIATPNGAGLSNNHFRDYNVGANGLILNNATGKTQGTQLGGIILGNP

NLKGQAAQVILNQVTGGNRSTLAGYTEVAGQSARVIVANPHGITCQGCGF

INTPRATLTTGKPIMDGQRLERFQVDGGDIVVEGAELNVGNLEQFDLITR

SAKLNAKLYAKNLNIVTGRNDVQADSLQATPRAADGSEKPQLAIDSSALG

GMYAGAIRLVGTEQGVGVKLAGDMAASGGDIRIDASGKLSLAQASSQGDL

KIAAQAVELNGKTYAGGSAEIRSAEELVNRQSLAARERIALEAAHIDNAG

VIEAGVEPDERRNARGDLELRSGTLRNAGSLVASRALEAKASQALDNQGG

SLKGATVRVDGGHLDNRGGKLLAEGELRVEASSLDNRQDGLLQSRDRAVV

KTRGDLDNRGGQVVGLNELQVQAAALDNRSAGLLSSKGDMDIEFARLDNS

-continued

AGGKLVSERRTLLKADRLDNRSGRIVAGQDLDLSSRLIDNRAGDISSTSR

VVASAREQLDNRGGKIVGDSGLDITTPRMLNQDKGVLASRDGLRLSATEL

FNGAGGLLSSQKGIDVSLAGAFDNQAGSLDSRGFLTVKSAWLDNQGGTLS

SAGALAVTSQGALNNQGGRLASDAGLSLSSASLDNSQAGAISGKGAVEIR

TGNLNNSRKASIGSDAGLTLVAARVDNSQAGRIAAKGVIDADLQGLDQHD

RGNLVSDTGITLDLNKGSLVNRAQGLIATPGTLLLRQLGVVDNSGGEISS

DRAFTLATSALNNQGGRLLSGGALTLRIAQALDNSLEGIVSGAGGLDIQA

FVLDNRSGSIGSKGAIDIGVTRLENDAGTLIAERGLKLVADEANSSKGRI

AANGSLHAKVGTLSQKGGELTSQDSLTLDLGILNNNAGRIAGNQGVDITA

RQVDNSVGEIASQGVVALNLTEQLDNRGGKIVGDSGLGITAPHVLNQDKG

VLASRDGLRLSATELFNGAGGLLSSQKGIDVSLAGAFDNQAGSLDSRGFL

TVKSAWLDNQGGTLSSAGALAVTSQGALNNQGGRLASDAGLSLSSASLDN

SQAGAISGKGAVEIRTGNLNNSRKASIGSDAGLTLVAARVDNSQAGRIAA

KGAIDAALQGLDQHDRGSLVSDTGITLDLNKGSLVNRAQGLIATPGTLLL

RQLGVVDNSGGEISSDRAFTLATSALNNQGGRLLSGGALTLRIAQALDNS

LEGIVSGAGGLDIQAFVLDNRSGSIGSKGAIDIGVTRLENDAGTLIAERG

LKLAADEANNSKGRIVAKDELRAKLGALVQNGGELTTQGALALDADKVDN

GAGRIAGNRGVVIDARQVDNRAGEIASQGVATLNLTEQLDNRGGKVVADS

GLGITAPRVLNQDKGVIASRDGLRLSGTELFNGNAGLLSSQRHIEVTLDG

VLDNQGKGALLSDGTLTVSAGRIHNQDATLSSAGALRLSSQEAVDNRGGK

LVTDSSLRLTSASLDNSRSGIISANAAAEIHTGVLNNSQKGNLGSNDGLG

LIATEVDNSQEGRITAKGMIDANIKGLDQQGKGRLVSNAGIILDLNEGTL

ANGAQGLIATPGTLLLRQLGMVDNSGGEISSDRAFTLTTSALTNQGGRLR

SGGVLTLRIAQALDNSLEGVLSGTGGLDIRALALDNRSGSIGSKGAVDID

VSRLENDDGDLLSEGRLKLTAERANSVRGRIAARGDLHASVTAFNQAGGE

LSSEGALMLEADSLDNRSGGLVSADGNLTVSARRIDNRAGEIASPGQVTL

DVAEQLDNRGKAIGDSGLRLAAPRVLNQDGGVLASRDGLRLNGAELFNGN

GGLLSSQQSIDVILDGVLGNQAGSLSSQGRLSVKSGRLDNQGGAVSSAGT

LSLSSQGALNNQGGRVVTDAGAVLRSASLDNSQGGIVSAKGAAEIRTGSL

NNSQKGGIGSGAGLALVADLVDNSQNGRITAKGAIDANLKGLDQQGSGRL

VSDTAIALDLRGGELVNRAQGLIATPGALLLRQLGVVDNSGGGEISSDRS

FTLAATALSNRGGRVISGDSLTLRIAQALDNSLQGVLSASGGLDVAALVF

DNHSGIVASKGDTHIGVNRLENEAGRVVSEGALDLTAKQVSSAKGRIAAK

GDLQVTVGTLEQQGGELASQGTLTLDADSLDNRNGGLVSADGGVTAEARQ

IDNRGGEISSVAKVALAVREQLDNRGGKVIGDSELSLTVQRLLNQAKGVL

ASRDGLHLDGAELLNGDGGLLSSQRLVDVTLSGALDNQGSGALVSEESLT

VKADQVNNQAGTFSSAGSLLVTSRGELNNQGGRLVTDAGATLNSTGFDNS

RAGLVSAKGAVAIRTGALNNSQKGSIGGNTGVTLVAGLVDNGREGRISTK

GTLDANLKGLLQQGGGSLVGERGVTLDLNGGTLDNHDLGLVSTPGALLLR

-continued

QLGMVDNSVGGEISSDRAFTLAANTLNNQGGRLISSEALTLRIAKTLDNS

LKGQVLATDGLAIESQVLDNRAGTIGSKGDARISVTSLDNAEQGSLVSEG

RLELVADQVSNGNQGRIAARGVLEAAVGTLLQQGGELVSQGSLDLRADTL

DNSQSGLIAANGGIAIEARQVDNRAGEISSTSKVAVNAREQLDNRGGKVI

GDSGLRLTVQRLLNQAKGVLAGRDGLSLDGGELFNGDGGRLDSQNSLSVS

LGGVLDNQGGALVSEGSLTARAARLDNRGGTFSSAGALALTSQAVLDNQG

GRLLSDAGVTLKGASLDNSRSGVISAKGAVDIRTGVLDNSRNGGIGSNAG

ITLVAARLDNGQQGRVSAKGLLDANLKGLDQRGGGVLVSETGVTLDLNGG

TLVNRDGGLIATPGALLLRQLGAVDNGAGGEISSDRAFTLAAASLDNRGG

RLIGADSLTLRIAQADNSLAGVISGAAGLDIAAARLDNSAKGTLASRAGI

DLRVDGALDNHAEGTVSGARLTLASASLDNSGKGLLSGNAGLSVATGALD

NAEGGQLISQGVLDVSSADLDNRGGALSGKQSLRLSAANLDNRGGLLTSD

GEELTAGRVDSADGGEISARGDLRLTVERLVQRQGRLIGERGVSLDLRGG

DLDNQGGLISARGPLSIERLNVLDNRQGGEIYSQQGFELLARRIDNGQQG

RIISAGKLRLDADALGNAGAGLLSGWQGLTVTGGSLDNSAGGTLSSKDGE

LAISLGGALDNHGQGALVSKGAQRIDAASLDNAQGIVSGESDVTLSIAGK

LDNGQGGLVSAQRALSFERDDTLLNNAGGRINGGSLLLKGASLDNSDGQL

ISQGRLDAILGGALVNAGAARLASGGDLLLRSASVDNRGGKLVSQGLLEI

SAGSLDNSASGTLASQADMSLRLGGGALRNQQDGLIFSQAGALEVQAGSL

DNRQGTLQAQGDNRLRIGGALDNQAGRLDSRAGNLDLQSGSLDNGAGGVL

NSAKGWLKLVTGLFDNSAGVTQAQSLEIRAGQGVRNQQGHLSALGGDNRI

VTADFDNQGGGLYASGLLSLDGQRFLNQGAAAGQGGKVGAGRIDFSLAGA

LANRFGQLESESELHLRAAAIDNSGGSLRALGRSGSTRLVAGDLNNAYGV

LESANQDLDLQLGSLANAGGRILHTGNGTFGLDSGQVIRAGGELTTNGLL

DIRASEWTNSSVLQAGRLNLDIGTFRQTAEGKLLAVQSFTGRGGDWSNDG

LLASNGSLRLELSGGYRGNGRATSLGDFALNAASLDLGNAASLAGGANVT

LGAGNLLVNRGRITAAGDLVASAASLNNYGTLGGGGNLRLNAPALLNERG

LLFSGADMTLRAGDITNLYGDVYSLGRLDIARDDAGGWANRLENISGNLE

STGDMRFSVSSLLNRRETLEIEGDLQNSAIGVRCTGCQLSERWGKTRSSS

ELVWIREYKSTLGDSSAAASITAGRDLLVVGASLQNIASNISAVRDATLS

LSNFENKGYALGEYAVRGVYSPPSKFGEELLMRILAYNAVNDPSYGEGYA

STGGRLPNIHYFDKNFNEKVSPLEVIHGNGKNGGPGWHLYFGTLDVEYPD

TDRWNKAIGRIPAPNYSSKKTDAIPDLLKGLAPLDELTINKGANSTVGAV

VQAGGRVTVNAAESFNNSVLQGFQAVQETQLPHQDIAVSSTTSAVVTLKS

QLPADLARQQINPLTLPGFSLPQGQNGLFRLASQGAQVNQASGALKSASD

LTQSGHGVSVSAQTGSGASGWSTQARRVGDDRVTSLAGSAYQGRVAEAID

ALRASAPISGDGGNTGRFQAGEHQATTGLGGLVEGNASGHSGNGVILADL

RGGLPSFSSLPASDHVQGTVPGHDGNGTILANWQGAQATVQASPSTVRVE

GVVSSPGGNGSILADLPAEQSSVQALPSAVRAQGSLPRLEERSALLAEPP

-continued

VGQPALQTLPSVARVEGVPSNATPSNSHKYLIETNPALTELKQFLNSDYL

LGGLGINPDDSKKRLGDGLYEQRLVREAIVQRTGQRFIAGLNSDEAMFRY

LMDNAIASKDVLGLTPGVTLSAAQVAALTHDIVWLEEVEVNGEKVLAPVV

YLAQAEGRLGPNGALIQGRDVNLITGGDLRNAGTLRAQNDLSATAGNIDN

SGLIEAGNRLDLLASGSIRNDQGGIIAGREVSLSALTGDVINERTVTQHQ

SSYRGTGTTEAFADSAARIEAAQKLTVSAGRDVANIGGVIDSKGDLALQG

GRDVLVSAAVAERGWTAGSQAYQTQTTQMGAEVVAGRDISVSAGRDISVV

GSRIDARRDVTFEAGRDVGLVAAANEEHAYGKTKKVTFQDDKITQQATRV

DAGGDLAINAGQDLRLVASQASAGDEAYLVAGDKLELLAANDSSYYLYDK

KSKGSFGSKKTRRDEITDVTAVGSQISSGGDLTLLSGGDQTYQGAKLESG

NDLAIVSGGAVTFEAVKDLHQESHEKSKGDLAWQSSKGKGQTDETVRQSQ

IVAQGNLAIKAVEGLKIDLKHIDQKTVSQTIDAMVQADPQLAWLKQMEQR

GDVDWRRVQELHDSWKYSNSGLGVGAQLAIAIVVAYFTAGAASAALGSMA

GVGAGSGSMMAAAGSTAMVQAGTAVGTAAAGWANAAGTAVAMGMASNGAI

-continued

STINNRGNLGDVVKDVTSSDALRGYVVAGTTAGLTAGVYDKWTSTQTGTS

TALPNTGAVAPAAGLGTWQGVGQFTSNQLLQNGTSVLLDRALGGKGSLGD

ALQNSLANAFAAYGFKLIGDTTHGVLDDGSLGKIGLHALMGGLAAEAVGG

DFRTGALAAGVNEALVDSLAKQYASLPIDDKKGLLIMSSQLIGVLAASTQ

GDADAKSLQTGAWVAGNATQHNYLSHWQEEKKRQEVDGCKDKQLCKTGIE

AKWAIISAQQDVGIVVGVGGGIGLSTAETAVGVYELVKNWRETYAALEQL

ATSPEFRQQFGDNYLKGLEERAAFLTQAYEDAGWQGSVTAGVEGGRFAAE

LVGVLTAVKGGAQITAKLPTAAKNLVNAIAESPVSGSMSSQLGAVGDLGR

LGGGGKGYVDILSHEAKQHILYGDKPGSGGHLWPGQAGKTVFPQNWSADK

IVHEVGDIATSPSTKWYAQTGTGGVYTSKGDPAKWVAYEVRDGVRMRVVY

QPATGKVITAFPDNAPIPPYKPIK

[0314] The corresponding nucleic acid sequences (DNA in SEQ ID NOs. 31-60 and RNA in SEQ ID NOs: 61-90) are set forth in the electronic sequence listing that forms part of the present application.

SEQUENCE LISTING

```
<160> NUMBER OF SEQ ID NOS: 90

<210> SEQ ID NO 1
<211> LENGTH: 66
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 1

Met Ser Gln Glu Pro His Val His Gly Pro Asn Cys Asn His Asp His
1               5                   10                  15

Asp His His His Asp His Gly His Gly His Val His Gly Pro His Cys
            20                  25                  30

Asn His Ser His Glu Pro Val Arg Asn Pro Leu Lys Ala Val Gly Arg
        35                  40                  45

Asn Asp Pro Cys Pro Cys Gly Ser Glu Lys Lys Phe Lys Lys Cys His
    50                  55                  60

Gly Ala
65


<210> SEQ ID NO 2
<211> LENGTH: 78
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 2

Met Lys Lys Thr Val Thr Leu Ala Leu Leu Leu Ala Ala Ser Leu Gly
1               5                   10                  15

Leu Ala Ala Cys Asp Lys Lys Glu Glu Asp Lys Ala Ala Ala Pro Ala
            20                  25                  30

Ala Pro Ala Thr Glu Thr Gln Pro Ser Ala Pro Ala Thr Pro Pro Ala
        35                  40                  45

Glu Pro Ser Ala Pro Ala Pro Ser Ser Asp Thr Pro Ala Thr Pro Gln
    50                  55                  60
```

-continued

```
Thr Pro Ala Pro Thr Pro Glu Gln Pro Gln Gln Asn Gln Gln
65                  70                  75


<210> SEQ ID NO 3
<211> LENGTH: 104
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 3

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

Gly Val Ala Ser Val Gly Ala His Ala Ala Gln Asn Pro Phe Ala Val
            20                  25                  30

Gln Glu Leu Ser Ser Gly Tyr Ser Val Ala Ala Ala Glu Lys Ala Lys
        35                  40                  45

Glu Gly Ser Cys Gly Glu Ala Lys Cys Gly Ala Asp Lys Gly Lys Arg
    50                  55                  60

Glu Ala Ser Lys Ala Gly His Glu Gly Ser Cys Gly Ala Asp Arg Lys
65                  70                  75                  80

Ala Lys Glu Gly Ser Cys Gly Gly Glu Lys Lys Ala Gly Glu Gly Asn
                85                  90                  95

Cys Gly Ala Asp Lys Lys Lys Ser
            100


<210> SEQ ID NO 4
<211> LENGTH: 155
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 4

Met Ser Val Phe Asp Ser Arg Gln Lys Thr Ser Ala Ser Leu Leu Gly
1               5                   10                  15

Ala Val Leu Val Gly Gly Met Leu Leu Gly Gly Ser Ala Phe Ala Val
            20                  25                  30

Glu Pro Leu Gly Gln Gly Leu Gln Val Ala Ala Ala Ser Ala Gly Glu
        35                  40                  45

Gly Lys Cys Gly Glu Gly Lys Cys Gly Ser Gly Gly Ser Ala Lys Thr
    50                  55                  60

Pro Ala Lys Ala Gly Ala Glu Gly Lys Cys Gly Glu Gly Lys Cys Gly
65                  70                  75                  80

Asp Ala Ser Phe Ala Arg Thr Asp Thr Asp His Asp Gly Lys Val Ser
                85                  90                  95

Arg Ala Glu Phe Leu Ala Val Ala Lys Asp Arg Ala Gly Glu Phe Asp
            100                 105                 110

Ser Ile Asp Ser Asp His Asp Gly Phe Ile Ser Glu Ala Glu Ala Tyr
        115                 120                 125

Glu His Leu Arg Lys Thr Tyr Glu Ala Asn Gly Lys Pro Met Pro Ala
    130                 135                 140

Gly Leu Phe Ser Lys Leu Glu Gln Gly Gln His
145                 150                 155


<210> SEQ ID NO 5
<211> LENGTH: 179
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas aeruginosa
```

-continued

```
<400> SEQUENCE: 5

Met Arg Ser Leu Ser Leu Leu Leu Leu Leu Ser Leu Ala Ser Thr Cys
1               5                   10                  15

Glu Ala Ala Ala Val Phe Arg Cys Glu Asp Ala Ser Gly His Val Ser
            20                  25                  30

Phe Thr Gln Leu Gly Cys Pro Ala Gly Gln Ala Gly Glu Thr Val Val
        35                  40                  45

Ala Asp Asn Pro Pro Pro Gly Gly Arg Ser Val Thr Pro Met Ala Glu
    50                  55                  60

Thr Lys Thr Lys Lys Ala Ser Ile Gly Arg Lys Ser Val Pro Leu Ala
65                  70                  75                  80

Val Ile Gly Glu Arg Glu Asp Arg Cys Gly Arg Arg Leu Asp Glu Lys
                85                  90                  95

Glu Arg Arg Lys Ala Ile Val Glu Gln Arg Ile Met Ala Gly Met Thr
            100                 105                 110

Arg Ser Asp Val Glu Arg Ala Leu Gly Lys Pro Asp Arg Val Ser Gly
        115                 120                 125

Asn Asn Ala Glu Val Arg Tyr Gln Tyr Lys Ala Asp Lys Arg Arg Gly
    130                 135                 140

Ala Arg Ser Val Ser Phe Asp Gln Glu Gly Cys Val Lys Gly Arg Glu
145                 150                 155                 160

Gly Thr Gly Trp Ser Glu Ser Ile Pro Gly Ala Lys Ala Gly Pro Ser
                165                 170                 175

Ser Tyr Arg


<210> SEQ ID NO 6
<211> LENGTH: 304
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 6

Met Ser Gln Pro Ser Glu Asn Arg Leu Ile Thr Ser Ala Arg Tyr Ala
1               5                   10                  15

Leu Cys Leu Leu Thr Ala Ser Gly Val Leu Leu Ser Gly Cys Ala Ser
            20                  25                  30

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

Ser Cys Tyr Glu Pro Val Ser His Leu Arg Ser Thr Asp Asn Ala Val
    50                  55                  60

Arg Asn Ser Ala Ile Thr Gly Ala Ile Thr Gly Gly Leu Leu Gly Gly
65                  70                  75                  80

Leu Ala Gly Gly Leu Ala Ser Asp Glu Asn Arg Gly Arg Asn Ala Ala
                85                  90                  95

Leu Ala Ala Ala Gly Gly Ala Leu Ala Gly Gly Ala Ala Gly Tyr Tyr
            100                 105                 110

Met Glu Lys Gln Lys Gln Ile Ser Asp Asp Arg Ala Arg Ile Gly Ser
        115                 120                 125

Tyr Gly Thr Asp Val Asp Arg Ser Thr Val Glu Ile Asn Arg Ser Val
    130                 135                 140

Ala Tyr Ala Lys Ser Ala Gln Ser Cys Tyr Gln Ser Gln Phe Lys Ala
145                 150                 155                 160

Leu Leu Asp Gly Arg Lys Asn Lys Ser Ile Asn Glu Ala Glu Gly Arg
```

-continued

```
                165                 170                 175

Lys Arg Leu Ala Glu Ile Val Ser Gly Leu Gln Glu Thr Asn Ala Leu
            180                 185                 190

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

Gln Ala Tyr Glu Lys Asp Leu Gln Gln Val Gly Val Pro Arg Ala Glu
    210                 215                 220

Val Thr Lys Val Ala Glu Ala Glu Asn Arg Ala Ser Thr Thr Lys Gly
225                 230                 235                 240

Gly Ser Lys Pro Lys Thr Gly Ser Asn Pro Lys Val Pro Lys Glu Ala
                245                 250                 255

Val Ala Thr Glu Gln Thr Ile Arg Lys Ala Gln Asp Ala Gln Ser Glu
            260                 265                 270

Gly Asn Lys Val Ala Ser Gln Gly Gln Gly Met Ile Arg Glu Val Cys
        275                 280                 285

Asn Ser Pro Asp Met Gly Asp Trp Ala Pro Pro Ser Cys Ala Lys Ala
    290                 295                 300


<210> SEQ ID NO 7
<211> LENGTH: 309
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 7

Met Ala Gly Lys Lys Lys Ser Glu Lys Glu Ser Ser Trp Ile Gly Glu
1               5                   10                  15

Ile Glu Lys Tyr Ser Arg Gln Ile Trp Leu Ala Gly Leu Gly Ala Tyr
            20                  25                  30

Ser Lys Val Ser Lys Asp Gly Ser Lys Leu Phe Glu Thr Leu Val Lys
        35                  40                  45

Asp Gly Glu Lys Ala Glu Lys Glu Ala Lys Ser Asp Val Asp Ala Gln
    50                  55                  60

Val Gly Ala Ala Lys Ala Ser Ala Arg Ser Ala Lys Ser Lys Val Asp
65                  70                  75                  80

Glu Val Arg Asp Arg Ala Leu Gly Lys Trp Ser Glu Leu Glu Glu Ala
                85                  90                  95

Phe Asp Lys Arg Leu Asn Ser Ala Ile Ser Arg Leu Gly Val Pro Ser
            100                 105                 110

Arg Asn Glu Val Lys Glu Leu His Ser Lys Val Asp Thr Leu Thr Lys
        115                 120                 125

Gln Ile Glu Lys Leu Thr Gly Val Ser Val Lys Pro Ala Ala Lys Ala
    130                 135                 140

Ala Ala Lys Pro Ala Ala Lys Pro Ala Ala Lys Pro Ala Ala Lys Thr
145                 150                 155                 160

Ala Ala Ala Lys Pro Ala Ala Lys Pro Ala Ala Lys Ala Ala Ala Lys
                165                 170                 175

Pro Ala Ala Lys Pro Ala Ala Lys Lys Thr Ala Ala Lys Thr Ala Ala
            180                 185                 190

Ala Lys Pro Ala Ala Lys Pro Ala Ala Lys Pro Thr Ala Lys Ala Ala
        195                 200                 205

Ala Lys Pro Ala Thr Lys Pro Ala Ala Lys Ala Ala Ala Lys Pro Ala
    210                 215                 220
```

-continued

```
Ala Lys Pro Ala Ala Ala Lys Pro Ala Ala Lys Pro Ala Ala Lys Pro
225                 230                 235                 240

Ala Ala Ala Thr Ala Ala Lys Pro Ala Ala Lys Pro Ala Ala Lys Pro
                245                 250                 255

Ala Ala Lys Lys Pro Ala Ala Lys Lys Pro Ala Ala Lys Pro Ala Ala
            260                 265                 270

Ala Lys Pro Ala Ala Pro Ala Ala Ser Ser Ser Ala Pro Ala Ala Pro
        275                 280                 285

Ala Ala Thr Pro Ala Ala Ser Ala Pro Ala Ala Asn Ala Pro Ala Thr
    290                 295                 300

Pro Ser Ser Gln Gly
305


<210> SEQ ID NO 8
<211> LENGTH: 340
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 8

Met Lys Ala Thr Met Val Leu Thr Pro Leu Ala Leu Ala Met Ala Ala
1               5                   10                  15

Val Leu Ser Val Ser Ala Tyr Ala Gly Asn Glu Gly Gly Trp His Pro
            20                  25                  30

Pro Lys Pro Asn Pro Gln Ser Asn Asn Lys Gly Gly Ala Thr Ala Leu
        35                  40                  45

Val Val Asp Thr Gln Gln Asn Tyr Asn Asn Lys Val Ser Asn Phe Gly
    50                  55                  60

Thr Leu Asn Asn Ala Ser Val Ser Gly Ser Ile Lys Asp Ala Ser Gly
65                  70                  75                  80

Asn Val Gly Val Asn Val Ala Ala Gly Asp Asn Asn Gln Gln Ala Asn
                85                  90                  95

Ala Ala Ala Leu Ala Ser Ala Asp Ala Ser Phe Val Phe Gly Thr Ala
            100                 105                 110

Thr Ala Ser Thr Ser Val Leu Gln Ser Gly Tyr Gly Asn Thr Leu Asn
        115                 120                 125

Asn Tyr Ser Asn Pro Asn Thr Ala Ser Leu Ser Asn Ser Ala Asn Asn
    130                 135                 140

Val Ser Gly Asn Leu Gly Val Asn Val Ala Ala Gly Asn Phe Asn Gln
145                 150                 155                 160

Gln Lys Asn Asp Leu Ala Ala Ala Val Ser Asn Gly Gln Tyr Ser Thr
                165                 170                 175

Ala Gly Ser Ala Ala Ser Gln Thr Ser Thr Gly Asn Thr Thr Val Asn
            180                 185                 190

Ser Ala Asn Tyr Ala Tyr Gly Gly Thr Tyr Val Ser Leu Lys Leu Asn
        195                 200                 205

Ala Asp Gly Ser Tyr Lys Gly Thr Ser Asp Gln Ile Gly Asp Val Tyr
    210                 215                 220

Leu Asp Thr Trp Glu Gly Gln Thr His Pro Gly Gly Ser Asn Thr Gly
225                 230                 235                 240

His Ile Asp Val Asp Ser Gln Ala Gln Gly Ala Lys Asp Leu Asn His
                245                 250                 255

Asp Gly Gly Ala Phe Ala Phe Lys Glu Lys Gly Asp Val Asp Leu Lys
            260                 265                 270
```

-continued

```
Gly Thr Val Ser Gly Phe Ile Pro Ala Ile Val Gly Phe Lys Thr Pro
        275                 280                 285

Val Thr Asn Asn Ala Ser Leu Ser Asn Ser Leu Gln Asn Val Ser Gly
    290                 295                 300

Asn Val Gly Val Asn Ile Ala Ala Gly Gly Gly Asn Gln Gln Ser Asn
305                 310                 315                 320

Ser Leu Ser Ile Ala Ala Gly Cys Ser Ser Cys Pro Ala Gly Gly Glu
                325                 330                 335

Ser Leu Gly Phe
            340


<210> SEQ ID NO 9
<211> LENGTH: 347
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 9

Met Lys Gln Gln Phe Glu Arg Ser Pro Ser Glu Ser Tyr Phe Trp Pro
1               5                   10                  15

Val Val Leu Ala Val Val Leu His Val Leu Ile Phe Ala Met Leu Phe
            20                  25                  30

Val Ser Trp Ala Phe Ala Pro Glu Leu Pro Pro Ser Lys Pro Ile Val
        35                  40                  45

Gln Ala Thr Leu Tyr Gln Leu Lys Ser Lys Ser Gln Ala Thr Thr Gln
    50                  55                  60

Thr Asn Gln Lys Ile Ala Gly Glu Ala Lys Lys Thr Ala Ser Lys Gln
65                  70                  75                  80

Tyr Glu Val Glu Gln Leu Glu Gln Lys Lys Leu Glu Gln Gln Lys Leu
                85                  90                  95

Glu Gln Gln Lys Leu Glu Gln Gln Gln Val Ala Ala Ala Lys Ala Ala
            100                 105                 110

Glu Gln Lys Lys Ala Asp Glu Ala Arg Lys Ala Glu Ala Gln Lys Ala
        115                 120                 125

Ala Glu Ala Lys Lys Ala Asp Glu Ala Lys Lys Ala Ala Glu Ala Lys
    130                 135                 140

Ala Ala Glu Gln Lys Lys Gln Ala Asp Ile Ala Lys Lys Arg Ala Glu
145                 150                 155                 160

Asp Glu Ala Lys Lys Lys Ala Ala Glu Asp Ala Lys Lys Lys Ala Ala
                165                 170                 175

Glu Asp Ala Lys Lys Lys Ala Ala Glu Glu Ala Lys Lys Lys Ala Ala
            180                 185                 190

Ala Glu Ala Ala Lys Lys Lys Ala Ala Val Glu Ala Ala Lys Lys Lys
        195                 200                 205

Ala Ala Ala Ala Ala Ala Ala Ala Arg Lys Ala Ala Glu Asp Lys Lys
    210                 215                 220

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

Ala Leu Ala Asp Glu Val Gly Ser Glu Val Thr Gly Ser Leu Asp Asp
                245                 250                 255

Leu Ile Val Asn Leu Val Ser Gln Gln Trp Arg Arg Pro Pro Ser Ala
            260                 265                 270

Arg Asn Gly Met Ser Val Glu Val Leu Ile Glu Met Leu Pro Asp Gly
```

-continued

```
        275                 280                 285

Thr Ile Thr Asn Ala Ser Val Ser Arg Ser Ser Gly Asp Lys Pro Phe
    290                 295                 300

Asp Ser Ser Ala Val Ala Ala Val Arg Asn Val Gly Arg Ile Pro Glu
305                 310                 315                 320

Met Gln Gln Leu Pro Arg Ala Thr Phe Asp Ser Leu Tyr Arg Gln Arg
                325                 330                 335

Arg Ile Ile Phe Lys Pro Glu Asp Leu Ser Leu
            340                 345


<210> SEQ ID NO 10
<211> LENGTH: 352
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 10

Met Ser Ala Asn Lys Lys Pro Val Thr Thr Pro Leu His Leu Leu Gln
1               5                   10                  15

Gln Leu Ser His Ser Leu Val Glu His Leu Glu Gly Ala Cys Lys Gln
            20                  25                  30

Ala Leu Val Asp Ser Glu Lys Leu Leu Ala Lys Leu Glu Lys Gln Arg
        35                  40                  45

Gly Lys Ala Gln Glu Lys Leu His Lys Ala Arg Thr Lys Leu Gln Asp
    50                  55                  60

Ala Ala Lys Ala Gly Lys Thr Lys Ala Gln Ala Lys Ala Arg Glu Thr
65                  70                  75                  80

Ile Ser Asp Leu Glu Glu Ala Leu Asp Thr Leu Lys Ala Arg Gln Ala
                85                  90                  95

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

Leu Lys Leu Ala Gln Gly Val Gly Lys Val Lys Glu Ala Ala Gly Lys
        115                 120                 125

Ala Leu Glu Ser Arg Lys Ala Lys Pro Ala Thr Lys Pro Ala Ala Lys
    130                 135                 140

Ala Ala Ala Lys Pro Ala Val Lys Thr Val Ala Ala Lys Pro Ala Ala
145                 150                 155                 160

Lys Pro Ala Ala Lys Pro Ala Ala Lys Pro Ala Ala Lys Pro Ala Ala
                165                 170                 175

Lys Thr Ala Ala Ala Lys Pro Ala Ala Lys Pro Thr Ala Lys Pro Ala
            180                 185                 190

Ala Lys Pro Ala Ala Lys Pro Ala Ala Lys Thr Ala Ala Ala Lys Pro
        195                 200                 205

Ala Ala Lys Pro Ala Ala Lys Pro Val Ala Lys Pro Ala Ala Lys Pro
    210                 215                 220

Ala Ala Lys Thr Ala Ala Ala Lys Pro Ala Ala Lys Pro Ala Ala Lys
225                 230                 235                 240

Pro Val Ala Lys Pro Thr Ala Lys Pro Ala Ala Lys Thr Ala Ala Ala
                245                 250                 255

Lys Pro Ala Ala Lys Pro Ala Ala Lys Pro Ala Ala Lys Pro Ala Ala
            260                 265                 270

Lys Pro Val Ala Lys Ser Ala Ala Ala Lys Pro Ala Ala Lys Pro Ala
        275                 280                 285
```

-continued

```
Ala Lys Pro Ala Ala Lys Pro Ala Ala Lys Pro Ala Ala Lys Pro Val
    290                 295                 300

Ala Ala Lys Pro Ala Ala Thr Lys Pro Ala Thr Ala Pro Ala Ala Lys
305                 310                 315                 320

Pro Ala Ala Thr Pro Ser Ala Pro Ala Ala Ala Ser Ser Ala Ala Ser
                325                 330                 335

Ala Thr Pro Ala Ala Gly Ser Asn Gly Ala Ala Pro Thr Ser Ala Ser
            340                 345                 350


<210> SEQ ID NO 11
<211> LENGTH: 420
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 11

Met Trp Gly Leu Thr Met Lys Phe Ala Ser Leu Ile Leu Met Leu Leu
1               5                   10                  15

Phe Ala Thr Val Ala Arg Ala Glu Asp Tyr Tyr Trp Lys Ile Gln Ser
            20                  25                  30

Leu Pro Glu Arg Phe Ser Ser Pro Ser Ala Ala Cys Ala Ala Trp Ala
        35                  40                  45

Lys Ala Thr Gly Arg Pro Gly Glu Phe Thr Phe Thr Gly Ser Met Lys
    50                  55                  60

Ala Arg Asp Gln Thr Ser Phe Trp Cys Glu Phe Thr Asn Asn Glu Thr
65                  70                  75                  80

Gly Lys Thr Ala Ala Gly Tyr Gly Pro Ala Gly Arg Tyr Gly Asp Ser
                85                  90                  95

Cys Pro Glu Gly Thr Glu Tyr Asp Lys Ala Thr Gly Val Cys Lys Ser
            100                 105                 110

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

Asp Ser Pro Val Val Thr Ser Gly Gly Arg Asn Tyr Val Gly Asp Gly
    130                 135                 140

Gly Ala Pro Thr Ala Cys Tyr Gln Ser Cys Glu Tyr Gly Gly Asn Pro
145                 150                 155                 160

Ser Pro Ala Ser Cys Tyr Leu Val Lys Gly Ser Thr Thr Thr Gly Phe
                165                 170                 175

Cys Asn Tyr Ile Leu Lys Gly Thr Gly Gln Asn Cys Gly Ala Asp Ser
            180                 185                 190

Tyr Thr Phe Ser Gln Thr Gly Asp Ser Leu Asn Pro Pro Asp Thr Pro
        195                 200                 205

Asn Thr Asp Pro Ser Asp Pro Asn Asp Pro Gly Cys Pro Pro Gly Trp
    210                 215                 220

Ser Trp Ser Gly Thr Thr Cys Val Lys Ala Pro Thr Asp Pro Thr Asp
225                 230                 235                 240

Pro Thr Asp Pro Thr Thr Pro Gly Ser Asp Gly Gly Gly Asp Gly Asn
                245                 250                 255

Gly Gly Gly Asn Asn Asn Gly Gly Gly Asn Asp Gly Gly Thr Gly Asn
            260                 265                 270

Gly Gly Asp Gly Ser Gly Gly Gly Asp Gly Asn Gly Gly Gly Asp Gly
        275                 280                 285

Ser Gly Asp Gly Asp Gly Ser Gly Thr Gly Gly Asp Gly Asn Gly Thr
    290                 295                 300
```

-continued

```
Cys Asp Pro Ala Lys Glu Asn Cys Ser Thr Gly Pro Glu Gly Pro Gly
305                 310                 315                 320

Gly Glu Leu Lys Glu Pro Thr Pro Gly Thr Trp Asp Asp Ala Ile Ala
                325                 330                 335

Thr Trp Glu Lys Lys Val Glu Asp Ala Lys Gln Glu Leu Lys Thr Lys
            340                 345                 350

Val Lys Ala Asn Val Asp Gln Met Lys Gly Ala Phe Asp Leu Asn Leu
        355                 360                 365

Ala Glu Gly Gly Gly Gln Leu Pro Cys Glu Ser Met Thr Ile Trp Gly
    370                 375                 380

Lys Ser Tyr Ser Leu Cys Ile Ser Asp Tyr Ala Gly Gln Leu Ser Ser
385                 390                 395                 400

Leu Arg Val Ala Leu Leu Leu Met Ala Ala Leu Ile Ala Ala Leu Ile
                405                 410                 415

Leu Leu Lys Asp
            420
```

<210> SEQ ID NO 12
<211> LENGTH: 427
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 12

```
Met Ala Val Ala Pro Gly Val Leu Leu Pro Pro Thr Pro Asp Val Lys
1               5                   10                  15

Pro Lys Ala Ala Ala Pro Lys Ser Gln Gln Lys Thr Pro Glu Pro Ser
            20                  25                  30

Asn Asp Lys Thr Ser Ser Phe Ser Asp Met Tyr Ala Lys Glu Thr Ala
        35                  40                  45

Lys Lys Pro Ala Glu Arg Ala Asp Gly Pro Ala Lys Gly Ser Arg Asp
    50                  55                  60

Lys Pro Arg Asp Ala Gly Lys Asp Ala Ala Glu Ala Gln Pro Thr Asp
65                  70                  75                  80

Ala Val Arg Gln Pro Ala Val Ala Glu Asp Gly Lys Pro Leu Pro Ala
                85                  90                  95

Asp Gly Gln Ala Lys Ala Asp Gly Glu Asp Lys Val Glu Thr Pro Val
            100                 105                 110

Asp Pro Leu Gln Leu Leu Gly Leu Gly Gly Ala Val Pro Leu Leu Asp
        115                 120                 125

Glu Asn Thr Gln Ala Thr Leu Leu Pro Pro Ala Val Pro Thr Ala Ser
    130                 135                 140

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

Lys Leu Asn Gly Val Pro Ala Val Asn Met Ala Leu Glu Gln Gly Ala
                165                 170                 175

Gln Asp Ala Ala Gln Thr Ala Lys Gly Gly Pro Ala Lys Ser Ala Asp
            180                 185                 190

Pro Arg Gln Ala Asn Leu Gly Asp Ala Leu Ala Gly Leu Thr Ser Asp
        195                 200                 205

Ser Leu Thr Lys Ala Val Asp Gly Lys Ala Leu Glu Ala Gln Leu Gln
    210                 215                 220

Gln Thr Ala Glu Pro Ala Val Ala Ser Ala Ala Ser Glu Ser Leu Leu
```

-continued

```
225                 230                 235                 240

Glu Ser Lys Ala Glu Pro Arg Gly Glu Pro Phe Ala Ala Lys Leu Asn
                245                 250                 255

Gly Leu Thr Gln Ala Met Ala Gln Gln Ala Leu Thr Asn Arg Pro Val
            260                 265                 270

Asn Gly Thr Val Pro Gly Gln Pro Val Ala Met Gln Gln Asn Gly Trp
        275                 280                 285

Ser Glu Ala Val Val Asp Arg Val Met Trp Met Ser Ser Gln Asn Leu
    290                 295                 300

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

Val Arg Ile His Met Thr Ala Asp Gln Thr Gln Val Thr Phe Ala Ser
                325                 330                 335

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

Arg Asp Met Phe Ser Gln Gln Gly Met Asn Gln Leu Asp Val Asn Val
        355                 360                 365

Ser Asp Gln Ser Leu Ala Arg Gly Trp Gln Gly Gln Gln Gln Gly Glu
    370                 375                 380

Gly Gly Ser Ala Arg Gly Arg Gly Leu Ala Gly Glu Ala Ser Gly Asp
385                 390                 395                 400

Glu Glu Thr Leu Ala Gly Val Ser Glu Ile Arg Ser Arg Pro Gly Ala
                405                 410                 415

Ser Ala Ala Arg Gly Leu Val Asp Tyr Tyr Ala
            420                 425


<210> SEQ ID NO 13
<211> LENGTH: 428
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 13

Met Leu Arg Leu Leu Pro Leu Leu Leu Ser Leu Ala Cys Leu Ala Pro
1               5                   10                  15

Ala Phe Ala Asp Glu Arg Ala Asp Thr Gln Arg Gln Leu Glu Gln Thr
            20                  25                  30

Gln Lys Asp Ile Gly Glu Leu Lys Lys Leu Leu Asp Gly Ile Gln Gln
        35                  40                  45

Glu Lys Ser Gly Val Gln Lys Gln Leu Lys Ser Thr Glu Thr Glu Met
    50                  55                  60

Gly Asp Leu Glu Lys Gln Ile Lys Ala Leu Gln Asp Glu Leu Asp Lys
65                  70                  75                  80

Ser Glu Ala Glu Leu Lys Arg Leu Asp Gly Glu Lys Lys Lys Leu Gln
                85                  90                  95

Asp Ala Arg Ile Glu Gln Gln Arg Leu Leu Ala Ile Gln Ala Arg Ala
            100                 105                 110

Ala Tyr Gln Ser Gly Arg Glu Glu Tyr Leu Lys Leu Leu Leu Asn Gln
        115                 120                 125

Glu His Pro Glu Lys Phe Ser Arg Thr Leu Thr Tyr Tyr Asp Tyr Ile
    130                 135                 140

Asn Lys Ala Arg Leu Glu Gln Leu Ala Ser Phe Asn Glu Thr Leu Arg
145                 150                 155                 160
```

-continued

Gln Leu Ala Asn Val Glu Gln Asp Ile Ser Ala Gln Lys Ala Glu Gln
165 170 175

Leu Ser Lys Gln Gly Glu Leu Asp Ser Arg Arg Glu Ala Leu Ala Ala
180 185 190

Thr Arg Lys Glu Arg Gln Gln Ala Leu Ala Lys Leu Asn Ser Asp Tyr
195 200 205

Arg Glu Arg Asp Gln Lys Leu Lys Ser Arg Gln Gln Asp Gln Ala Glu
210 215 220

Leu Ala Lys Val Leu Arg Thr Ile Glu Glu Thr Leu Ala Arg Gln Ala
225 230 235 240

Arg Glu Ala Ala Ala Ala Ala Glu Arg Glu Arg Gln Arg Ala Leu Ala
245 250 255

Ala Glu Arg Glu Arg Ala Arg Gln Gln Gln Ala Ala Pro Gly Arg Val
260 265 270

Thr Ser Pro Pro Arg Glu Pro Ala Pro Gly Pro Leu Val Ser Ser Thr
275 280 285

Gly Ala Val Tyr Gly Gly Ala Phe Gly Ser Ala Arg Gly Lys Leu Pro
290 295 300

Trp Pro Val Asn Gly Arg Val Val Ala Arg Phe Gly Ser Gln Arg Gly
305 310 315 320

Asp Asp Pro Arg Ala Lys Trp Asp Gly Val Leu Ile Ser Ala Ser Ala
325 330 335

Gly Ser Thr Val Arg Ala Val His Gly Gly Arg Val Val Phe Ala Asp
340 345 350

Trp Leu Arg Gly Ala Gly Leu Leu Val Ile Leu Asp His Gly Gly Gly
355 360 365

Tyr Leu Ser Leu Tyr Gly His Asn Gln Ser Leu Leu Lys Asp Ala Gly
370 375 380

Asp Thr Val Lys Ala Gly Asp Pro Ile Ala Thr Val Gly Thr Ser Gly
385 390 395 400

Gly Gln Ser Ser Pro Ala Val Tyr Phe Ala Ile Arg His Gln Gly Arg
405 410 415

Pro Ala Asp Pro Thr Thr Trp Cys Arg Ala Gln Gly
420 425

<210> SEQ ID NO 14
<211> LENGTH: 568
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 14

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

Ser Thr Leu Leu Leu Ser Ala Cys Asn Gln Gly Asp Asp Ala Pro Lys
20 25 30

Pro Ala Ala Val Ala Pro Gln Pro Ala Ala Pro Ser Met Ala Ala Leu
35 40 45

Ser Ile Pro Leu Cys Leu Asn Gly Gln Cys Ala Val Ile Asp Gln Asp
50 55 60

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

Ser Ala Tyr Gln Gly Thr Leu Met Ala Ala Arg Glu Glu Arg Trp Asn
85 90 95

-continued

```
Leu Ile Gln Ala Lys Asp Gly Lys Val Leu Arg Asp Asp Ile Gly Glu
            100                 105                 110

Ala Leu Ser Leu Leu Thr Pro Asn Leu Tyr Gly Phe Val Arg Asp Gly
        115                 120                 125

Lys Tyr Gly Val Val Asp Gly Gln Gly Lys Glu Val Gln Ala Pro Arg
    130                 135                 140

Phe Asp Asp Ile Tyr Pro Asn Ser Ala Asn Glu Phe Ile Ile Tyr Glu
145                 150                 155                 160

Ile Asp Gly Lys Arg Gly Ile Leu Asp Ala Lys Gly Lys Gln Leu Thr
                165                 170                 175

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

Gly Gly Leu Ile Ser Ala Glu Arg Gly Glu Glu Lys Trp Ile Ile Asn
        195                 200                 205

Leu Ala Thr Gly Glu Gln Lys Ala Val Ala Tyr Glu Ser Leu Gly Asp
    210                 215                 220

Leu His Asp Gly Val Met Ser Ala Ser Val Ile Gly Lys Gly Ser Gln
225                 230                 235                 240

Leu Val Asp Ala Lys Gly Asp Val Val Gly Asp Gly Lys Ser Tyr Asp
                245                 250                 255

Tyr Leu Gly Thr Pro Ala Asn Gly Leu Val Ala Phe Arg Glu Lys Tyr
            260                 265                 270

Asp Ser Pro Cys Gly Tyr Leu Asp Tyr Gln Gly Lys Val Ala Ile Ala
        275                 280                 285

Ala Gln Phe Ala Gly Cys Gly Ala Phe Gly Lys Gln Gly Gly Leu Ala
    290                 295                 300

Gln Gln Arg Met Glu Asp Gly Ser Ser Gly Lys Tyr Gly Leu Ile Asp
305                 310                 315                 320

Arg Ser Gly Ala Trp Lys Val Gln Pro Gln Tyr Asp Ser Ala Asp Ser
                325                 330                 335

Ala Gly Leu Thr Ala Leu Gly Tyr Thr Val Asp Val Pro Gly Leu Ala
            340                 345                 350

Ala Val Gly Val Ser Thr Gly Leu Phe Ser Ala Asp Phe Gly Ile Phe
        355                 360                 365

Asn Leu Asp Glu Gly Ser Glu Trp Val Lys Pro Gly Tyr Ala Gln Ile
    370                 375                 380

Gly Ala Leu Gly Asn Asp Leu Phe Val Val Ala Lys Lys Gly Gly Pro
385                 390                 395                 400

Gln Lys Thr Val Ser Phe Met Gly Ser Glu Ser Gln Val Pro Val Val
                405                 410                 415

Gly Leu Met Asp Arg Ser Gly Lys Met Leu Leu Glu Pro Asp Glu Leu
            420                 425                 430

Ile Ser Ile Gln Ser Ala Tyr Asp Gly Arg Phe Leu Glu Gly Leu Asp
        435                 440                 445

Gly Met Asp Asn Ala Ala His Thr Val Leu Leu Asp Arg Gln Gly Arg
    450                 455                 460

Thr Leu Val Pro Ala Leu Trp Gln Lys Leu Glu Val Asn Pro Gln Gln
465                 470                 475                 480

Gly Tyr Ile Leu Gly Tyr Glu Val Ser Gly Thr Gly Asp Glu Ala Thr
                485                 490                 495
```

-continued

```
Glu Thr Leu Arg Ala Leu Tyr Asp Leu Asn Gly Lys Pro Arg Phe Thr
            500                 505                 510

Val Ala Thr Thr Asp Cys Gly Ala Glu Gln Leu Leu Asp Gly Asn Gly
        515                 520                 525

Lys Ala Ile Trp Pro Gln Asp Pro Thr Pro Tyr Cys Gln Ser Asp Asp
    530                 535                 540

Glu Gln Asp Asp Glu Gly Glu Pro Glu Gln Glu Pro Ala Pro Val Glu
545                 550                 555                 560

Glu Ser Glu Glu Thr Ser Glu Ser
                565


<210> SEQ ID NO 15
<211> LENGTH: 579
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 15

Met Leu Arg Pro Ala Arg Ser Leu Ser Leu Cys Ser Ala Leu Val Ile
1               5                   10                  15

Leu Leu Ala Ala Cys Gly Glu Gly Glu Pro Leu Leu Pro Ala Asp Ala
            20                  25                  30

Arg Leu Pro Asp Gly Ala Arg Tyr Arg Gly Glu Leu Val Asp Gly Arg
        35                  40                  45

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

Gly Arg Phe Glu His Gly Leu Leu His Gly His Gly Thr Trp Gln Gly
65                  70                  75                  80

Ala Asp Gly Ser Arg Tyr Ser Gly Gly Phe Ala Ala Gly Leu Phe Asp
                85                  90                  95

Gly Gln Gly Arg Leu Ala Met Ala Asp Gly Ser Val Tyr Gln Gly Gly
            100                 105                 110

Phe Arg Gln Gly Leu Phe Asp Gly Glu Gly Ser Leu Glu Gln Gln Gly
        115                 120                 125

Thr Arg Tyr Arg Gly Gly Phe Arg Lys Gly Leu Tyr Ser Gly Gln Gly
    130                 135                 140

Thr Leu Asp Gly Ser Asp Gly Ser Arg Tyr Gln Gly Ser Phe Arg Gln
145                 150                 155                 160

Gly Arg Leu Glu Gly Glu Gly Ser Phe Ser Asp Ser Gln Gly Asn Gln
                165                 170                 175

Tyr Ala Gly Thr Phe Arg Asp Gly Gln Leu Asn Gly Lys Gly Arg Trp
            180                 185                 190

Ser Gly Pro Asp Gly Asp Arg Tyr Val Gly Gln Phe Lys Asp Asn Gln
        195                 200                 205

Phe His Gly Gln Gly Arg Tyr Glu Ser Ala Ser Gly Asp Val Trp Ile
    210                 215                 220

Gly Arg Phe Ser Glu Gly Ala Leu Asn Gly Pro Gly Glu Leu Leu Gly
225                 230                 235                 240

Ala Asp Gly Ser Arg Tyr Arg Gly Gly Phe Gln Phe Trp Arg Phe His
                245                 250                 255

Gly Gln Gly Leu Leu Glu Gln Leu Asp Gly Thr Arg Tyr Glu Gly Gly
            260                 265                 270

Phe Ala Ala Gly Ala Tyr Ala Gly Gln Gly Thr Leu Asp Arg Ala Asp
        275                 280                 285
```

-continued

```
Gly Ser Arg Glu Gln Gly Leu Trp Ala Asp Gly Lys Arg Ile Arg Asp
    290                 295                 300

Ala Ala Gly Lys Ala Leu Pro Asp Thr Leu Glu Val Gly Leu Leu Ala
305                 310                 315                 320

Gln Gly Arg Leu Leu Asp Glu Glu Leu Arg Lys Ile Pro Ala Ser Thr
                325                 330                 335

Pro Ala Ser Glu Leu Tyr Ala Leu Ser Leu Gly Gly Asp Gly Arg Gln
            340                 345                 350

Gly Val Phe Leu Arg Glu Ala Asp Tyr Ala Gly Asp Leu Leu Gly Gln
        355                 360                 365

Arg Phe Ala Ala Arg Gly Val Ile Arg Leu Val Asn His Arg Asp His
    370                 375                 380

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

Arg Thr Leu Ala Glu Arg Ser Gly Pro Glu Asp Leu Val Phe Ile Tyr
                405                 410                 415

Leu Thr Ser His Gly Ser Ser Asp His Gln Leu Ala Leu Asp Met Pro
            420                 425                 430

Gly Leu Asn Leu Gly Asp Leu Pro Ala Ala Glu Leu Ala Glu Leu Leu
        435                 440                 445

Ala Pro Leu Arg Gln Arg Asp Lys Val Leu Val Val Ser Ala Cys Tyr
    450                 455                 460

Ser Gly Gly Phe Ile Pro Pro Leu Lys Asp Glu Arg Thr Leu Ile Leu
465                 470                 475                 480

Thr Ala Ala Arg Ala Asp Arg Val Ser Phe Gly Cys Ser Asp Asp Ala
                485                 490                 495

Asp Phe Thr Tyr Phe Gly Arg Ala Leu Leu Ala Asn Ala Leu Asn Arg
            500                 505                 510

Thr Asp Asp Leu Ser Lys Ala Phe Glu Leu Ala Lys Glu Glu Val Arg
        515                 520                 525

Gln Arg Glu Lys Glu Glu Gly Phe Glu Ala Ser Glu Pro Gln Ala Trp
    530                 535                 540

Leu Pro Glu Arg Val Leu Ala His Trp Arg Thr Leu Arg Gly Gln Gln
545                 550                 555                 560

Ala Glu Arg Ala Leu Ala Ser Arg Glu Gly Lys Thr Gly Glu Gly Ala
                565                 570                 575

Ala Gly Lys


<210> SEQ ID NO 16
<211> LENGTH: 621
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 16

Met Leu Gln Asn Ile Arg Asp Asn Ser Gln Gly Trp Ile Ala Lys Thr
1               5                   10                  15

Ile Ile Gly Val Ile Ile Val Leu Leu Ser Leu Thr Gly Phe Asp Ala
            20                  25                  30

Ile Ile Arg Ala Thr Asp His Ser Asn Val Ala Ala Lys Val Asn Gly
        35                  40                  45

Asp Asp Ile Ser Leu Asn Glu Val Gln Gln Ala Val Asp Met Gln Arg
    50                  55                  60
```

-continued

```
Arg Gln Leu Leu Gln Arg Leu Gly Lys Asp Phe Asp Pro Ser Met Leu
65                  70                  75                  80

Asp Asp Lys Leu Leu Lys Glu Ala Ala Leu Lys Gly Leu Ile Glu Arg
                85                  90                  95

Thr Leu Leu Leu Gln Ala Ala Lys Asp Asp Lys Phe Ala Phe Ser Asp
            100                 105                 110

Gln Ala Leu Asp Gln Leu Ile Leu Gln Thr Pro Glu Phe Gln Val Asp
        115                 120                 125

Gly Lys Phe Asn Ala Asp Arg Phe Asp Gln Val Ile Arg Gln Met Asn
    130                 135                 140

Tyr Ser Arg Met Gln Phe Arg Gln Met Leu Gly Gln Glu Met Leu Ile
145                 150                 155                 160

Gly Gln Leu Arg Ala Gly Leu Ala Gly Thr Gly Phe Val Thr Asp Asn
                165                 170                 175

Glu Leu Gln Ser Phe Ala Arg Leu Glu Lys Gln Thr Arg Asp Phe Ala
            180                 185                 190

Thr Leu Ala Ile Lys Ala Asp Ala Ser Lys Ser Ser Val Ser Asp Asp
        195                 200                 205

Glu Val Lys Ala Phe Tyr Glu Gly His Lys Ser Glu Phe Met Thr Pro
    210                 215                 220

Glu Gln Val Val Val Glu Tyr Val Glu Leu Lys Lys Ser Ser Phe Phe
225                 230                 235                 240

Asp Gln Val Lys Val Lys Gln Glu Asp Leu Glu Ala Leu Tyr Gln Lys
                245                 250                 255

Glu Ile Ala Asn Leu Ser Glu Gln Arg Asp Ala Ala His Ile Leu Ile
            260                 265                 270

Glu Val Asn Asp Lys Val Gly Asp Glu Gln Ala Lys Ala Lys Ile Asp
        275                 280                 285

Glu Ile Lys Ala Arg Leu Ala Lys Gly Glu Asp Phe Ala Ala Leu Ala
    290                 295                 300

Lys Glu Phe Ser Gln Asp Ile Gly Ser Ala Ala Thr Gly Gly Asp Leu
305                 310                 315                 320

Gly Tyr Ala Gly Arg Gly Val Tyr Asp Pro Ala Phe Glu Glu Ala Leu
                325                 330                 335

Tyr Ala Leu Lys Gln Gly Glu Val Ser Ala Pro Val Lys Thr Pro Tyr
            340                 345                 350

Gly Tyr His Leu Ile Lys Leu Leu Gly Val Gln Ala Pro Glu Val Pro
        355                 360                 365

Ser Leu Glu Ser Leu Lys Pro Lys Leu Glu Asp Glu Leu Lys Lys Gln
    370                 375                 380

Met Val Glu Gln Arg Phe Val Glu Ala Thr Lys Asp Leu Glu Ser Ser
385                 390                 395                 400

Ala Tyr Glu Ala Ala Asp Leu Ser Gln Pro Ala Gln Glu Met Gly Leu
                405                 410                 415

Lys Val Gln Thr Ser Gln Pro Phe Gly Arg Ser Gly Gly Asp Gly Ile
            420                 425                 430

Ala Ala Asn Arg Gln Ile Val Gln Thr Ala Phe Ser Ala Glu Val Leu
        435                 440                 445

Glu Glu Ala Ala Asn Ser Gly Ala Ile Glu Leu Asp Pro Asp Thr Val
    450                 455                 460
```

-continued

```
Val Val Leu Arg Val Lys Glu His Asn Lys Pro Lys Glu Gln Pro Leu
465                 470                 475                 480

Glu Gln Val Ala Ala Asn Ile Arg Glu Arg Leu Ala Ala Glu Lys Ala
                485                 490                 495

Ala Glu Glu Ala Gln Lys Arg Gly Glu Ala Leu Ile Ala Glu Leu Arg
            500                 505                 510

Glu Gly Arg Thr Ser Ser Ala Ala Gly Glu Ser Trp Lys Val Val Glu
        515                 520                 525

Ala Ala Ser Arg Gly His Glu Gly Val Asp Pro Lys Leu Leu Gln Ala
    530                 535                 540

Val Phe Arg Met Gln Arg Pro Glu Ala Lys Asp Lys Pro Ser Phe Ser
545                 550                 555                 560

Gly Val Thr Leu Ala Asn Gly Asp Tyr Val Val Ile Arg Leu Asn Gly
                565                 570                 575

Val Ser Glu Pro Glu Glu Ala Ile Ser Asp Asp Glu Lys Ala Met Tyr
            580                 585                 590

Arg Arg Phe Leu Ala Ser Arg Ser Gly Gln Ala Asp Phe Ala Ala Phe
        595                 600                 605

Arg Arg Gln Leu Gln Asp Lys Ala Glu Val Glu Lys Tyr
    610                 615                 620


<210> SEQ ID NO 17
<211> LENGTH: 688
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 17

Met Asp Met Thr Ser Leu Met Pro Leu Leu Leu Gly Val Gly Leu Val
1               5                   10                  15

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

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

Pro Lys Val His Phe Thr Gly Ala Leu Val Tyr Pro Val Ile His Leu
    50                  55                  60

Lys Glu Phe Met Arg Ile Ser Leu Ile Thr Leu Glu Val Asp Arg Arg
65                  70                  75                  80

Gly Lys Asp Gly Leu Ile Cys Arg Asp Asn Met Arg Ala Asp Ile Thr
                85                  90                  95

Val Ala Phe Tyr Leu Arg Val Asn Glu Thr Gln Asp Asp Val Leu Lys
            100                 105                 110

Val Ala Lys Ala Ile Gly Val Asp Arg Ala Ser Asp Arg Ser Ala Val
        115                 120                 125

Asn Glu Leu Phe Asn Ala Lys Phe Ser Glu Ala Leu Lys Thr Val Gly
    130                 135                 140

Lys Gln Phe Asp Phe Val Gln Leu Phe Glu Asn Arg Gln Asp Phe Arg
145                 150                 155                 160

Asp Arg Ile Ile Glu Val Ile Gly Asn Asp Leu Asn Gly Tyr Val Leu
                165                 170                 175

Glu Asp Val Ala Ile Asp Tyr Leu Glu Gln Thr Ala Lys Asn Ser Leu
            180                 185                 190

Asp Pro Ser Asn Ile Leu Asp Ala Glu Gly Ile Arg Lys Ile Thr Glu
        195                 200                 205
```

-continued

```
Leu Thr Ala Thr Gln Asn Val Ile Thr Asn Glu Leu Glu Arg Asn Glu
    210                 215                 220

Glu Leu Ala Ile Lys Lys Lys Asn Val Glu Thr Arg Glu Ala Ala Leu
225                 230                 235                 240

Ala Leu Glu Arg Gln Gln Ala Asp Ala Glu Ala Arg Gln Lys Arg Glu
                245                 250                 255

Ile Glu Thr Ile Arg Ala Arg Glu Glu Ala Glu Thr Ala Arg Val Lys
            260                 265                 270

Glu Glu Glu Arg Leu Lys Ala Glu Gln Ala Arg Ile Gln Ala Gln Gln
        275                 280                 285

Glu Ile Asp Val Arg Thr Glu Asn His Gln Arg Glu Val Glu Val Ala
    290                 295                 300

Gln Gln Asn Arg Gln Arg Ala Val Val Ile Glu Val Glu Lys Val Thr
305                 310                 315                 320

Arg Ala Lys Asp Leu Glu Ile Val Ala Arg Glu Arg Glu Val Glu Leu
                325                 330                 335

Gln Lys Ile Glu Lys Glu Lys Ala Leu Glu Glu Gln Arg Lys Asn Ile
            340                 345                 350

Ala Asn Val Ile Arg Glu Arg Val Ala Val Glu Lys Thr Val Ala Gln
        355                 360                 365

Glu Glu Glu Arg Ile Lys Glu Val Arg Glu Val Ser Glu Ala Glu Arg
    370                 375                 380

Val Lys Gln Val Ile Leu Leu Gln Ala Gln Ala Glu Ala Glu Gln Glu
385                 390                 395                 400

Leu Val Arg Gln Val Lys Gln Ala Glu Ala Asp Glu Ala Arg Ser Lys
                405                 410                 415

His Lys Ala Val Glu Ile Asn Thr Met Ala Gln Ala Glu Leu Glu Ala
            420                 425                 430

Ala Ser Lys Gln Ala Glu Ala Lys Lys Arg Leu Ala Glu Gly Ile Glu
        435                 440                 445

Ala Glu Arg Ala Ala Pro Gly Leu Ala Asp Ala Arg Val Leu Glu Val
    450                 455                 460

Thr Ala Ala Ala Lys Glu Lys Asp Gly Leu Ala Ala Ala Arg Val Arg
465                 470                 475                 480

Ala Glu Gln Leu Ile Ala Glu Ala Arg Gly Asp Glu Glu Arg Gly Leu
                485                 490                 495

Ala Asp Ala Arg Val Leu Glu Ala Gln Ala Ala Ala Lys Glu Lys Asp
            500                 505                 510

Gly Leu Ala Glu Ala Lys Val Leu Ala Glu Lys Leu Gly Ala Gln Ala
        515                 520                 525

Arg Gly Glu Glu Gln Leu Gly Ala Ala Lys Ala Lys Ala Thr Lys Asp
    530                 535                 540

Gln Gly Ser Ala Glu Ala Glu Val Leu Leu Gln Arg Leu Asn Ala Glu
545                 550                 555                 560

Ala Glu Gly Leu Gly Lys Lys Phe Gly Ala Leu Asp Ala Leu Ser Asp
                565                 570                 575

Ser Ala Arg Gln His Glu Glu Phe Arg Met Gln Leu Glu Lys Ser Phe
            580                 585                 590

Glu Glu Ala Met Ala Ala Ile Ala Ala Asn Lys Asp Ile Ala Lys Asp
        595                 600                 605
```

-continued

```
Gln Ala Glu Val Leu Ala Thr Ala Leu Gly Lys Ala Asn Ile Glu Ile
    610                 615                 620

Val Gly Gly Glu Gly Asp Phe Phe Asn Ser Phe Ala Lys Ser Leu Ser
625                 630                 635                 640

Val Gly Lys Ala Ile Glu Gly Val Val Gly Lys Ser Pro Val Val Gln
                645                 650                 655

Asp Val Leu Ala Arg Leu Leu Asn Gly Arg Gly Ala Ala Ala Ala Val
            660                 665                 670

Met Pro Glu Arg Lys Ser Gly His Glu Asn Glu Pro Ala Ala Glu Val
        675                 680                 685


<210> SEQ ID NO 18
<211> LENGTH: 742
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 18

Met Tyr Pro Gln Phe Arg Arg Gly His Leu Ala Ala Ala Val Leu Phe
1               5                   10                  15

Ala Ser Ser Ser Leu Leu Gly Gly Gln Ala Leu Ala Glu Asp Glu Arg
            20                  25                  30

Leu Glu Glu Leu Asp Glu Arg Ala Glu Ser Val Val Gln Leu Gly Asp
        35                  40                  45

Glu Val Val Leu Gly Thr Ala Glu Gln Glu Leu Lys Gln Ala Pro Gly
    50                  55                  60

Val Ser Ile Ile Thr Ala Glu Asp Ile Arg Lys Arg Pro Pro Val Asn
65                  70                  75                  80

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

Asn Ser Ser Ser Gly Gln Arg Gly Asn Asn Arg Gln Ile Asp Ile Arg
            100                 105                 110

Gly Met Gly Pro Glu Asn Thr Leu Ile Leu Val Asp Gly Lys Pro Val
        115                 120                 125

Ser Ser Arg Asn Ser Val Arg Tyr Gly Trp Arg Gly Glu Arg Asp Thr
    130                 135                 140

Arg Gly Asp Ser Asn Trp Val Pro Pro Glu Glu Val Glu Arg Ile Glu
145                 150                 155                 160

Val Leu Arg Gly Pro Ala Ala Ala Arg Tyr Gly Ser Gly Ala Ala Gly
                165                 170                 175

Gly Val Val Asn Ile Ile Thr Lys Arg Pro Thr Asp Arg Leu Arg Gly
            180                 185                 190

Ser Met Thr Val Phe Thr Asn Ile Pro Glu Ser Ser Lys Asp Gly Ala
        195                 200                 205

Thr Arg Arg Ala Asn Phe Ser Leu Ser Gly Pro Leu Thr Glu Ala Leu
    210                 215                 220

Ser Phe Arg Ala Tyr Gly Ser Ala Asn Lys Thr Asp Ser Asp Asp Thr
225                 230                 235                 240

Asp Ile Asn Leu Gly His Thr Val Asn Pro Ser Arg Thr Val Ala Gly
                245                 250                 255

Arg Glu Gly Val Arg Asn Arg Asp Leu Ser Gly Met Leu Ser Trp Gln
            260                 265                 270

Val Thr Pro Asp Gln Val Val Asp Phe Glu Ala Gly Phe Ser Arg Gln
        275                 280                 285
```

-continued

```
Gly Asn Ile Tyr Ala Gly Asp Thr Gln Asn Asn Asn Gly Thr Ala Asn
    290                 295                 300

Thr Gln Gly Leu Ala Asp Asp Gly Ala Glu Thr Asn Arg Met Tyr Arg
305                 310                 315                 320

Glu Asn Tyr Ala Ile Thr His Asn Gly Thr Trp Ser Phe Gly Thr Ser
                325                 330                 335

Arg Phe Val Ala Gln Tyr Asp Ser Thr Arg Asn Asn Arg Leu Glu Glu
            340                 345                 350

Gly Leu Ala Gly Ser Val Glu Gly Gln Ile Gly Ala Asp Arg Ser Phe
        355                 360                 365

Ser Ala Ser Lys Leu Glu Asn Tyr Arg Leu Ser Gly Glu Leu Asn Leu
    370                 375                 380

Pro Leu His Ala Leu Phe Glu Gln Val Leu Thr Val Gly Ala Glu Trp
385                 390                 395                 400

Asn Lys Glu Thr Leu Asn Asp Pro Ser Ser Leu Lys Gln Gly Phe Val
                405                 410                 415

Gly Ser Asp Ser Leu Pro Gly Thr Pro Ala Ala Gly Ser Arg Ser Pro
            420                 425                 430

Lys Ser Lys Ala Glu Ile Arg Ala Leu Tyr Val Glu Asp Asn Ile Glu
        435                 440                 445

Leu Arg Pro Gly Thr Met Leu Thr Pro Gly Leu Arg Leu Asp Asp His
    450                 455                 460

Ser Asp Phe Gly Leu Asn Trp Ser Pro Ser Leu Asn Ala Ser Gln Thr
465                 470                 475                 480

Leu Gly Glu Tyr Phe Thr Val Lys Ala Gly Ile Ala Arg Ala Phe Lys
                485                 490                 495

Ala Pro Asn Leu Tyr Gln Ser Asn Pro Asn Tyr Leu Leu Tyr Thr Arg
            500                 505                 510

Gly Asn Gly Cys Pro Ile Gln Thr Ser Ser Gly Gly Cys Tyr Leu Val
        515                 520                 525

Gly Asn Glu Asn Leu Asp Ala Glu Thr Ser Val Asn Lys Glu Leu Gly
    530                 535                 540

Ile Glu Phe Arg Arg Asp Gly Trp Val Ala Gly Leu Thr Tyr Phe Arg
545                 550                 555                 560

Asn Asp Tyr Lys Asn Lys Ile Val Ala Pro Leu Asp Val Met Gly Gln
                565                 570                 575

Thr Gly Thr Gly Asn Asn Ile Leu Gln Trp Ser Asn Ala Lys Lys Ala
            580                 585                 590

Val Val Glu Gly Leu Glu Gly Asn Leu Leu Val Pro Leu His Glu Asp
        595                 600                 605

Leu Ser Trp Ser Thr Asn Leu Thr Tyr Met Leu Gln Ser Lys Asp Lys
    610                 615                 620

Asp Thr Gly Asn Pro Leu Ser Val Ile Pro Glu Tyr Thr Leu Asn Ser
625                 630                 635                 640

Thr Leu Asp Trp Gln Ala Ser Glu Arg Leu Ser Thr Gln Leu Thr Ser
                645                 650                 655

Thr Ile Tyr Gly Arg Gln Glu Pro Pro Lys His Gly Thr Ser Arg Asn
            660                 665                 670

Thr Pro Val Val Ser Arg Lys Glu Val Gly Thr Tyr Gly Ile Trp Gly
        675                 680                 685
```

-continued

```
Val Ser Ala Gly Tyr Thr Phe Ser Glu Asn Leu Ser Val Arg Gly Gly
    690                 695                 700

Val Ser Asn Leu Phe Asp Lys Arg Leu Tyr Arg Gln Gly Asn Ser Phe
705                 710                 715                 720

Asp Ala Gly Ala Ala Thr Tyr Asn Glu Pro Gly Arg Ala Tyr Tyr Val
                725                 730                 735

Ser Met Thr Thr Ser Phe
            740


<210> SEQ ID NO 19
<211> LENGTH: 746
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 19

Met Ser Ser Arg Ala Leu Pro Ala Val Pro Phe Leu Leu Leu Ser Ser
1               5                   10                  15

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

Val Ile Glu Leu Gly Glu Gln Thr Val Val Ala Thr Ala Gln Glu Glu
        35                  40                  45

Thr Lys Gln Ala Pro Gly Val Ser Ile Ile Thr Ala Glu Asp Ile Ala
    50                  55                  60

Lys Arg Pro Pro Ser Asn Asp Leu Ser Gln Ile Ile Arg Thr Met Pro
65                  70                  75                  80

Gly Val Asn Leu Thr Gly Asn Ser Ser Ser Gly Gln Arg Gly Asn Asn
                85                  90                  95

Arg Gln Ile Asp Ile Arg Gly Met Gly Pro Glu Asn Thr Leu Ile Leu
            100                 105                 110

Val Asp Gly Lys Pro Val Ser Ser Arg Asn Ser Val Arg Tyr Gly Trp
        115                 120                 125

Arg Gly Glu Arg Asp Ser Arg Gly Asp Thr Asn Trp Val Pro Ala Asp
    130                 135                 140

Gln Val Glu Arg Ile Glu Val Ile Arg Gly Pro Ala Ala Ala Arg Tyr
145                 150                 155                 160

Gly Asn Gly Ala Ala Gly Gly Val Val Asn Ile Ile Thr Lys Gln Ala
                165                 170                 175

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

His Lys Ala Glu Gly Ala Ser Glu Arg Met Ser Phe Gly Leu Asn Gly
        195                 200                 205

Pro Leu Thr Glu Asn Leu Ser Tyr Arg Val Tyr Gly Asn Ile Ala Lys
    210                 215                 220

Thr Asp Ser Asp Asp Trp Asp Ile Asn Ala Gly His Glu Ser Asn Arg
225                 230                 235                 240

Thr Gly Lys Gln Ala Gly Thr Leu Pro Ala Gly Arg Glu Gly Val Arg
                245                 250                 255

Asn Lys Asp Ile Asp Gly Leu Leu Ser Trp Arg Leu Thr Pro Glu Gln
            260                 265                 270

Thr Leu Glu Phe Glu Ala Gly Phe Ser Arg Gln Gly Asn Ile Tyr Thr
        275                 280                 285

Gly Asp Thr Gln Asn Thr Asn Ser Asn Asn Tyr Val Lys Gln Met Leu
    290                 295                 300
```

-continued

```
Gly His Glu Thr Asn Arg Met Tyr Arg Glu Thr Tyr Ser Val Thr His
305                 310                 315                 320

Arg Gly Glu Trp Asp Phe Gly Ser Ser Leu Ala Tyr Leu Gln Tyr Glu
                325                 330                 335

Lys Thr Arg Asn Ser Arg Ile Asn Glu Gly Leu Ala Gly Gly Thr Glu
            340                 345                 350

Gly Ile Phe Asp Pro Asn Asn Ala Gly Phe Tyr Thr Ala Thr Leu Arg
        355                 360                 365

Asp Leu Thr Ala His Gly Glu Val Asn Leu Pro Leu His Leu Gly Tyr
    370                 375                 380

Glu Gln Thr Leu Thr Leu Gly Ser Glu Trp Thr Glu Gln Lys Leu Asp
385                 390                 395                 400

Asp Pro Ser Ser Asn Thr Gln Asn Thr Glu Glu Gly Gly Ser Ile Pro
                405                 410                 415

Gly Leu Ala Gly Lys Asn Arg Ser Ser Ser Ser Ser Ala Arg Ile Phe
            420                 425                 430

Ser Leu Phe Ala Glu Asp Asn Ile Glu Leu Met Pro Gly Thr Met Leu
        435                 440                 445

Thr Pro Gly Leu Arg Trp Asp His His Asp Ile Val Gly Asp Asn Trp
    450                 455                 460

Ser Pro Ser Leu Asn Leu Ser His Ala Leu Thr Glu Arg Val Thr Leu
465                 470                 475                 480

Lys Ala Gly Ile Ala Arg Ala Tyr Lys Ala Pro Asn Leu Tyr Gln Leu
                485                 490                 495

Asn Pro Asp Tyr Leu Leu Tyr Ser Arg Gly Gln Gly Cys Tyr Gly Gln
            500                 505                 510

Ser Thr Ser Cys Tyr Leu Arg Gly Asn Asp Gly Leu Lys Ala Glu Thr
        515                 520                 525

Ser Val Asn Lys Glu Leu Gly Ile Glu Tyr Ser His Asp Gly Leu Val
    530                 535                 540

Ala Gly Leu Thr Tyr Phe Arg Asn Asp Tyr Lys Asn Lys Ile Glu Ser
545                 550                 555                 560

Gly Leu Ser Pro Val Asp His Ala Ser Gly Gly Lys Gly Asp Tyr Ala
                565                 570                 575

Asn Ala Ala Ile Tyr Gln Trp Glu Asn Val Pro Lys Ala Val Val Glu
            580                 585                 590

Gly Leu Glu Gly Thr Leu Thr Leu Pro Leu Ala Asp Gly Leu Lys Trp
        595                 600                 605

Ser Asn Asn Leu Thr Tyr Met Leu Gln Ser Lys Asn Lys Glu Thr Gly
    610                 615                 620

Asp Val Leu Ser Val Thr Pro Arg Tyr Thr Leu Asn Ser Met Leu Asp
625                 630                 635                 640

Trp Gln Ala Thr Asp Asp Leu Ser Leu Gln Ala Thr Val Thr Trp Tyr
                645                 650                 655

Gly Lys Gln Lys Pro Lys Lys Tyr Asp Tyr His Gly Asp Arg Val Thr
            660                 665                 670

Gly Ser Ala Asn Asp Gln Leu Ser Pro Tyr Ala Ile Ala Gly Leu Gly
        675                 680                 685

Gly Thr Tyr Arg Leu Ser Lys Asn Leu Ser Leu Gly Ala Gly Val Asp
    690                 695                 700
```

-continued

```
Asn Leu Phe Asp Lys Arg Leu Phe Arg Ala Gly Asn Ala Gln Gly Val
705                 710                 715                 720

Val Gly Ile Asp Gly Ala Gly Ala Ala Thr Tyr Asn Glu Pro Gly Arg
                725                 730                 735

Thr Phe Tyr Thr Ser Leu Thr Ala Ser Phe
            740                 745


<210> SEQ ID NO 20
<211> LENGTH: 784
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 20

Met Ser Pro Ser Arg Ala Leu Ser Pro Leu Ser Arg Ala Leu Leu Leu
1               5                   10                  15

Ala Cys Leu Gly Gly Pro Val Leu Val Ser Ala Gly Ser Ala Cys Ala
            20                  25                  30

Ala Glu Ile Arg Thr Asp Ala Arg Gln Tyr Tyr Arg Leu Pro Ala Glu
        35                  40                  45

Pro Leu Glu Gln Ala Leu Asn His Leu Gly Arg Gln Ala Gly Val Leu
    50                  55                  60

Ile Ala Phe Ser Pro Glu Gln Thr Ala Ala Arg Arg Ser Gln Ala Leu
65                  70                  75                  80

Asp Gly Glu Tyr Thr Leu Glu Glu Ala Leu Ala Ala Leu Leu Val Gly
                85                  90                  95

Ser Gly Leu Glu Ala Arg Ala Arg Gly Asp Gly Ala Tyr Thr Leu Glu
            100                 105                 110

Ala Leu Pro Val Glu Asp Pro Ala Asn Leu Gln Ala Leu Thr Val Val
        115                 120                 125

Gly Asp Trp Leu Ala Asp Ala Ser Ala Ala Asp Val Phe Glu His Pro
    130                 135                 140

Gly Ala Arg Asp Val Val Arg Arg Glu Gln Phe Gln Ala Gln Gly Ala
145                 150                 155                 160

Ala Ser Thr Arg Glu Val Leu Glu Arg Ile Pro Gly Val Ser Ala Pro
                165                 170                 175

Leu Asn Asn Gly Thr Gly Ser His Asp Leu Ala Leu Asn Phe Gly Ile
            180                 185                 190

Arg Gly Leu Asn Pro Arg Leu Ala Ser Arg Ser Thr Val Leu Met Asp
        195                 200                 205

Gly Ile Pro Val Pro Phe Ala Pro Tyr Gly Gln Pro Gln Leu Ser Leu
    210                 215                 220

Ala Pro Val Ser Ile Gly Asn Met Asp Ala Val Asp Val Val Arg Gly
225                 230                 235                 240

Gly Gly Ala Val Arg Tyr Gly Pro Gln Asn Val Gly Gly Ile Val Asn
                245                 250                 255

Phe Val Thr Arg Ala Ile Pro Glu Asp Phe Ala Thr Lys Leu Asp Val
            260                 265                 270

His Ser Glu Leu Ser Pro Ser Ser Ser Gln Asp Gly Leu Lys Thr Thr
        275                 280                 285

His Asn Val Leu Ile Gly Gly Thr Gly Ala Asn Gly Leu Gly Gly Ala
    290                 295                 300

Leu Leu Tyr Ser Gly Thr Arg Gly Gly Asp Trp Arg Glu His Ser Asp
305                 310                 315                 320
```

-continued

```
Thr Arg Ile Asp Asp Leu Ile Leu Lys Gly Arg Phe Gln Pro Ser Asp
                325                 330                 335

Glu His Thr Phe Ser Ala Met Thr Gln Tyr Tyr Asp Gly Glu Ala Asp
            340                 345                 350

Met Pro Gly Gly Leu Gly Thr Ala Ala Tyr His Asp Asp Pro Tyr Gln
        355                 360                 365

Ser Thr Arg Pro Tyr Asp Lys Phe Trp Gly Arg Arg Thr Leu Ala Ser
    370                 375                 380

Ala Ser Tyr Glu Tyr Thr Pro Asn Ala Ser Gln Lys Leu Asn Val Thr
385                 390                 395                 400

Gly Phe Phe Thr Lys Thr Leu Arg Ser Gly Tyr Leu Asp Gln Gly Arg
                405                 410                 415

Asn Leu Thr Leu Ser Pro Arg Glu Tyr Trp Val Arg Gly Leu Glu Thr
            420                 425                 430

Arg Phe Ser Gln Gly Phe Glu Leu Gly Glu Ser Arg His Glu Val Gly
        435                 440                 445

Ile Gly His Arg Tyr Val Asn Glu Ala Ser His Glu Leu Arg Tyr Trp
    450                 455                 460

Thr Arg Ala Asp Ser Gly Gln Leu Pro Ser Thr Gly Ser Arg Asn Asp
465                 470                 475                 480

Arg Asp Thr Arg Gly Ser Thr Glu Ala Asn Ala Phe Tyr Ile Asp Asp
                485                 490                 495

Arg Ile Asp Ile Gly Asn Trp Thr Ile Thr Pro Gly Ile Arg Tyr Glu
            500                 505                 510

Lys Ile Asp Ser Glu Gln Lys Asn Leu Leu Lys Asn Ser Lys Asp Ser
        515                 520                 525

Gly Arg Tyr Asn Ala Ser Leu Pro Ala Leu Asn Val Ile Tyr His Leu
    530                 535                 540

Thr Pro Ser Trp Asn Leu Tyr Ala Asn Thr Glu Gly Ser Phe Gly Thr
545                 550                 555                 560

Val Gln Tyr Ser Gln Met Gly Lys Ala Val Arg Ser Gly Asp Ile Glu
                565                 570                 575

Pro Glu Lys Ala Arg Thr Trp Glu Leu Gly Ser Arg Tyr Asp Asp Gly
            580                 585                 590

Ile Leu Arg Ala Glu Leu Gly Ala Phe Leu Ile Asn Phe Asp Asn Gln
        595                 600                 605

Tyr Glu Ser Asn Gln Gln Thr Asp Ser Val Thr Ala Arg Gly Lys Thr
    610                 615                 620

Arg His Lys Gly Ile Glu Ala Ala Ile Ala Tyr Asp Leu Ala Asp Leu
625                 630                 635                 640

Asp Pro Leu Leu Ser Gly Phe Asp Val Tyr Ala Ser Tyr Ala Tyr Val
                645                 650                 655

Asp Ala Ser Ile Arg Glu Asp Gly Pro Asn Lys Gly Asn Gln Val Pro
            660                 665                 670

Phe Ser Ser Lys His Lys Gly Thr Leu Gly Ala Asn Tyr Arg Thr Gly
        675                 680                 685

Ala Trp Ser Tyr Asn Leu Asp Gly Ser Phe Gln Thr Ser Gln Tyr Ala
    690                 695                 700

Asp Asn Ala Asn Thr Glu Ser Glu Ser Ala Asp Gly Ser Thr Gly Arg
705                 710                 715                 720
```

-continued

```
Ile Ala Gly Trp Met Val Trp Ser Ala Arg Gly Thr Tyr Asp Phe Gly
                725                 730                 735

Pro Gln Leu Asn Asp Leu Lys Leu Gly Leu Gly Val Lys Asn Leu Phe
            740                 745                 750

Asp Arg Arg Tyr Tyr Thr Arg Ser Phe Asp Asp Asn Asn Lys Gly Leu
        755                 760                 765

Tyr Val Gly Gln Pro Arg Thr Leu Tyr Val Gln Ala Ser Val Gly Phe
    770                 775                 780


<210> SEQ ID NO 21
<211> LENGTH: 851
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 21

Met Thr Leu Pro Phe Thr Arg Ala Ala Trp Arg Pro Leu Cys Ser Ala
1               5                   10                  15

Ala Val Leu Gly Ala Ala Leu Trp Ala Ala Gly Ala Ser Ala Ala Glu
            20                  25                  30

Arg Arg Phe Asp Leu Pro Ala Gln Pro Leu Ala Ala Ser Leu Ser Arg
        35                  40                  45

Leu Ala Gln Gln Ala Gln Val Gln Val Leu Phe Asp Glu Ser Leu Leu
    50                  55                  60

Arg Gly Leu Arg Ala Pro Ala Leu Ser Gly Ser Tyr Gly Val Arg Glu
65                  70                  75                  80

Ala Leu Glu Arg Leu Leu Val Gly Ser Glu Leu Glu Leu Val Glu Ala
                85                  90                  95

Gly Gly Gly Tyr Val Val Arg Arg Arg Gln Val Asp Ala Tyr Ser Asp
            100                 105                 110

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

Val Asp Ala Ser Asn Val Gly Arg Ser Thr Leu Thr Arg Arg Asp Ile
    130                 135                 140

Glu Arg Gln Gln Ala Asp Asn Ile Pro Ser Leu Leu Gln Thr Leu Pro
145                 150                 155                 160

Gly Val Thr Met Gly Gly Ser Pro Lys Pro Gly Gly Gln Thr Thr Asn
                165                 170                 175

Ile Trp Gly Leu Gly Asp Ala Glu Asp Val Pro Tyr Thr Leu Asp Gly
            180                 185                 190

Ala Gln Lys Ser Gly Phe Glu Arg Tyr Gln Gln Gly Thr Val Phe Ile
        195                 200                 205

Glu Pro Glu Met Ile Lys Arg Ile Glu Val Glu Lys Gly Pro His Ser
    210                 215                 220

Val Phe Thr Gly Asn Gly Gly Phe Gly Gly Thr Val His Met Glu Thr
225                 230                 235                 240

Lys Asp Ala Pro Asp Leu Leu Arg Glu Gly Arg Asp Val Gly Ala Met
                245                 250                 255

Leu Lys Tyr Gly Tyr His Ser Asn Asp Gln Gln Lys Ile Tyr Ser Gly
            260                 265                 270

Ala Val Phe Gly Arg Ser Glu Asp Arg Arg Val Asp Ala Leu Leu Tyr
        275                 280                 285

Leu Asn Gly Arg Asp Gly Arg Asp Met Lys Leu Ala Asp Asn Leu Pro
    290                 295                 300
```

-continued

```
Leu Ser Pro Thr Asp Tyr Pro Ile Asn Pro Lys Arg Leu Pro Asn Ser
305                 310                 315                 320

Ala Gln Asp Glu Lys Thr Gly Leu Phe Lys Leu Asn Leu His Pro Thr
                325                 330                 335

Glu Glu His Asp Leu Gly Phe Thr Tyr Leu Arg Ser Lys Ser Ser Arg
            340                 345                 350

Trp Thr Pro Phe Ser Ala Ser Ser Tyr Pro Thr Pro Pro Ser Gln Trp
        355                 360                 365

Thr Ile Asp Arg Tyr Gly Tyr Glu Leu Gly Leu Thr Arg Leu Leu Ala
    370                 375                 380

His Arg Asp Thr Thr Asp Thr Thr Trp Thr Gly Lys Tyr Asn Tyr His
385                 390                 395                 400

Pro Leu Asp Asn Pro Trp Ile Asp Leu Gln Leu Ser Tyr Ser Asp Ala
                405                 410                 415

Arg Thr Glu Gln Leu Asp Arg Arg Glu Asp Thr Ala Phe Tyr Gln Leu
            420                 425                 430

Ala Thr Gly Gly Lys Arg Met Arg Thr Glu Tyr Gln Asp Lys Val Leu
        435                 440                 445

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

Leu Thr Leu Gly Ala Ala Leu His Lys His Lys Arg Asp Ile Leu Met
465                 470                 475                 480

His Met Pro Gly Lys Thr Tyr Glu Thr Pro Arg Tyr Asn Tyr Gly Trp
                485                 490                 495

Leu Gln Pro Ala Phe Met Pro Ala Gly Lys Gln Asp Thr Gln Ser Phe
            500                 505                 510

Tyr Ile Gln Asp Ala Ile Thr Tyr Gly Ser Leu Thr Val Thr Pro Ser
        515                 520                 525

Met Arg Phe Asp Ser Val Arg Asn Asp Gly Gln Ala Asn Leu Ala Pro
    530                 535                 540

Ile Tyr Asp Asn Pro Lys Leu Gly His Asp Tyr Arg Ala Gln Thr Tyr
545                 550                 555                 560

Ser Gly Trp Ser Pro Arg Leu Ser Val Phe Trp Thr Ala Thr Pro Asn
                565                 570                 575

Leu Ala Phe Phe Ala Asp Tyr Thr Glu Thr Trp Arg Ala Pro Val Ile
            580                 585                 590

Asp Glu Gln Tyr Glu Val Gln Asn Ser Ser Thr Ile Gly Gly Ser Ser
        595                 600                 605

Arg Asp Leu Asp Ala Glu Arg Ile His Ala Ile Arg Gly Gly Ser Val
    610                 615                 620

Ile Asn Leu Pro Asp Leu Leu Val Ala Gly Asp Ser Leu Gln Ile Arg
625                 630                 635                 640

Thr Thr Leu Phe Gln Asn Arg Ile Lys Asp Glu Ile Phe Arg Thr Arg
                645                 650                 655

Ser Val Gly Cys Arg Gln Gln Ser Ile Asp Asn Gly Ser Ile Gly Gly
            660                 665                 670

Ser Cys Gly Asp Met Leu Pro Leu Ser Asn Tyr Arg Asn Leu Pro Gly
        675                 680                 685

Leu Thr Ile Lys Gly Phe Glu Ile Glu Ser Phe Tyr Asp Ser Gln Arg
    690                 695                 700
```

-continued

```
Leu Phe Gly Ser Leu Ser Tyr Ser Trp Met Thr Gly Lys His Asp Gly
705                 710                 715                 720

Ala Tyr Ser Asn Pro Trp Gly Pro Asn Val Trp Ala Arg Asp Ile Pro
                725                 730                 735

Pro Pro Lys Trp Val Ala Met Leu Gly Leu Lys Val Pro Glu Trp Asp
            740                 745                 750

Ala Lys Leu Gly Trp Gln Gly Glu Phe Val Arg Lys Thr Asp Arg Leu
        755                 760                 765

Pro Ser Asp Arg Tyr Ser Gly Gly Met Gly Thr Gly Ser Gly Asp Ile
    770                 775                 780

Tyr Trp Asp His Ala Ala Asn Asp Ser Tyr Asp Thr His Arg Leu Phe
785                 790                 795                 800

Ala Glu Trp Val Pro Ala Lys Leu Gly Leu Lys Asp Thr Arg Ile Asp
                805                 810                 815

Phe Thr Val Asp Asn Leu Phe Asn Arg Ser Tyr Arg Gln Pro Leu Gly
            820                 825                 830

Gly Asp Leu Val Tyr Ser Gln Gly Arg Asn Ala Lys Ile Ser Val Thr
        835                 840                 845

Gln Phe Phe
    850


<210> SEQ ID NO 22
<211> LENGTH: 880
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 22

Met His Arg Ser Leu His Thr Asp Ala Pro Leu Gly Ala Ala Leu Leu
1               5                   10                  15

Leu Ala Leu Gln Leu Ala Pro Gly Ser Ala Ala Ala Ala Glu Glu Gln
            20                  25                  30

Ala Pro Val Asp Pro Pro Thr Val Gln Leu Gln Arg Ile Glu Val Thr
        35                  40                  45

Gly Ser Ala Ile Arg Arg Val Asp Ala Glu Thr Ala Val Pro Ile Ser
    50                  55                  60

Val Leu Arg Ala Glu Glu Leu Arg Gln Gln Gly Val Thr Ser Thr Glu
65                  70                  75                  80

Glu Leu Ile Gly Arg Leu Ser Gly Asn Gln Gly Val Tyr Asn Ser Ser
                85                  90                  95

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

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

Ala Asn Asn Ala Ile Asp Gly Ser Ala Val Asp Leu Asn Thr Ile Pro
    130                 135                 140

Phe Ala Ala Ile Asp Arg Val Glu Val Leu Arg Asp Gly Ala Ser Ala
145                 150                 155                 160

Leu Tyr Gly Thr Asp Ala Ile Gly Gly Val Ile Asn Phe Ile Thr Arg
                165                 170                 175

Lys Ser Leu Asn Glu Gly Arg Phe Asp Ser Gly Tyr Ala Ser Pro Thr
            180                 185                 190

His Asp Gly Gly Gly Asn Gln Arg Asn Val Ser Ala Ser Trp Gly Phe
        195                 200                 205
```

-continued

```
Gly Glu Leu Glu Glu Asp Arg Phe Asn Val Phe Ala Val Ala Asn Tyr
    210                 215                 220

Asp Lys Gln Glu Arg Leu Gly Ala Lys Asp Arg Gly Tyr Thr Tyr Asn
225                 230                 235                 240

Tyr Gln Pro Gly Arg Gly Leu Asp Tyr Ser Ser Gly Thr Ala Phe Pro
                245                 250                 255

Gly Asn Trp Ser Gln Gly Ala Asn Ala Ser Asn Pro Leu Ala Ala Gly
            260                 265                 270

Gly Cys Lys Gly Ala Asp Leu Ile Pro Arg Asn Gly Ile Cys Arg Gln
        275                 280                 285

Ser Leu Trp Arg Tyr Leu Asp Leu Val Pro Glu Thr Glu Lys Thr Ser
    290                 295                 300

Val Phe Ser Arg Ala Thr Gly Lys Leu Ala Asp Glu His Asn Val Ser
305                 310                 315                 320

Leu Glu Tyr Phe Trp Ser Arg Ser Asp Asn Ala Thr Gln Val Gly Pro
                325                 330                 335

Gly Thr Leu Thr Gly Leu Gln Ile Asp Pro Gly Thr Ala Phe Tyr Pro
            340                 345                 350

Gly Asn Gly Ile Thr Pro Gly Pro Gly Gly Phe Val Leu Asp Pro Ser
        355                 360                 365

Arg Pro Val Glu Val Asn Trp Arg Gln Ser Val Leu Gly Pro Arg Leu
    370                 375                 380

Gln Ser Ser Gln Asn Thr Gly Gln Arg Leu Leu Leu Gly Phe Asp Gly
385                 390                 395                 400

Gln Phe Ala Gly Trp Asp Tyr Asp Ile Gly Ala Ser Tyr Asn Gln Asn
                405                 410                 415

Lys Val Val Asp His Ile His Ser Gly Tyr Val Asp Asp Arg Ala Ala
            420                 425                 430

Ala Leu Gly Ile Ala Asn Gly Thr Leu Asn Pro Phe Gly Pro Gln Thr
        435                 440                 445

Asp Ala Gly Leu Ala Tyr Leu Gly Ser His Ala Leu Ser Gly Asp Phe
    450                 455                 460

Arg Thr Ser Val Gly Arg Val Lys Gly Leu Asp Ala Arg Ala Ser Arg
465                 470                 475                 480

Glu Ile Gly Asp Trp Phe Gly Ala Gly Pro Ala Ala Leu Ala Leu Gly
                485                 490                 495

Gly Glu Phe Arg Lys Glu Ala Phe His Gln Asp Ile Gln Asp Phe Ala
            500                 505                 510

Gly Asn Val Gln Ser Leu Gly Val Asp Pro Ala Ala Thr Val Ser Gly
        515                 520                 525

Glu Arg Asn Leu Lys Ala Gln Tyr Ala Glu Leu Asn Val Pro Val Leu
    530                 535                 540

Asp Ser Leu Glu Leu Ser Ala Ala Ile Arg His Asp Lys Tyr Ser Asp
545                 550                 555                 560

Phe Gly Ser Thr Ser Asn Pro Lys Tyr Ser Phe Arg Phe Gln Pro Phe
                565                 570                 575

Arg Gln Leu Val Leu Arg Gly Ala Tyr Ser Glu Gly Phe Arg Ala Pro
            580                 585                 590

Ser Leu Tyr Glu Leu Tyr Asn Pro Thr Phe Thr Thr Tyr Thr Ser Ala
        595                 600                 605
```

-continued

Asn Tyr Asp Asp Pro Arg Leu Cys Ala Gly Gly Gln Pro Ser Gln Gly
610 615 620

Gly Ile Ala Asn Arg Asp Cys Ala Gln Gln Phe Tyr Asn Ala Thr Gly
625 630 635 640

Gly Asn Thr Asp Leu Arg Pro Glu Thr Ala Arg Asn Val Thr Leu Gly
645 650 655

Leu Val Tyr Gln Pro Leu Arg Asp Leu Ser Val Gly Leu Asp Phe Trp
660 665 670

Trp Ile Arg Ile Ala Asn Gln Ile Ala Glu Phe Pro Glu Ala Ala Ile
675 680 685

Phe Ala Asp Pro Gln Ala Tyr Ala Gly Arg Ile Val Arg Lys Ala Asp
690 695 700

Gly Ser Ile Asp His Val Val Thr Gly Leu Ala Asn Leu Gly Lys Val
705 710 715 720

Lys Thr Ser Gly Val Asp Leu Ser Leu Asp Tyr Arg Phe Pro Ala Ser
725 730 735

Arg Tyr Gly Gln Phe Gly Leu Asp Leu Gln Gly Thr Tyr Val Ser Arg
740 745 750

Tyr Asp Phe Gln Gln Gln Ile Gly Gly Gln Tyr Leu Asp Asn Val Gly
755 760 765

Asp Phe Gln Gly Val Gly Val Ile Ala Arg Trp Lys His Val Ala Asn
770 775 780

Ala Thr Trp Ser Arg Asp Ala Trp Gln Ala Thr Leu Ser Asn Arg Tyr
785 790 795 800

Thr Ser Gly Tyr Asn Asp Tyr Asp Arg Ala Ser His Gly Lys Val Gly
805 810 815

Ser Trp Asn Leu Trp Asp Leu Ala Gly Ser Tyr Arg Leu Ser His Ala
820 825 830

Leu Gly Leu Thr Leu Gly Val Lys Asn Leu Phe Asp Arg Glu Pro Pro
835 840 845

Phe Ser Asn Gln Thr Tyr Thr Phe Gln Ser Gly Tyr Asp Pro Arg Tyr
850 855 860

Thr Asp Pro Tyr Gly Arg Ile Leu Phe Gly Arg Leu Ser Tyr Ser Phe
865 870 875 880

<210> SEQ ID NO 23
<211> LENGTH: 919
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 23

Met Val Arg Leu Arg Thr Leu Val Arg Ala Ile Ala Ala Ala Ser Val
1 5 10 15

Leu Thr Ser Gly Met Ala His Gly Leu Gly Leu Gly Glu Ile Thr Leu
20 25 30

Lys Ser Ala Leu Asn Gln Pro Leu Asp Ala Glu Ile Glu Leu Leu Glu
35 40 45

Val Arg Asp Leu Gly Ser Gly Glu Val Ile Pro Ser Leu Ala Ser Pro
50 55 60

Glu Glu Phe Ser Lys Ala Gly Val Asp Arg Leu Tyr Tyr Leu Thr Asp
65 70 75 80

Leu Lys Phe Thr Pro Val Val Lys Pro Asn Gly Lys Ser Val Ile Arg
85 90 95

-continued

```
Val Thr Ser Ser Lys Pro Val Gln Glu Pro Tyr Leu Asn Phe Leu Val
            100                 105                 110

Gln Val Leu Trp Pro Asn Gly Arg Leu Leu Arg Glu Tyr Thr Val Leu
        115                 120                 125

Leu Asp Pro Pro Leu Tyr Ser Pro Gln Ala Ala Ala Ser Ala Pro Gln
    130                 135                 140

Ala Pro Val Ser Ala Pro Arg Ala Thr Gly Ala Pro Arg Ala Pro Gln
145                 150                 155                 160

Ala Pro Ala Pro Val Arg Thr Thr Ala Pro Ala Gly Ser Asp Thr Tyr
                165                 170                 175

Arg Thr Val Ser Asn Asp Thr Leu Trp Glu Ile Ala Gln Arg Asn Arg
            180                 185                 190

Thr Asp Arg Val Ser Val Pro Gln Ala Met Leu Ala Phe Gln Glu Leu
        195                 200                 205

Asn Pro Gly Ala Phe Val Asp Gly Asn Ile Asn Arg Leu Lys Ser Gly
    210                 215                 220

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

Arg Glu Ala Leu Ser Gln Val Gln Ala Gln Asn Gln Ser Trp Arg Gly
                245                 250                 255

Ser Arg Asn Pro Ala Ala Gly Ser Ala Gly Ala Arg Gln Leu Asp Ala
            260                 265                 270

Thr Gln Arg Asn Ala Ala Gly Ser Ala Pro Ser Lys Val Asp Ala Thr
        275                 280                 285

Asp Asn Leu Arg Leu Val Ser Gly Glu Gly Lys Ala Ser Lys Gly Ala
    290                 295                 300

Asp Lys Gly Gly Lys Gly Asp Ser Lys Ala Ile Ala Asp Thr Leu Ala
305                 310                 315                 320

Val Thr Lys Glu Ser Leu Asp Ser Thr Arg Arg Glu Asn Glu Glu Leu
                325                 330                 335

Gln Ser Arg Met Gln Asp Leu Gln Ser Gln Leu Asp Lys Leu Gln Lys
            340                 345                 350

Leu Ile Gln Leu Lys Asp Ala Gln Leu Ala Lys Leu Gln Gly Gln Leu
        355                 360                 365

Gly Ala Glu Gly Gln Gly Ala Ala Gln Pro Asn Ala Ala Leu Pro Asp
    370                 375                 380

Ala Ser Gln Pro Asn Ala Ala Ala Gln Ala Pro Ala Gln Pro Gly Thr
385                 390                 395                 400

Pro Ala Ala Ala Ala Pro Thr Pro Ala Pro Ala Gly Glu Ala Pro Ala
                405                 410                 415

Ala Pro Ala Gln Pro Pro Val Ala Pro Pro Pro Ala Pro Ala Ala Glu
            420                 425                 430

Lys Pro Pro Ala Pro Ala Val Pro Ala Pro Ala Pro Val Gln Ala Ala
        435                 440                 445

Glu Gln Pro Ala Pro Ser Phe Leu Asp Glu Leu Leu Ala Asn Pro Leu
    450                 455                 460

Trp Leu Ala Val Ile Gly Gly Ser Ala Leu Leu Ala Leu Leu Val Leu
465                 470                 475                 480

Leu Met Ile Leu Ser Arg Arg Asn Ala Gln Lys Glu Lys Glu Glu Ala
                485                 490                 495
```

-continued

```
Gln Ala Phe Ala Ala Asp Thr Gly Glu Glu Gln Glu Asp Ala Leu Asp
            500                 505                 510

Leu Gly Lys Asp Gly Phe Asp Asp Leu Thr Leu Asp Glu Pro Glu Pro
        515                 520                 525

Gln Val Ala Ala Val Ala Pro Gln Val Glu Lys Thr Thr Ala Gln Thr
    530                 535                 540

Ser Asp Ala Leu Gly Glu Ala Asp Ile Tyr Ile Ala Tyr Gly Arg Phe
545                 550                 555                 560

Asn Gln Ala Ala Glu Leu Leu Gln Asn Ala Ile Tyr Asp Glu Pro Gln
                565                 570                 575

Arg Thr Asp Leu Arg Leu Lys Leu Met Glu Val Tyr Ala Glu Met Gly
            580                 585                 590

Asp Arg Glu Gly Phe Ala Arg Gln Glu Asn Glu Leu Arg Glu Ile Gly
        595                 600                 605

Gly Ala Gln Pro Gln Val Glu Gln Leu Lys Ser Arg Tyr Pro Ala Met
    610                 615                 620

Val Ala Val Ala Ala Val Ala Gly Leu Ala Gly Ala Lys Leu Ala Gln
625                 630                 635                 640

Asp Glu Leu Asp Ser Phe Ser Leu Asp Asp Leu Ser Leu Asp Asp Ser
                645                 650                 655

Gly His Ala Ala Lys Pro Asp Ala Ala Gly Gln Asp Leu Asp Asp Ala
            660                 665                 670

Phe Asp Leu Ser Leu Asp Asp Leu Gly Gly Asp Asp Val Gln Ala Asp
        675                 680                 685

Leu Lys Ser Asp Ser Gly Ala Leu Asp Asp Leu Thr Leu Asp Ser Asp
    690                 695                 700

Leu Asp Leu Ala Ala Ser Thr Pro Ala Asp Lys Pro Val Asp Asp Leu
705                 710                 715                 720

Asp Phe Gly Leu Asp Phe Ala Glu Leu Ala Glu Thr Pro Ser Gln Pro
                725                 730                 735

Lys His Asp Asp Leu Gly Asp Phe Ser Leu Asp Leu Asp Ala Pro Glu
            740                 745                 750

Asp Lys Leu Ser Asp Asp Asp Phe Leu Leu Ser Leu Asn Asp Glu Val
        755                 760                 765

Pro Ala Ala Ala Pro Ala Asp Asn Glu Phe Thr Leu Asp Thr Glu Ala
    770                 775                 780

Ala Glu Glu Pro Ala Leu Ser Leu Pro Asp Asp Phe Asp Leu Ser Leu
785                 790                 795                 800

Ala Asp Glu Pro Thr Glu Pro Ala Ala Pro Glu Lys Gly Glu Asp Ser
                805                 810                 815

Phe Ala Ala Gln Leu Asp Glu Val Ser Ala Gln Leu Asp Glu Leu Ala
            820                 825                 830

Ser Asn Leu Asp Glu Pro Lys Ser Ala Thr Pro Ser Phe Ser Ala Glu
        835                 840                 845

Asp Ala Ala Val Ala Ser Ala Leu Asp Gly Asp Ala Asp Asp Asp Phe
    850                 855                 860

Asp Phe Leu Ser Gly Ala Asp Glu Ala Ala Thr Lys Leu Asp Leu Ala
865                 870                 875                 880

Arg Ala Tyr Ile Asp Met Gly Asp Ser Glu Gly Ala Arg Asp Ile Leu
                885                 890                 895

Asp Glu Val Leu Ala Glu Gly Asn Asp Ser Gln Gln Ala Glu Ala Arg
```

-continued

```
            900                 905                 910

Glu Leu Leu Glu Arg Leu Ala
        915


<210> SEQ ID NO 24
<211> LENGTH: 995
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 24

Met Thr Asp Asp His Ser Phe Arg Pro Arg Pro Thr Ser Leu Ser Ala
1               5                   10                  15

Ala Leu Leu Leu Gly Ala Trp Ile Ala Gln Pro Ala Thr Ala Ala Tyr
            20                  25                  30

Val Glu Ala Gly Arg Pro Gly Asp Pro Ala Ser Trp Arg Ser Ala Glu
        35                  40                  45

Tyr Gln Gln Asp Trp Gly Leu Glu Arg Met Arg Ala Asp Gln Ala Tyr
    50                  55                  60

Ala Ala Gly Ile Asp Gly Gln Gly Val Lys Ile Gly Glu Met Asp Ser
65                  70                  75                  80

Gly Phe Asp Pro Ser His Pro Asp Thr Pro Ala Ser Arg Tyr Gln Pro
                85                  90                  95

Val Thr Ala Ser Gly Thr Tyr Val Asp Gly Thr Pro Phe Ser Val Ser
            100                 105                 110

Gly Ala Met Asn Gly Asn Asn Asp Ser His Gly Thr His Val Gly Gly
        115                 120                 125

Thr Leu Gly Ala Ser Arg Asp Gly Val Gly Met His Gly Val Ala Tyr
    130                 135                 140

Ala Ala Gln Val Tyr Val Ala Asn Thr Asn Gln Asn Asp Ser Phe Leu
145                 150                 155                 160

Phe Gly Pro Thr Pro Asp Pro Asn Tyr Phe Lys Ala Ala Tyr Gln Ala
                165                 170                 175

Leu Ala Asp Ala Gly Val Arg Ala Ile Asn Asn Ser Trp Gly Ser Gln
            180                 185                 190

Pro Lys Asp Val Ser Tyr Glu Thr Leu Asp Gly Leu His Ala Ala Tyr
        195                 200                 205

Ala Gln His Tyr Gly Arg Ser Thr Trp Leu Asp Ala Ala Ala Gly Val
    210                 215                 220

Ser Arg Gln Gly Val Ile Asn Val Phe Ser Ala Gly Asn Ser Gly Tyr
225                 230                 235                 240

Ala Asn Ala Ser Val Arg Ser Ala Leu Pro Tyr Phe Gln Pro Asp Leu
                245                 250                 255

Glu Gly His Trp Leu Ala Val Ser Gly Leu Asp Gln Gln Asn Gly Gln
            260                 265                 270

Arg Tyr Asn Arg Cys Gly Ile Ala Lys Tyr Trp Cys Ile Thr Thr Pro
        275                 280                 285

Gly Arg Leu Ile Asn Ser Thr Met Pro Gly Gly Gly Tyr Ala Asn Lys
    290                 295                 300

Ser Gly Thr Ser Met Ala Ala Pro His Ala Thr Gly Ala Leu Ala Leu
305                 310                 315                 320

Val Met Gln Arg Tyr Pro Tyr Leu Asn Asn Glu Gln Ala Leu Gln Val
                325                 330                 335
```

-continued

```
Leu Leu Thr Thr Ala Thr Gln Leu Asp Gly Thr Pro Thr Gly Ala Pro
            340                 345                 350

Thr Asp Thr Val Gly Trp Gly Val Pro Asp Leu Gly Arg Ala Met His
        355                 360                 365

Gly Pro Gly Gln Leu Leu Gly Arg Phe Glu Ala Asn Leu Pro Ala Gly
    370                 375                 380

Leu Arg Asp Glu Trp Ser Asn Pro Ile Ser Asp Ser Ala Leu Leu Gln
385                 390                 395                 400

Arg Gln Ala Glu Asp Ala Ala Glu His Ala Ala Trp Gln Arg Thr Leu
                405                 410                 415

Lys Asp Lys Gly Trp Glu Asn Gly Leu Pro Ala Gly Ala Ser Gln Gln
            420                 425                 430

Glu Arg Thr Asp Tyr Ala Ile Gly Met Ala Arg Asp Gln Ala Ala Ala
        435                 440                 445

Gln Arg Gln Tyr Gln Gly Ser Leu Val Lys Ala Gly Ala Gly Ser Leu
    450                 455                 460

Val Leu Ser Gly Asp Ser Thr Tyr Arg Gly Pro Thr Leu Val Asp Gly
465                 470                 475                 480

Gly Leu Leu Ser Val Asp Gly Ser Leu Leu Ser Ala Val Glu Val Asn
                485                 490                 495

Ala Gly Gly Thr Leu Gly Gly Ser Gly Arg Ile Gly Gly Leu Leu Ala
            500                 505                 510

Arg Ser Gly Gly Thr Val Ala Ala Gly Asn Ser Ile Gly Thr Leu Glu
        515                 520                 525

Val Ala Gly Asp Leu Arg Phe Glu Ser Gly Ser Thr Tyr Ala Val Glu
    530                 535                 540

Leu Ser Glu Ser Ala Ser Asp Arg Ile Val Ala Ser Gly Lys Ala Ser
545                 550                 555                 560

Ile Ala Gly Gly Asn Val Thr Leu Ala Met Glu Asn Ser Pro Asp Leu
                565                 570                 575

Leu Ser Gln Ser Gln Val Glu Ser Leu Val Gly Arg Arg Tyr Asp Ile
            580                 585                 590

Leu Asp Ala Ala Gly Gly Ile Asp Gly Arg Phe Asp Ala Val Leu Pro
        595                 600                 605

Asn Tyr Leu Phe Leu Gly Gly Thr Leu Asp Tyr Ala Ala Asn Ala Ile
    610                 615                 620

Arg Leu Asp Ile Gly Arg Asn Gly Thr Thr Leu Ala Ser Val Ala Gln
625                 630                 635                 640

Thr Pro Asn Gln Ala Ala Val Ala Gly Ala Val Glu Thr Leu Gly Ala
                645                 650                 655

Gly Asn Pro Val Tyr Glu Ser Leu Leu Leu Ser Glu Asn Ala Ala Thr
            660                 665                 670

Ala Gln Arg Ala Phe Gln Gln Leu Ser Gly Glu Ile Tyr Pro Ala Leu
        675                 680                 685

Ala Gly Leu Leu Leu Asn Asp Ser Arg Tyr Leu Arg Asp Ser Val Gly
    690                 695                 700

Glu Arg Leu Arg Gln Thr Ser Asp Gly Glu Ala Gly Gly Glu Ala Pro
705                 710                 715                 720

Glu Gly Trp Phe Lys Ala Leu Gly Ser Trp Gly Lys Ser Ala Asp Gly
                725                 730                 735

Ser His Gly Ser Glu Gly Tyr Arg His Ser Val Gly Gly Phe Leu Leu
```

-continued

```
            740                 745                 750

Gly Val Asp Ser Gln Val Ala Ser Asp Thr Arg Leu Gly Leu Val Ala
        755                 760                 765

Gly Tyr Ser Asn Ser Ser Leu Asn Met Asp Ser Ser Leu Gln Ser Ser
    770                 775                 780

Ala Ser Ile Asp Ser Tyr His Leu Gly Ala Tyr Leu Gly Arg Gln Leu
785                 790                 795                 800

Gln Gln Trp Arg Leu Ser Leu Gly Ala Ala His Ala Trp His Arg Ala
            805                 810                 815

Glu Val Lys Arg Asp Leu Gln Tyr Gly Ala Val Ala Gly Lys Gln Lys
            820                 825                 830

Ala Lys Leu Asp Ala Gln Ser Ser Gln Leu Phe Ala Glu Ala Ala Tyr
        835                 840                 845

Ala Leu Gly Trp Arg Ser Leu Glu Leu Glu Pro Phe Ala Gly Leu Ala
    850                 855                 860

Tyr Val His Val Ala Ser Asp Asp Phe Arg Glu Arg Gly Ser Ala Ala
865                 870                 875                 880

Ala Leu Glu Gly Gly Asp Asp Asn Leu Asp Ala Ala Phe Thr Thr Leu
            885                 890                 895

Gly Leu Arg Ala Lys Arg His Phe Glu Leu Asp Ala Gly Arg Arg Leu
            900                 905                 910

Ala Leu Ser Gly Thr Leu Gly Trp Arg His Asn Leu Ser Asp Thr Thr
        915                 920                 925

Pro Gln Arg His Leu Ala Phe Ala Ser Gly Ser Gln Pro Phe Ser Val
    930                 935                 940

Glu Ser Val Ala Leu Ser Arg Asp Ala Ala Leu Leu Gly Val Asp Ala
945                 950                 955                 960

Ser Leu Ala Val Asn Arg Glu Val Ser Val Arg Leu Gly Tyr Asn Gly
            965                 970                 975

Leu Leu Gly Ser Arg Glu Lys Asp His Gly Val Gly Leu Ala Val Asp
            980                 985                 990

Trp Arg Phe
        995


<210> SEQ ID NO 25
<211> LENGTH: 1057
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 25

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

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

Ala Arg Glu Gln Lys Lys Ala Asn Ile Tyr Lys Gly Arg Ile Thr Arg
        35                  40                  45

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

His Gly Phe Leu Pro Leu Lys Glu Ile Ser Arg Glu Tyr Phe Lys Lys
65                  70                  75                  80

Ser Pro Glu Gly Arg Ile Asn Ile Lys Glu Val Leu Ser Glu Gly Gln
                85                  90                  95
```

-continued

```
Glu Val Ile Val Gln Val Glu Lys Glu Glu Arg Gly Asn Lys Gly Ala
            100                 105                 110

Ala Leu Thr Thr Phe Ile Ser Leu Ala Gly Arg Tyr Leu Val Leu Met
        115                 120                 125

Pro Asn Asn Pro Arg Ala Gly Gly Ile Ser Arg Arg Ile Glu Gly Glu
    130                 135                 140

Glu Arg Asn Glu Leu Arg Glu Ala Leu Asn Gly Leu Asn Ala Pro Ala
145                 150                 155                 160

Asp Met Gly Leu Ile Val Arg Thr Ala Gly Leu Gly Arg Ser Thr Glu
                165                 170                 175

Glu Leu Gln Trp Asp Leu Asp Tyr Leu Leu Gln Leu Trp Ser Ala Ile
            180                 185                 190

Lys Glu Ala Ser Gly Glu Arg Gly Ala Pro Phe Leu Ile Tyr Gln Glu
        195                 200                 205

Ser Asn Val Ile Ile Arg Ala Ile Arg Asp Tyr Leu Arg Gln Asp Ile
    210                 215                 220

Gly Glu Val Leu Ile Asp Ser Ile Asp Ala Gln Glu Glu Ala Leu Asn
225                 230                 235                 240

Phe Ile Arg Gln Val Met Pro Gln Tyr Ala Ser Lys Val Lys Leu Tyr
                245                 250                 255

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

Glu Thr Ala Phe Gln Arg Glu Val Lys Leu Pro Ser Gly Gly Ser Ile
        275                 280                 285

Val Ile Asp Pro Thr Glu Ala Leu Val Ser Ile Asp Ile Asn Ser Ala
    290                 295                 300

Arg Ala Thr Lys Gly Gly Asp Ile Glu Glu Thr Ala Leu Gln Thr Asn
305                 310                 315                 320

Leu Glu Ala Ala Glu Glu Ile Ala Arg Gln Leu Arg Leu Arg Asp Ile
                325                 330                 335

Gly Gly Leu Ile Val Ile Asp Phe Ile Asp Met Thr Pro Ala Lys Asn
            340                 345                 350

Gln Arg Ala Val Glu Glu Arg Val Arg Glu Ala Leu Glu Ala Asp Arg
        355                 360                 365

Ala Arg Val Gln Val Gly Arg Ile Ser Arg Phe Gly Leu Leu Glu Met
    370                 375                 380

Ser Arg Gln Arg Leu Arg Pro Ser Leu Gly Glu Thr Ser Gly Ile Val
385                 390                 395                 400

Cys Pro Arg Cys Asn Gly Gln Gly Ile Ile Arg Asp Val Glu Ser Leu
                405                 410                 415

Ser Leu Ala Ile Leu Arg Leu Ile Glu Glu Glu Ala Leu Lys Asp Arg
            420                 425                 430

Thr Ala Glu Val Arg Ala Arg Val Pro Phe Gln Val Ala Ala Phe Leu
        435                 440                 445

Leu Asn Glu Lys Arg Asn Ala Ile Thr Lys Ile Glu Leu Arg Thr Arg
    450                 455                 460

Ala Arg Ile Phe Ile Leu Pro Asp Asp His Leu Glu Thr Pro His Phe
465                 470                 475                 480

Glu Val Gln Arg Leu Arg Asp Asp Ser Pro Glu Leu Val Ala Gly Gln
                485                 490                 495

Thr Ser Tyr Glu Met Ala Thr Val Glu His Glu Glu Ala Gln Pro Val
```

-continued

```
            500                 505                 510

Ser Ser Thr Arg Thr Leu Val Arg Gln Glu Ala Ala Val Lys Thr Val
        515                 520                 525

Ala Pro Gln Gln Pro Ala Pro Gln His Thr Glu Ala Pro Val Glu Pro
    530                 535                 540

Ala Lys Pro Met Pro Glu Pro Ser Leu Phe Gln Gly Leu Val Lys Ser
545                 550                 555                 560

Leu Val Gly Leu Phe Ala Gly Lys Asp Gln Pro Ala Ala Lys Pro Ala
                565                 570                 575

Glu Thr Ser Lys Pro Ala Ala Glu Arg Gln Thr Arg Gln Asp Glu Arg
            580                 585                 590

Arg Asn Gly Arg Gln Gln Asn Arg Arg Arg Asp Gly Arg Asp Gly Asn
        595                 600                 605

Arg Arg Asp Glu Glu Arg Lys Pro Arg Glu Glu Arg Ala Glu Arg Gln
    610                 615                 620

Pro Arg Glu Glu Arg Ala Glu Arg Pro Asn Arg Glu Glu Arg Ser Glu
625                 630                 635                 640

Arg Arg Arg Glu Glu Arg Ala Glu Arg Pro Ala Arg Glu Glu Arg Gln
                645                 650                 655

Pro Arg Glu Gly Arg Glu Glu Arg Ala Glu Arg Thr Pro Arg Glu Glu
            660                 665                 670

Arg Gln Pro Arg Glu Gly Arg Glu Gly Arg Glu Glu Arg Ser Glu Arg
        675                 680                 685

Arg Arg Glu Glu Arg Ala Glu Arg Pro Ala Arg Glu Glu Arg Gln Pro
    690                 695                 700

Arg Glu Gly Arg Glu Glu Arg Ala Glu Arg Pro Ala Arg Glu Glu Arg
705                 710                 715                 720

Gln Pro Arg Glu Asp Arg Gln Ala Arg Asp Ala Ala Ala Leu Glu Ala
                725                 730                 735

Glu Ala Leu Pro Asn Asp Glu Ser Leu Glu Gln Asp Glu Gln Asp Asp
            740                 745                 750

Thr Asp Gly Glu Arg Pro Arg Arg Arg Ser Arg Gly Gln Arg Arg Arg
        755                 760                 765

Ser Asn Arg Arg Glu Arg Gln Arg Glu Val Ser Gly Glu Leu Glu Gly
    770                 775                 780

Ser Glu Ala Thr Asp Asn Ala Ala Ala Pro Leu Asn Thr Val Ala Ala
785                 790                 795                 800

Ala Ala Ala Ala Gly Ile Ala Val Ala Ser Glu Ala Val Glu Ala Asn
                805                 810                 815

Val Glu Gln Ala Pro Ala Thr Thr Ser Glu Ala Ala Ser Glu Thr Thr
            820                 825                 830

Ala Ser Asp Glu Thr Asp Ala Ser Thr Ser Glu Ala Val Glu Thr Gln
        835                 840                 845

Gly Ala Asp Ser Glu Ala Asn Thr Gly Glu Thr Ala Asp Ile Glu Ala
    850                 855                 860

Pro Val Thr Val Ser Val Val Arg Asp Glu Ala Asp Gln Ser Thr Leu
865                 870                 875                 880

Leu Val Ala Gln Ala Thr Glu Glu Ala Pro Phe Ala Ser Glu Ser Val
                885                 890                 895

Glu Ser Arg Glu Asp Ala Glu Ser Ala Val Gln Pro Ala Thr Glu Ala
            900                 905                 910
```

-continued

```
Ala Glu Glu Val Ala Ala Pro Val Pro Val Glu Val Ala Ala Pro Ser
        915                 920                 925

Glu Pro Ala Ala Thr Glu Glu Pro Thr Pro Ala Ile Ala Ala Val Pro
    930                 935                 940

Ala Asn Ala Thr Gly Arg Ala Leu Asn Asp Pro Arg Glu Lys Arg Arg
945                 950                 955                 960

Leu Gln Arg Glu Ala Glu Arg Leu Ala Arg Glu Ala Ala Ala Ala Ala
                965                 970                 975

Glu Ala Ala Ala Gln Ala Ala Pro Ala Val Glu Glu Ile Pro Ala Val
            980                 985                 990

Ala Ser Glu Glu Ala Ser Ala Gln  Glu Glu Pro Ala Ala  Pro Gln Ala
        995                 1000                 1005

Glu Glu  Ile Thr Gln Ala Asp  Val Pro Ser Gln Ala  Asp Glu Ala
    1010                 1015                 1020

Gln Glu  Ala Val Gln Ala Glu  Pro Glu Ala Ser Gly  Glu Gly Ala
    1025                 1030                 1035

Ala Asp  Thr Glu His Ala Lys  Lys Thr Glu Glu Ser  Glu Thr Ser
    1040                 1045                 1050

Arg Pro  His Ala
    1055


<210> SEQ ID NO 26
<211> LENGTH: 1161
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 26

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

Leu Ser Gly Ala Val Leu Leu Ser Ala Gln Thr Thr His Ala Ala Ala
            20                  25                  30

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

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

Ala Pro Asp Ser Ile Ser Gly Tyr Gly Asn Tyr Thr Phe Phe Ala Ser
65                  70                  75                  80

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

Pro Lys Lys Leu Thr Leu Val Asn Gly Gln Val Gln Ile Gln Asp Tyr
            100                 105                 110

Pro Ala Pro Asn Phe Ser Ser Ala Trp Arg Asn Gly Phe Thr Arg Ser
        115                 120                 125

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

Arg Gly Tyr Asp Lys Glu Ser Thr Ile Lys Ala Asp Ala Ala Tyr Tyr
145                 150                 155                 160

Tyr Asp Phe Thr Gly Ser Ser Ser Cys Asn Arg Thr Asn Gln Ala Cys
                165                 170                 175

Tyr Thr Arg Arg Tyr Val Ser Thr Glu Gln Arg Gln Asn Phe Ala Asn
            180                 185                 190

Trp Tyr Ser Phe Tyr Arg Thr Arg Ala Leu Ala Thr Gln Thr Ala Ala
```

-continued

```
        195                 200                 205

Asn Leu Ala Phe Tyr Ser Leu Pro Glu Asn Ala Arg Val Ser Trp Gln
    210                 215                 220

Leu Leu Asn Asp Ser Asn Cys Asn Gln Met Gly Ser Gly Ser Ser Ser
225                 230                 235                 240

Gly Asn Cys Phe Ser Asn Tyr Leu Arg Asp Phe Thr Gly Gln His Arg
                245                 250                 255

Val Asn Phe Phe Asn Trp Leu Glu Lys Leu Ser Val Asn Gly Gly Thr
            260                 265                 270

Pro Leu Arg Gln Ala Met Thr Arg Ala Gly Glu Phe Leu Lys Lys Thr
        275                 280                 285

Gly Val Asn Gly Pro Tyr Ala Tyr Arg Pro Gly Thr Gln Thr Ala Pro
    290                 295                 300

Glu Tyr Ser Cys Arg Gly Ser Tyr His Ile Leu Met Thr Asp Gly Leu
305                 310                 315                 320

Trp Asn Asn Asp Ser Ala Asn Val Gly Asn Ala Asp Ser Thr Ala Arg
                325                 330                 335

Asn Leu Pro Asp Gly Lys Ser Tyr Ser Ser Gln Thr Pro Tyr Arg Asp
            340                 345                 350

Gly Thr Phe Asp Thr Leu Ala Asp Gln Ala Phe His Tyr Trp Ala Thr
        355                 360                 365

Asp Ala Arg Pro Asp Ile Asp Asp Asn Ile Lys Pro Tyr Ile Pro Tyr
    370                 375                 380

Pro Asp Gln Ala Asn Pro Ser Ala Glu Tyr Trp Asn Pro Arg Asn Asp
385                 390                 395                 400

Pro Ala Thr Trp Gln His Met Val Thr Tyr Thr Leu Gly Leu Gly Leu
                405                 410                 415

Thr Thr Ser Leu Thr Ser Pro Arg Trp Glu Gly Ser Thr Phe Ser Gly
            420                 425                 430

Gly Tyr Asn Asp Ile Val Ala Gly Asn Leu Ser Trp Pro Arg Ala Ser
        435                 440                 445

Asn Asn Asp Ser Asn Asn Val Tyr Asp Leu Trp His Ala Ala Val Asn
    450                 455                 460

Ser Arg Gly Glu Phe Phe Ser Ala Asp Ser Pro Asp Gln Leu Val Ala
465                 470                 475                 480

Ala Phe Gln Asp Ile Leu Asn Arg Ile Ser Gly Lys Asp Leu Pro Ala
                485                 490                 495

Ser Arg Pro Ala Ile Ser Ser Ser Leu Gln Glu Asp Asp Thr Gly Asp
            500                 505                 510

Lys Leu Thr Arg Phe Ala Tyr Gln Thr Ser Phe Ala Ser Asp Lys Asn
        515                 520                 525

Trp Ala Gly Asp Leu Thr Arg Tyr Ser Leu Thr Thr Gln Asp Lys Ala
    530                 535                 540

Thr Val Gln Thr Lys Leu Trp Ser Ala Gln Ser Ile Leu Asp Ala Met
545                 550                 555                 560

Pro Asn Gly Gly Ala Gly Arg Lys Ile Met Met Ala Gly Ser Gly Thr
                565                 570                 575

Ser Gly Leu Lys Glu Phe Thr Trp Gly Ser Leu Ser Ala Asp Gln Gln
            580                 585                 590

Arg Gln Leu Asn Arg Asp Pro Asp Arg Asn Asp Val Ala Asp Thr Lys
        595                 600                 605
```

-continued

```
Gly Gln Asp Arg Val Ala Phe Leu Arg Gly Asp Arg Arg Lys Glu Asn
    610                 615                 620

Ser Asp Asn Phe Arg Thr Arg Asn Ser Ile Leu Gly Asp Ile Ile Asn
625                 630                 635                 640

Ser Ser Pro Ala Thr Val Gly Lys Ala Gln Tyr Leu Thr Tyr Leu Ala
                645                 650                 655

Gln Pro Ile Glu Pro Ser Gly Asn Tyr Ser Thr Phe Ala Glu Ala Gln
            660                 665                 670

Lys Thr Arg Ala Pro Arg Val Tyr Val Gly Ala Asn Asp Gly Met Leu
        675                 680                 685

His Gly Phe Asp Thr Asp Gly Asn Glu Thr Phe Ala Phe Ile Pro Ser
    690                 695                 700

Ala Val Phe Glu Lys Leu His Lys Leu Thr Ala Arg Gly Tyr Gln Gly
705                 710                 715                 720

Gly Ala His Gln Phe Tyr Val Asp Gly Ser Pro Val Val Ala Asp Ala
                725                 730                 735

Phe Phe Gly Gly Ala Trp His Thr Val Leu Ile Gly Ser Leu Arg Ala
            740                 745                 750

Gly Gly Lys Gly Leu Phe Ala Leu Asp Val Thr Asp Pro Ala Asn Ile
        755                 760                 765

Lys Leu Leu Trp Glu Ile Gly Val Asp Gln Glu Pro Asp Leu Gly Tyr
    770                 775                 780

Ser Phe Pro Lys Pro Thr Val Ala Arg Leu His Asn Gly Lys Trp Ala
785                 790                 795                 800

Val Val Thr Gly Asn Gly Tyr Ser Ser Leu Asn Asp Lys Ala Ala Leu
                805                 810                 815

Leu Ile Ile Asp Leu Glu Thr Gly Ala Ile Thr Arg Lys Leu Glu Val
            820                 825                 830

Thr Gly Arg Thr Gly Val Pro Asn Gly Leu Ser Ser Pro Arg Leu Ala
        835                 840                 845

Asp Asn Asn Ser Asp Gly Val Ala Asp Tyr Ala Tyr Ala Gly Asp Leu
    850                 855                 860

Gln Gly Asn Leu Trp Arg Phe Asp Leu Ile Ala Gly Lys Val Asn Gln
865                 870                 875                 880

Asp Asp Pro Phe Ser Arg Ala Asn Asp Gly Pro Ala Val Ala Ser Ser
                885                 890                 895

Phe Arg Val Ser Phe Gly Gly Gln Pro Leu Tyr Ser Ala Val Asp Ser
            900                 905                 910

Ala Gly Ala Ala Gln Ala Ile Thr Ala Ala Pro Ser Leu Val Arg His
        915                 920                 925

Pro Thr Arg Lys Gly Tyr Ile Val Ile Phe Gly Thr Gly Lys Tyr Phe
    930                 935                 940

Glu Asn Ala Asp Ala Arg Ala Asp Thr Ser Arg Ala Gln Thr Leu Tyr
945                 950                 955                 960

Gly Ile Trp Asp Gln Gln Thr Lys Gly Glu Ala Ala Gly Ser Thr Pro
                965                 970                 975

Arg Leu Thr Arg Gly Asn Leu Gln Gln Gln Thr Leu Asp Leu Gln Ala
            980                 985                 990

Asp Ser Thr Phe Ala Ser Thr Ala  Arg Thr Ile Arg Ile  Ala Ser Gln
        995                 1000                 1005
```

-continued

```
Asn Pro  Val Asn Trp Leu Asn  Asn Asp Gly Ser Thr  Lys Gln Ser
    1010                 1015                 1020

Gly Trp  Tyr Leu Asp Phe Met  Val Asn Gly Thr Leu  Lys Gly Glu
    1025                 1030                 1035

Met Leu  Ile Glu Asp Met Ile  Ala Ile Gly Gln Val  Val Leu Leu
    1040                 1045                 1050

Gln Thr  Ile Thr Pro Asn Asp  Asp Pro Cys Ala Asp  Gly Ala Ser
    1055                 1060                 1065

Asn Trp  Thr Tyr Gly Leu Asp  Pro Tyr Thr Gly Gly  Arg Thr Ser
    1070                 1075                 1080

Phe Thr  Val Phe Asp Leu Ala  Arg Gln Gly Val Val  Asp Ser Lys
    1085                 1090                 1095

Ser Asp  Tyr Ser Tyr Asn Lys  Gln Asn Val Ala Val  Ser Gly Thr
    1100                 1105                 1110

Glu Gln  Lys Gly Leu Gly Gly  Leu Thr Leu Ser Thr  Asn Glu Gln
    1115                 1120                 1125

Gly Asn  Pro Glu Val Cys Ser  Ser Gly Glu Cys Leu  Thr Val Asn
    1130                 1135                 1140

Pro Gly  Pro Asn Thr Arg Gly  Arg Gln Asn Trp Arg  Pro Ile Glu
    1145                 1150                 1155

Gly Lys  Asn
    1160


<210> SEQ ID NO 27
<211> LENGTH: 1211
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 27

Met Lys Ile Leu Ala Ile Arg Leu Lys Asn Leu Ala Ser Leu Ala Gly
1               5                   10                  15

Glu Gln Glu Ile Asp Phe Thr Arg Glu Pro Leu Ser Ser Ala Gly Leu
            20                  25                  30

Phe Ala Ile Thr Gly Pro Thr Gly Ala Gly Lys Ser Thr Val Leu Asp
        35                  40                  45

Ala Leu Cys Leu Ala Leu Phe Gly Ser Thr Pro Arg Leu Glu Ser Thr
    50                  55                  60

Ser Ala Ser Ser Lys Val Pro Asp Gly Arg Asn Glu Leu Ser Ser Asn
65                  70                  75                  80

Asp Glu Arg Asn Leu Leu Arg Arg Gly Cys Ala Ser Gly Tyr Ala Glu
                85                  90                  95

Val Asp Phe Val Gly Ile Asp Gly His Arg Tyr Arg Ala Arg Trp Glu
            100                 105                 110

Thr Arg Arg Ser Arg Asp Lys Ala Asp Gly Ala Leu Gln Lys Ser Gln
        115                 120                 125

Gln Ser Leu Gln Asp Leu Glu Thr Gln Gln Met Leu Ala Ala Asn Lys
    130                 135                 140

Lys Ser Glu Phe Arg Glu Gln Leu Glu Gln Lys Leu Gly Leu Asn Phe
145                 150                 155                 160

Ala Gln Phe Thr Arg Ala Val Leu Leu Ala Gln Ser Glu Phe Ser Ala
                165                 170                 175

Phe Leu Lys Ala Ser Asp Asn Asp Arg Gly Ala Leu Leu Glu Lys Leu
            180                 185                 190
```

-continued

```
Thr Asp Thr Gly Leu Tyr Ser Gln Leu Ser Lys Ala Ala Tyr Gln Arg
        195                 200                 205

Ala Ser Gln Ala Asp Glu Gln Arg Lys Gln Leu Glu Gln Arg Leu Glu
    210                 215                 220

Gly Ser Leu Pro Leu Ala Glu Gln Ala Arg Ala Gly Leu Glu Ala Ala
225                 230                 235                 240

Leu Glu Ser His Ala Gln Ala Arg Leu Gln Glu Gln Gln Ala Leu Gln
                245                 250                 255

Arg Leu Glu Gly Gln Gln Gln Trp Phe Thr Glu Glu Gln Arg Leu Leu
            260                 265                 270

Gln Ser Cys Glu His Ala Gln Gly Gln Leu Ala Glu Ala Arg Gln Ala
        275                 280                 285

Trp Asp Ala Leu Ala Thr Glu Arg Glu Thr Leu Gln Trp Leu Glu Arg
    290                 295                 300

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

Glu Leu Arg His Ser Glu Gln Gln Gln Arg Gln Arg Thr Glu Gln Gln
                325                 330                 335

Ala Ala Gly Thr Glu Arg Leu Gln Gly Leu Gln Ala Arg Leu Gln Glu
            340                 345                 350

Ala Arg Glu Arg Gln Ala Gln Ala Asp Asn His Leu Arg Gln Ala Gln
        355                 360                 365

Ala Pro Leu Arg Glu Ala Phe Gln Leu Glu Ser Glu Ala Arg Arg Leu
    370                 375                 380

Glu Arg Thr Leu Ala Glu Arg Gln Glu Leu His Arg Gln Ser Asn Gln
385                 390                 395                 400

Arg His Ala Gln Gln Ser Asp Ala Ala Arg Gln Leu Asp Met Glu Gln
                405                 410                 415

Gln Arg His Val Ala Glu Gln Ala Gln Leu Gln Ala Ala Leu Arg Asp
            420                 425                 430

Ser Gln Ala Leu Ala Ala Leu Gly Asp Ala Trp Val Thr His Gln Gly
        435                 440                 445

Gln Leu Ala Thr Phe Val Gln Arg Arg Gln Arg Ala Leu Glu Ser Gln
    450                 455                 460

Ala Gln Leu Pro Glu Leu Glu Lys Ser Leu Ala His Ala Gly Glu Pro
465                 470                 475                 480

Leu Glu Arg Leu Gln Ala Gln Trp Thr Ala Leu His Gly Ser Glu Pro
                485                 490                 495

Asp Asp Leu Ala Ala Arg Leu Val Glu Leu Arg Arg Gln Thr Asp Ser
            500                 505                 510

Leu Glu Arg Gln Gln Ala Leu His Lys Glu Trp Gln Gln Val Leu Asp
        515                 520                 525

Gln Arg Ala Gly Leu Ala Arg Arg Leu Gly Glu Leu Asp Gln Arg Met
    530                 535                 540

Val Glu Gln Glu Gln Ala Leu Leu Asp Leu Lys Arg Gln Gly Ser Gln
545                 550                 555                 560

Cys Ala Glu Glu Val Lys Ala Ala Glu Gln Ala Leu Gln Val Thr Arg
                565                 570                 575

Glu Leu Leu Gln Arg Gln Arg Leu Ala Arg Ser Ala Ser Val Glu Gln
            580                 585                 590
```

-continued

```
Leu Arg Ala Gly Leu Val Asp Gly Glu Ala Cys Pro Val Cys Gly Ser
        595                 600                 605

Gln Glu His Pro Tyr His His Ser Glu Gln Leu Leu Ala Ala Leu Gly
    610                 615                 620

Glu His Asp Asp Gln Glu Gln Val Arg Ala Glu Gln Ser Leu Glu Arg
625                 630                 635                 640

Leu Arg Gln Thr Leu Val Gly Leu Arg Glu Gly Tyr Ser Ser Gln Arg
            645                 650                 655

Glu Arg Leu Asn Gln Ser Arg Gln Glu Gln Gln Glu Leu Thr Gly Gln
                660                 665                 670

Leu Ala Ala Leu Asp Arg Gln Leu Asp Gln Trp Thr Leu Pro Glu Glu
        675                 680                 685

Leu Arg Leu Leu Gln Pro Ser Ala Gln Leu Glu Trp Leu Ala Gln Arg
    690                 695                 700

Leu Asp Asp Leu Ala Gly Gln Arg Gln Gln Cys Gln Arg Asp Phe Asp
705                 710                 715                 720

Arg Leu Ile Ala Arg Gln Arg Gln Thr Gln Gln Leu Gln Gln Glu Leu
            725                 730                 735

Arg Ala Ala Glu Thr Ile Leu Gln Gln Arg Gln Gln Ala Leu Thr Glu
                740                 745                 750

Gln Arg Gln Arg Tyr Glu His Leu Gln Gln Gln Val Glu Glu Asp Ser
        755                 760                 765

Gln Gln Leu Arg Pro Leu Leu Ser Asp Glu His Trp Gln Arg Trp Gln
    770                 775                 780

Ala Asp Pro Leu Arg Thr Phe Gln Ala Leu Gly Glu Ser Ile Glu Gln
785                 790                 795                 800

Arg Arg Gln Gln Gln Ala Arg Leu Gln Gln Ile Glu Gln Arg Leu Gln
            805                 810                 815

Glu Leu Lys Gln Arg Cys Asp Glu Ser Ser Trp Gln Leu Lys Gln Ser
                820                 825                 830

Asp Glu Gln Arg Asn Glu Ala Arg Gln Ala Glu Glu Arg Ala Gln Ala
        835                 840                 845

Glu Leu Ala Glu Leu Asn Gly Arg Leu Gly Ala His Leu Gly Gln His
    850                 855                 860

Ala Cys Ala Gln Asp Trp Gln Leu Ser Leu Glu His Ala Ala Gln Ala
865                 870                 875                 880

Ala Gln Ser Ala Val Glu Thr Leu Gln Ala Pro Leu Asp Ser Leu Arg
            885                 890                 895

Glu Glu Gln Leu Arg Leu Ala Glu Ala Leu Glu His Leu Gln Gln Gln
                900                 905                 910

Arg Gln Arg Gln Gln Asp Glu Phe Gln Arg Leu Gln Ala Asp Trp Gln
        915                 920                 925

Ala Trp Arg Glu Arg Gln Asp Asn Leu Asp Asp Ser Arg Leu Asp Ala
    930                 935                 940

Leu Leu Gly Leu Ser Glu Glu Gln Ala Thr Gln Trp Arg Glu Gln Leu
945                 950                 955                 960

Gln Arg Leu Gln Glu Glu Ile Thr Arg Gln Gln Thr Leu Glu Ala Glu
            965                 970                 975

Arg Gln Ala Gln Leu Leu Gln His Arg Arg Gln Arg Pro Glu Thr Asp
                980                 985                 990

Arg Glu Ala Leu Glu Asp Asn Leu  Arg Gln Gln Arg Glu  Arg Leu Ala
```

-continued

```
        995                 1000                 1005

Ala Ser  Glu Gln Ala Tyr Leu  Glu Thr Tyr Ser Gln  Leu Gln Ala
    1010                 1015                 1020

Asp Asn  Gln Arg Arg Glu Gln  Ser Gln Ala Leu Leu  Ala Glu Leu
    1025                 1030                 1035

Glu Arg  Ala Arg Ala Glu Phe  Arg Arg Trp Gly Arg  Leu Asn Glu
    1040                 1045                 1050

Leu Ile  Gly Ser Ser Ser Gly  Asp Lys Phe Arg Arg  Ile Ala Gln
    1055                 1060                 1065

Gly Tyr  Asn Leu Asp Leu Leu  Val Gln His Ser Asn  Val Gln Leu
    1070                 1075                 1080

Arg Gln  Leu Ala Arg Arg Tyr  Arg Leu Gln Arg Gly  Gly Ser Glu
    1085                 1090                 1095

Leu Gly  Leu Leu Val Val Asp  Thr Glu Met Gly Asp  Glu Leu Arg
    1100                 1105                 1110

Ser Val  Tyr Ser Leu Ser Gly  Gly Glu Thr Phe Leu  Ile Ser Leu
    1115                 1120                 1125

Ala Leu  Ala Leu Gly Leu Ala  Ser Met Ala Ser Ser  Lys Leu Arg
    1130                 1135                 1140

Ile Glu  Ser Leu Phe Ile Asp  Glu Gly Phe Gly Ser  Leu Asp Pro
    1145                 1150                 1155

Glu Ser  Leu Gln Leu Ala Met  Asp Ala Leu Asp Asn  Leu Gln Ala
    1160                 1165                 1170

Gln Gly  Arg Lys Val Ala Val  Ile Ser His Val Gln  Glu Met His
    1175                 1180                 1185

Glu Arg  Ile Pro Val Gln Val  Arg Val Gln Arg Glu  Gly Asn Gly
    1190                 1195                 1200

Met Ser  Ser Leu Lys Val Val  Gly
    1205                 1210


<210> SEQ ID NO 28
<211> LENGTH: 2468
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 28

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

Ala Ala Ala Val Glu Val Pro Glu Asn Gly Ile Leu Lys Leu Ser Gln
            20                  25                  30

Ser Ser Asn Val Ala Leu Asp Val Ala Pro Glu Ser Val Ala Gly Tyr
        35                  40                  45

Ser Lys Ser Gly Ser Asp Leu Ile Val Gln Leu Lys Thr Gly Glu Ser
    50                  55                  60

Val Arg Ile Ala Asn Phe Tyr Ala Glu Gly Gln Pro Ser Ser Gln Leu
65                  70                  75                  80

Phe Leu Ala Asp Lys Asp Lys Leu Val Ala Val Asp Leu Pro Pro Val
                85                  90                  95

Ala Ala Asp Gly Pro Leu Met Ala Gly Tyr Ile Pro Gln Glu Ser Leu
            100                 105                 110

Ala Gly Phe Glu Ser Leu Thr Gly Ala Gly Val Leu Gly Gly Met Ser
        115                 120                 125
```

-continued

```
Ala Gly Thr Ala Leu Leu Val Gly Ala Ala Ala Ile Gly Ala Gly Val
    130                 135                 140

Ala Ile Ser Asn Ser Ser Gly Gly Gly Gly Gly Gly Gly Ser Ser Val
145                 150                 155                 160

Pro Pro Asp Thr Thr Pro Pro Lys Ala Ala Ser Gly Leu Lys Ile Ala
                165                 170                 175

Pro Asp Gly Ser Ser Ile Ser Gly Gln Ala Glu Ala Gly Ala Ser Val
            180                 185                 190

Gly Ile Asp Thr Asn Gly Asp Gly Lys Pro Asp Leu Thr Val Ile Ala
        195                 200                 205

Asp Ala Asn Gly Asn Phe Thr Ala Pro Leu Asn Pro Pro Leu Thr Asn
    210                 215                 220

Gly Gln Thr Val Thr Val Val Val Thr Asp Pro Ala Gly Asn Ala Ser
225                 230                 235                 240

Pro Pro Ala Gln Val Thr Ala Pro Asp Thr Thr Ala Pro Ala Pro Ala
                245                 250                 255

Thr Asp Val Gln Val Ala Pro Asp Gly Ser Ser Val Thr Gly Lys Ala
            260                 265                 270

Glu Pro Gly Ser Thr Val Gly Val Asp Thr Asp Gly Asp Gly Gln Pro
        275                 280                 285

Asp Thr Thr Val Val Val Gly Pro Gly Gly Ser Phe Glu Val Pro Leu
    290                 295                 300

Asn Pro Pro Leu Thr Asn Gly Glu Thr Val Thr Val Ile Val Thr Asp
305                 310                 315                 320

Pro Ala Gly Asn Asn Ser Thr Pro Val Thr Val Glu Ala Pro Asp Thr
                325                 330                 335

Thr Ala Pro Ala Pro Ala Thr Asp Val Gln Val Ala Pro Asp Gly Ser
            340                 345                 350

Ser Val Thr Gly Asn Ala Glu Pro Gly Ala Thr Val Gly Val Asp Thr
        355                 360                 365

Asp Gly Asp Gly Gln Pro Asp Thr Thr Val Val Val Gly Pro Gly Gly
    370                 375                 380

Ser Phe Glu Val Pro Leu Asn Pro Pro Leu Thr Asn Gly Glu Thr Val
385                 390                 395                 400

Thr Val Ile Val Thr Asp Pro Ala Gly Asn Ser Ser Thr Pro Val Thr
                405                 410                 415

Ala Glu Ala Pro Asp Phe Pro Asp Ala Pro Gln Val Asn Ala Ser Asn
            420                 425                 430

Gly Ser Val Leu Ser Gly Thr Ala Glu Ala Gly Val Thr Ile Val Ile
        435                 440                 445

Thr Asp Gly Asn Gly Asn Pro Ile Gly Gln Thr Ser Ala Asp Ala Asn
    450                 455                 460

Gly Asn Trp Ser Phe Thr Pro Gly Ser Gln Leu Pro Asp Gly Thr Val
465                 470                 475                 480

Val Asn Val Val Ala Arg Asp Ala Ala Gly Asn Ser Ser Pro Ala Thr
                485                 490                 495

Ser Ile Thr Val Asp Gly Val Ala Pro Asn Ala Pro Val Val Glu Pro
            500                 505                 510

Ser Asn Gly Ser Glu Leu Ser Gly Thr Ala Glu Pro Gly Ser Ser Val
        515                 520                 525

Thr Leu Thr Asp Gly Asn Gly Asn Pro Ile Gly Gln Thr Thr Ala Asp
```

-continued

```
    530                 535                 540

Ala Asn Gly Asn Trp Ser Phe Thr Pro Ser Thr Pro Leu Pro Asp Gly
545                 550                 555                 560

Thr Val Val Asn Val Val Ala Arg Asp Ala Ala Gly Asn Ser Ser Pro
                565                 570                 575

Pro Ala Ser Val Thr Val Asp Ala Val Ala Pro Ala Thr Pro Thr Val
            580                 585                 590

Asp Pro Ser Asn Gly Thr Thr Leu Ser Gly Thr Ala Glu Pro Gly Ser
        595                 600                 605

Ser Val Thr Leu Thr Asp Gly Asn Gly Asn Pro Ile Gly Gln Val Thr
    610                 615                 620

Ala Asp Gly Ser Gly Asn Trp Thr Phe Thr Pro Ser Thr Pro Leu Pro
625                 630                 635                 640

Asn Gly Thr Val Val Asn Ala Thr Ala Thr Asp Pro Ser Gly Asn Ala
                645                 650                 655

Ser Ser Pro Ala Ser Val Thr Val Asp Ala Val Ala Pro Ala Thr Pro
            660                 665                 670

Val Val Asn Pro Ser Asn Gly Thr Thr Leu Ser Gly Thr Ala Glu Pro
        675                 680                 685

Gly Ala Thr Val Thr Leu Thr Asp Gly Asn Gly Asn Pro Ile Gly Gln
    690                 695                 700

Val Thr Ala Asp Gly Ser Gly Asn Trp Ser Phe Thr Pro Thr Thr Pro
705                 710                 715                 720

Leu Pro Asn Gly Thr Val Val Asn Ala Thr Ala Thr Asp Ala Ser Gly
                725                 730                 735

Asn Thr Ser Ala Gly Ser Ser Val Thr Val Asp Ser Val Ala Pro Ala
            740                 745                 750

Thr Pro Val Ile Asn Pro Ser Asn Gly Thr Thr Leu Ser Gly Thr Ala
        755                 760                 765

Glu Pro Gly Ser Ser Val Thr Leu Thr Asp Gly Asn Gly Asn Pro Ile
    770                 775                 780

Gly Gln Val Thr Ala Asp Gly Ser Gly Asn Trp Ser Phe Thr Pro Ser
785                 790                 795                 800

Thr Pro Leu Ala Asp Gly Thr Val Val Asn Ala Thr Ala Thr Asp Pro
                805                 810                 815

Ala Gly Asn Thr Ser Gly Gln Gly Ser Thr Thr Val Asp Gly Val Ala
            820                 825                 830

Pro Thr Thr Pro Thr Val Asn Leu Ser Asn Gly Ser Ser Leu Ser Gly
        835                 840                 845

Thr Ala Glu Pro Gly Ser Thr Val Ile Leu Thr Asp Gly Asn Gly Asn
    850                 855                 860

Pro Ile Ala Glu Val Thr Ala Asp Gly Ser Gly Asn Trp Thr Tyr Thr
865                 870                 875                 880

Pro Ser Thr Pro Ile Ala Asn Gly Thr Val Val Asn Val Val Ala Gln
                885                 890                 895

Asp Ala Ala Gly Asn Ser Ser Pro Gly Ala Ser Val Thr Val Asp Ser
            900                 905                 910

Gln Ala Pro Ala Ala Pro Val Val Asn Pro Ser Asn Gly Thr Thr Leu
        915                 920                 925

Ser Gly Thr Ala Glu Pro Gly Ala Thr Val Thr Leu Thr Asp Gly Asn
    930                 935                 940
```

-continued

```
Gly Asn Pro Ile Gly Gln Val Thr Ala Asp Gly Ser Gly Asn Trp Ser
945                 950                 955                 960

Phe Thr Pro Gly Thr Pro Leu Ala Asn Gly Thr Val Val Asn Ala Thr
                965                 970                 975

Ala Ser Asp Pro Thr Gly Asn Thr Ser Ala Pro Ala Ser Thr Thr Val
            980                 985                 990

Asp Ser Val Ala Pro Ala Ala Pro  Val Val Asn Pro Ser  Asn Gly Ala
        995                 1000                 1005

Glu Ile  Ser Gly Thr Ala Glu  Pro Gly Ala Thr Val  Thr Leu Thr
    1010                 1015                 1020

Asp Gly  Ser Gly Asn Pro Ile  Gly Gln Val Thr Ala  Asp Gly Ser
    1025                 1030                 1035

Gly Asn  Trp Ser Phe Thr Pro  Ser Thr Pro Leu Ala  Asp Gly Thr
    1040                 1045                 1050

Val Val  Asn Ala Thr Ala Thr  Asp Pro Ala Gly Asn  Thr Gly Gly
    1055                 1060                 1065

Gln Gly  Ser Thr Thr Val Asp  Ala Ile Ala Pro Ala  Thr Pro Thr
    1070                 1075                 1080

Val Asn  Leu Ser Asn Gly Ser  Ser Leu Ser Gly Thr  Ala Glu Pro
    1085                 1090                 1095

Gly Ser  Thr Val Ile Leu Thr  Asp Gly Asn Gly Asn  Pro Ile Ala
    1100                 1105                 1110

Glu Val  Thr Ala Asp Gly Ser  Gly Asn Trp Thr Tyr  Thr Pro Ser
    1115                 1120                 1125

Thr Pro  Ile Ala Asn Gly Thr  Val Val Asn Val Val  Ala Gln Asp
    1130                 1135                 1140

Ala Ser  Gly Asn Ser Ser Pro  Pro Ala Thr Val Thr  Val Asp Ser
    1145                 1150                 1155

Ser Ala  Pro Pro Ala Pro Val  Ile Asn Pro Ser Asn  Gly Val Val
    1160                 1165                 1170

Ile Ser  Gly Thr Ala Glu Ala  Gly Ala Thr Val Thr  Leu Thr Asp
    1175                 1180                 1185

Ala Gly  Gly Asn Pro Ile Gly  Gln Val Thr Ala Asp  Gly Ser Gly
    1190                 1195                 1200

Asn Trp  Ser Phe Thr Pro Gly  Thr Pro Leu Ala Asn  Gly Thr Val
    1205                 1210                 1215

Ile Val  Ala Thr Ala Thr Asp  Pro Thr Gly Asn Thr  Gly Pro Gln
    1220                 1225                 1230

Ala Ala  Thr Thr Val Asp Ala  Val Ala Pro Pro Ala  Pro Val Ile
    1235                 1240                 1245

Asp Pro  Ser Asn Gly Thr Thr  Ile Ser Gly Thr Ala  Glu Ala Gly
    1250                 1255                 1260

Ala Lys  Val Ile Leu Thr Asp  Gly Asn Gly Asn Pro  Ile Gly Glu
    1265                 1270                 1275

Thr Thr  Ala Asp Gly Ser Gly  Asn Trp Ser Phe Thr  Pro Gly Thr
    1280                 1285                 1290

Pro Leu  Ala Asn Gly Thr Val  Val Asn Ala Val Ala  Gln Asp Pro
    1295                 1300                 1305

Ala Gly  Asn Thr Gly Pro Gln  Gly Ser Thr Thr Val  Asp Ala Val
    1310                 1315                 1320
```

-continued

```
Ala Pro  Asn Thr Pro Val Val  Asn Pro Ser Asn Gly  Asn Leu Leu
    1325                 1330                 1335

Asn Gly  Thr Ala Glu Pro Gly  Ser Thr Val Thr Leu  Thr Asp Gly
    1340                 1345                 1350

Asn Gly  Asn Pro Ile Gly Gln  Thr Thr Ala Asp Gly  Ser Gly Asn
    1355                 1360                 1365

Trp Ser  Phe Thr Pro Gly Ser  Gln Leu Pro Asn Gly  Thr Val Val
    1370                 1375                 1380

Asn Val  Thr Ala Ser Asp Ala  Ala Gly Asn Thr Ser  Leu Pro Ala
    1385                 1390                 1395

Thr Thr  Thr Val Asp Ser Ser  Leu Pro Ser Ile Pro  Gln Val Asp
    1400                 1405                 1410

Pro Ser  Asn Gly Ser Val Ile  Ser Gly Thr Ala Asp  Ala Gly Asn
    1415                 1420                 1425

Thr Ile  Ile Ile Thr Asp Gly  Asn Gly Asn Pro Ile  Gly Gln Val
    1430                 1435                 1440

Thr Ala  Asp Gly Ser Gly Asn  Trp Ser Phe Thr Pro  Gly Ile Pro
    1445                 1450                 1455

Leu Pro  Asp Gly Thr Val Val  Asn Val Val Ala Arg  Ser Pro Ser
    1460                 1465                 1470

Asn Val  Asp Ser Ala Pro Ala  Val Ile Thr Val Asp  Gly Val Ala
    1475                 1480                 1485

Pro Ala  Ala Pro Val Ile Asp  Pro Ser Asn Gly Thr  Glu Ile Ser
    1490                 1495                 1500

Gly Thr  Ala Glu Ala Gly Ala  Thr Val Ile Leu Thr  Asp Gly Gly
    1505                 1510                 1515

Gly Asn  Pro Ile Gly Gln Ala  Thr Ala Asp Gly Ser  Gly Asn Trp
    1520                 1525                 1530

Thr Phe  Thr Pro Ser Thr Pro  Leu Ala Asn Gly Thr  Val Ile Asn
    1535                 1540                 1545

Ala Val  Ala Gln Asp Pro Ala  Gly Asn Thr Ser Gly  Pro Ala Ser
    1550                 1555                 1560

Val Thr  Val Asp Ala Ile Ala  Pro Pro Ala Pro Val  Ile Asn Pro
    1565                 1570                 1575

Ser Asn  Gly Val Val Ile Ser  Gly Thr Ala Glu Ala  Gly Ala Thr
    1580                 1585                 1590

Val Ile  Leu Thr Asp Gly Asn  Gly Asn Pro Ile Gly  Gln Val Thr
    1595                 1600                 1605

Ala Asp  Gly Ser Gly Asn Trp  Ser Phe Thr Pro Gly  Thr Pro Leu
    1610                 1615                 1620

Ala Asn  Gly Ser Val Ile Asn  Ala Leu Ala Gln Asp  Ala Ala Gly
    1625                 1630                 1635

Asn Asn  Ser Ser Pro Thr Ser  Ala Thr Val Asp Ser  Leu Ala Pro
    1640                 1645                 1650

Ala Ala  Pro Val Ile Asp Pro  Ser Asn Gly Ser Val  Ile Ala Gly
    1655                 1660                 1665

Thr Ala  Glu Ala Gly Ala Thr  Val Ile Leu Thr Asp  Gly Asn Gly
    1670                 1675                 1680

Asn Pro  Ile Gly Gln Val Thr  Ala Asp Gly Ser Gly  Asn Trp Ser
    1685                 1690                 1695

Phe Thr  Pro Gly Thr Pro Leu  Ser Asn Gly Thr Val  Val Asn Ala
```

-continued

```
    1700                 1705                 1710

Val Ala  Gln Asp Ala Ala Gly  Asn Thr Ser Gly Pro  Val Ser Thr
    1715                 1720                 1725

Thr Val  Asp Ala Val Ala Pro  Ala Thr Pro Val Ile  Asp Pro Ser
    1730                 1735                 1740

Asn Gly  Val Glu Leu Ser Gly  Thr Ala Glu Pro Gly  Val Arg Val
    1745                 1750                 1755

Ile Leu  Thr Asp Gly Asn Gly  Asn Pro Ile Gly Gln  Thr Leu Ala
    1760                 1765                 1770

Asp Gly  Ser Gly Asn Trp Ser  Phe Thr Pro Gly Thr  Pro Leu Ala
    1775                 1780                 1785

Asn Gly  Thr Val Val Asn Ala  Val Ala Gln Asp Pro  Ala Gly Asn
    1790                 1795                 1800

Thr Ser  Gly Pro Ala Ser Thr  Thr Val Asp Thr Val  Ala Pro Ala
    1805                 1810                 1815

Thr Pro  Val Ile Asn Pro Ser  Asn Gly Ser Val Ile  Thr Gly Thr
    1820                 1825                 1830

Ala Glu  Val Gly Ala Lys Val  Ile Leu Thr Asp Gly  Asn Gly Asn
    1835                 1840                 1845

Pro Ile  Gly Glu Thr Thr Ala  Asp Gly Ser Gly Asn  Trp Thr Phe
    1850                 1855                 1860

Thr Pro  Gly Thr Pro Leu Ala  Asn Gly Thr Val Ile  Asn Ala Val
    1865                 1870                 1875

Ala Glu  Asp Ala Ala Gly Asn  Ala Ser Gly Pro Ala  Ser Thr Thr
    1880                 1885                 1890

Val Asp  Ser Val Ala Pro Ser  Ala Pro Leu Leu Ser  Ile Ser Ala
    1895                 1900                 1905

Asp Gly  Ala Leu Leu Thr Gly  Thr Ala Glu Pro Asn  Ser Gln Val
    1910                 1915                 1920

Arg Ile  Val Val Asn Gly Asp  Thr Ala Asn Pro Ile  Thr Val Thr
    1925                 1930                 1935

Val Asp  Gly Ala Gly Asn Phe  Ser Leu Pro Phe Ala  Pro Pro Leu
    1940                 1945                 1950

Ile Thr  Gly Glu Leu Ile Ala  Gly Val Ala Val Asp  Ala Ala Gly
    1955                 1960                 1965

Asn Val  Ser Gly Pro Ala Thr  Ile Asn Ala Pro Asp  Leu Ala Pro
    1970                 1975                 1980

Pro Thr  Ile Ser Val Pro Glu  Ala Ala Asp Thr Trp  Ile Asn Ala
    1985                 1990                 1995

Ala Glu  Ile Gly Asp Gly Ile  Gln Val Asp Val Thr  Val Arg Pro
    2000                 2005                 2010

Thr Met  Gln Val Gly Gln Val  Val Thr Val Lys Phe  Ala Gly Gln
    2015                 2020                 2025

Asn Gly  Tyr Glu Ala Glu Val  Ser His Thr Leu Thr  Ala Gly Asp
    2030                 2035                 2040

Ile Ala  Ala Gly Asn Leu Thr  Leu Thr Leu Thr Pro  Pro Gly Gly
    2045                 2050                 2055

Met Gly  Pro Phe Pro Glu Gly  Ala Ser Thr Val Thr  Ala Asp Ile
    2060                 2065                 2070

Asn Gly  Gly Thr Ala Ser Thr  Pro Val Pro Phe Thr  Ile Asp Thr
    2075                 2080                 2085
```

-continued

```
Ile Pro  Pro Ala Thr Pro Val  Leu Ser Leu Val Gly  Asn Ile Leu
    2090                 2095                 2100

Thr Ile  Ser Ala Glu Pro Gly  Thr Glu Leu Thr Val  Thr Val Asp
    2105                 2110                 2115

Val Gly  Gly Val Thr Ala Thr  Ala Thr Val Thr Ala  Asp Asn Ser
    2120                 2125                 2130

Gly Leu  Ala Ser Leu Asn Leu  Leu Thr Asp Leu Asp  Ile Asp Phe
    2135                 2140                 2145

Ser Trp  Asp Gln Leu Leu Asn  Ala Gln Val Ser Val  Val Gly Arg
    2150                 2155                 2160

Asp Pro  Ala Gly Asn Pro Ser  Asn Thr Ala Ser Ile  Gly Val Gly
    2165                 2170                 2175

Thr Ser  Ile Glu Gln Pro Val  Thr Ile Gly Asn Phe  Gly Leu Asp
    2180                 2185                 2190

Val Ser  Leu Asn Pro Leu Asn  Pro Arg Phe Gly Phe  Ser Gly Thr
    2195                 2200                 2205

Thr Glu  Pro Asp Ser Ser Val  Val Ile Arg Val Ile  Thr Pro Ala
    2210                 2215                 2220

Leu Asn  Val Glu Leu Leu Pro  Ile Gln Ala Asp Ser  Ser Gly Asn
    2225                 2230                 2235

Phe Ser  Leu Asn Leu Leu Ser  Pro Thr Ile Leu Thr  Gln Leu Gly
    2240                 2245                 2250

Leu Asn  Ile Thr Asp Ile Leu  Asn Leu Gly Ser Gln  Ile Ser Phe
    2255                 2260                 2265

Asn Leu  Val Ser Thr Asp Ser  Asn Gly Asn Asp Ser  Ala Ala Tyr
    2270                 2275                 2280

Gly Ile  Thr Leu Thr Pro Asn  Gly Leu Ser Leu Asn  Ile Gly Gln
    2285                 2290                 2295

Ile Asp  Val Asn Gly Thr Ser  Gly Asp Asp Val Leu  Ser Gly Ala
    2300                 2305                 2310

Asn Gly  Ser Ser Glu His Ile  Asn Gly Gly Asp Gly  Ser Asp Leu
    2315                 2320                 2325

Ile Phe  Asn Val Gly Thr Gly  Asp His Val Val Ala  Gly Asn Gly
    2330                 2335                 2340

Asn Asp  Thr Ile Gln Ile Thr  Ala Thr Asp Phe Val  Ser Ile Asp
    2345                 2350                 2355

Gly Gly  Ala Gly Phe Asp Thr  Leu Val Leu Ala Asn  Gly Ile Asp
    2360                 2365                 2370

Leu Asp  Tyr Asn Ala Val Gly  Val Gly Thr Leu Ser  Asn Leu Glu
    2375                 2380                 2385

Arg Ile  Asp Leu Gly Lys Gly  Asp Ser Gly Ser Val  Leu Thr Leu
    2390                 2395                 2400

Thr Ala  Ala Glu Val Asp Ala  Ile Thr Asp Ala Asn  Asn Thr Leu
    2405                 2410                 2415

Gln Ile  Thr Gly Glu Asn Asn  Asp Thr Leu Asn Val  Val Gly Ala
    2420                 2425                 2430

Val Asn  Thr Gly Thr Thr Gln  Leu Ile Asn Gly Ile  Thr Tyr Asp
    2435                 2440                 2445

Val Tyr  Thr Phe Gly Ser Thr  Thr Leu Leu Ile Glu  Asp Asn Thr
    2450                 2455                 2460
```

-continued

```
Val Gln  Val Val Val
    2465


<210> SEQ ID NO 29
<211> LENGTH: 3535
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 29

Met Asp Ile Arg Ser Pro Leu Asn Gln Cys Ile Ala Leu Ser Leu Ala
1               5                   10                  15

Gly Ile Leu Phe Leu Asn Pro Ile Val Ala Ala Ala Ala Gly Leu Ala
            20                  25                  30

Leu Asp Lys Ala Ala Gly Gly Asn Thr Gly Leu Gly Gln Ala Gly Asn
        35                  40                  45

Gly Val Pro Ile Val Asn Ile Ala Thr Pro Asn Asp Ala Gly Leu Ser
    50                  55                  60

Asn Asn His Phe Arg Asp Tyr Asn Val Gly Ala Asn Gly Leu Ile Leu
65                  70                  75                  80

Asn Asn Ala Thr Gly Lys Thr Gln Gly Thr Gln Leu Gly Gly Ile Ile
                85                  90                  95

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

Gln Val Thr Gly Gly Asn Arg Ser Thr Leu Ala Gly Tyr Thr Glu Val
        115                 120                 125

Ala Gly Gln Ser Ala Arg Val Ile Val Ala Asn Pro His Gly Ile Thr
    130                 135                 140

Cys Gln Gly Cys Gly Phe Ile Asn Thr Pro Arg Ala Thr Leu Thr Thr
145                 150                 155                 160

Gly Lys Pro Ile Met Asp Gly Gln Arg Leu Glu Arg Phe Gln Val Asp
                165                 170                 175

Gly Gly Asp Ile Val Val Glu Gly Ala Glu Leu Asn Val Gly Asn Leu
            180                 185                 190

Glu Gln Phe Asp Leu Ile Thr Arg Ser Ala Lys Leu Asn Ala Lys Leu
        195                 200                 205

Tyr Ala Lys Asn Leu Asn Ile Val Thr Gly Arg Asn Asp Val Gln Ala
    210                 215                 220

Asp Ser Leu Gln Ala Thr Pro Arg Ala Ala Asp Gly Ser Glu Lys Pro
225                 230                 235                 240

Gln Leu Ala Ile Asp Ser Ser Ala Leu Gly Gly Met Tyr Ala Gly Ala
                245                 250                 255

Ile Arg Leu Val Gly Thr Glu Gln Gly Val Gly Val Arg Leu Ala Gly
            260                 265                 270

Asp Met Ala Ala Ser Gly Gly Asp Ile Arg Ile Asp Ala Ser Gly Lys
        275                 280                 285

Leu Ser Leu Ala Gln Ala Ser Ser Gln Gly Asp Leu Lys Ile Ala Ala
    290                 295                 300

Gln Ala Val Glu Leu Asn Gly Lys Thr Tyr Ala Gly Gly Ser Ala Glu
305                 310                 315                 320

Ile Arg Ser Ala Glu Glu Leu Val Asn Arg Gln Ser Leu Ala Ala Arg
                325                 330                 335

Glu Arg Ile Val Leu Glu Ala Ala His Ile Asp Asn Ala Gly Val Ile
            340                 345                 350
```

-continued

```
Glu Ala Gly Val Glu Pro Asp Glu Arg Arg Asn Ala Arg Gly Asp Leu
        355                 360                 365

Glu Leu Arg Ser Gly Thr Leu Arg Asn Ala Gly Ser Leu Val Ala Ser
    370                 375                 380

Arg Ala Leu Glu Ala Lys Ala Ser Gln Ala Leu Asp Asn Gln Gly Gly
385                 390                 395                 400

Ser Leu Lys Gly Ala Thr Val Arg Val Asp Ala Gly His Leu Asp Asn
                405                 410                 415

Arg Gly Gly Lys Leu Leu Ala Glu Gly Glu Leu Arg Val Glu Ala Ser
            420                 425                 430

Ser Leu Asp Asn Arg Gln Asp Gly Leu Leu Gln Ser Arg Asp Arg Ala
        435                 440                 445

Val Val Lys Thr Arg Gly Asp Leu Asp Asn Arg Gly Gly Gln Val Ile
    450                 455                 460

Gly Leu Asn Asp Leu Glu Val Gly Ala Ala Thr Leu Asp Asn Gly Gln
465                 470                 475                 480

Gln Gly Leu Leu Gly Ser Gln Gln Ser Thr Arg Val Ser Ala Gln Ala
                485                 490                 495

Leu Val Asn Arg Gly Asp Gly Glu Val Ser Gly Lys Arg Val Glu Ala
            500                 505                 510

Arg Val Gly Ser Leu Asp Asn Arg Gly Gly Lys Leu Ile Gly Asp Asp
        515                 520                 525

Leu Leu Val Val Ala Ser Gly Ala Ile Asp Asn Arg Leu Gly Leu Phe
    530                 535                 540

Ser Ala Ala Asn Arg Leu Asp Leu Arg Ala Arg Ser Leu Asp Asn Ser
545                 550                 555                 560

Gly Lys Gly Thr Leu Ser Ser Arg Gly Gly Leu Glu Val Ser Leu Gly
                565                 570                 575

Gly Leu Leu Asp Asn Arg Asp Glu Gly Asn Leu Leu Ser Gln Gly Ala
            580                 585                 590

Gln Arg Val Thr Val Gly Gln Leu Asp Asn Arg Ala Gly Gly Leu Leu
        595                 600                 605

Ser Ser Arg Ser Glu Leu Asn Val His Gly Ala Ser Leu Asp Asn Arg
    610                 615                 620

Gly Gly Val Leu Val Ala Asp Ala Gly Leu Ser Ala Thr Gly Gly Ala
625                 630                 635                 640

Phe Asp Asn Arg Asp Gly Gly Ser Ala Ser Gly Lys Ala Gly Val Arg
                645                 650                 655

Val Glu Val Ala Ser Leu Arg Asn Asp Gln Gly Gly Lys Leu Leu Ser
            660                 665                 670

Asp Gly Arg Leu Asp Leu Ala Ala Asn Ala Val Gly Asn Ala Gly Gly
        675                 680                 685

Arg Ile Ala Ala Lys Gly Asp Leu Gln Ala Thr Leu Gly Ser Leu Ala
    690                 695                 700

Gln Gln Gly Gly Glu Leu Val Ser Glu Lys Thr Leu Lys Val Ala Ala
705                 710                 715                 720

Asp Thr Leu Asp Asn Ser Gln Ser Gly Leu Ile Ala Ala Asn Gly Gly
                725                 730                 735

Ile Ala Ile Glu Ala Arg Gln Val Asp Asn Arg Ala Gly Glu Ile Ser
            740                 745                 750
```

-continued

```
Ser Thr Ser Lys Val Ala Val Asn Ala Arg Glu Gln Leu Asp Asn Arg
        755                 760                 765

Gly Gly Lys Val Ile Gly Asp Ser Gly Leu Arg Leu Thr Val Gln Arg
    770                 775                 780

Leu Leu Asn Gln Ala Lys Gly Val Leu Ala Gly Arg Asp Gly Leu Ser
785                 790                 795                 800

Leu Asp Gly Gly Glu Leu Phe Asn Gly Asp Gly Gly Arg Leu Asp Ser
                805                 810                 815

Gln Asn Ser Leu Ser Val Ser Leu Gly Gly Val Leu Asp Asn Gln Gly
            820                 825                 830

Gly Ala Leu Val Ser Glu Gly Ser Leu Thr Ala Arg Ala Ala Arg Leu
        835                 840                 845

Asp Asn Arg Gly Gly Thr Phe Ser Ser Ala Gly Ala Leu Ala Leu Thr
    850                 855                 860

Ser Gln Ala Ala Leu Asp Asn Gln Gly Gly Arg Leu Leu Ser Asp Ala
865                 870                 875                 880

Gly Val Thr Leu Gln Gly Ala Ser Leu Asp Asn Ser Arg Ser Gly Val
                885                 890                 895

Ile Ser Ala Lys Gly Ala Val Asp Ile Arg Thr Gly Val Leu Asp Asn
            900                 905                 910

Ser Arg Asn Gly Gly Ile Gly Ser Asn Ala Gly Ile Thr Leu Val Ala
        915                 920                 925

Ala Arg Leu Asp Asn Gly Gln Gln Gly Arg Val Ser Ala Lys Gly Leu
    930                 935                 940

Leu Asp Ala Asn Leu Lys Gly Leu Asp Gln Arg Gly Gly Gly Val Leu
945                 950                 955                 960

Ile Ser Glu Thr Gly Val Thr Leu Asp Leu Asn Gly Gly Thr Leu Val
                965                 970                 975

Asn Arg Asp Gly Gly Leu Ile Ala Thr Pro Gly Ala Leu Leu Leu Arg
            980                 985                 990

Gln Leu Gly Ala Val Asp Asn Gly  Ala Gly Gly Glu Ile  Ser Ser Asp
        995                 1000                 1005

Arg Ala  Phe Thr Leu Ala Ala  Ala Ser Leu Asp Asn  Arg Gly Gly
    1010                 1015                 1020

Arg Leu  Ile Gly Ala Ala Asn  Leu Thr Leu Arg Ile  Ala Gln Ala
    1025                 1030                 1035

Leu Asp  Asn Ser Leu Ala Gly  Val Ile Ser Gly Ala  Ala Gly Leu
    1040                 1045                 1050

Asp Ile  Ala Ala Ala Arg Leu  Asp Asn Ser Ala Lys  Gly Thr Leu
    1055                 1060                 1065

Ala Ser  Arg Ala Gly Ile Asp  Leu Arg Val Asp Gly  Ala Leu Asp
    1070                 1075                 1080

Asn His  Ala Glu Gly Thr Val  Ser Gly Ala Arg Leu  Thr Leu Ala
    1085                 1090                 1095

Ser Ala  Ser Leu Asp Asn Ser  Gly Lys Gly Leu Leu  Ser Gly Asn
    1100                 1105                 1110

Ala Gly  Leu Ser Val Ala Thr  Gly Ala Leu Asp Asn  Ala Glu Gly
    1115                 1120                 1125

Gly Gln  Leu Ile Ser Gln Gly  Val Leu Asp Val Ser  Ser Ala Asp
    1130                 1135                 1140

Leu Asp  Asn Arg Gly Gly Ala  Leu Ser Gly Lys Gln  Ser Leu Arg
```

-continued

```
    1145                1150                1155

Leu Ser  Ala Ala Asn Leu Asp  Asn Arg Gly Gly Leu  Leu Thr Ser
    1160                1165                1170

Asp Gly  Glu Leu Glu Leu Thr  Ala Gly Arg Val Asp  Ser Ala Asp
    1175                1180                1185

Gly Gly  Glu Ile Ser Ala Arg  Gly Asp Leu Arg Leu  Thr Val Glu
    1190                1195                1200

Arg Leu  Val Gln Arg Gln Gly  Arg Leu Val Gly Glu  Arg Gly Val
    1205                1210                1215

Ser Leu  Asp Leu Arg Gly Gly  Asp Leu Asp Asn Gln  Gly Gly Leu
    1220                1225                1230

Ile Ser  Ala Arg Gly Pro Leu  Ser Ile Glu Arg Leu  Ser Val Leu
    1235                1240                1245

Asp Asn  Arg Gln Gly Gly Glu  Ile Ser Ser Gln Gln  Gly Phe Glu
    1250                1255                1260

Leu Leu  Ala Arg Arg Ile Asp  Asn Gly Gln Gln Gly  Arg Ile Ile
    1265                1270                1275

Ser Ala  Gly Lys Leu Arg Leu  Asp Ala Asp Ala Leu  Gly Asn Ala
    1280                1285                1290

Gly Ala  Gly Leu Leu Ser Gly  Trp Gln Gly Leu Thr  Val Thr Gly
    1295                1300                1305

Gly Ser  Leu Asp Asn Ser Ala  Gly Gly Thr Leu Ser  Ser Lys Asp
    1310                1315                1320

Gly Glu  Leu Ala Ile Ser Leu  Gly Gly Ala Leu Asp  Asn His Gly
    1325                1330                1335

Gln Gly  Ala Leu Val Ser Lys  Gly Ala Gln Arg Ile  Asp Ala Ala
    1340                1345                1350

Ser Leu  Asp Asn Ala Gln Gly  Ile Val Ser Gly Glu  Ser Asp Val
    1355                1360                1365

Thr Leu  Ser Ile Ala Gly Lys  Leu Asp Asn Gly Gln  Gly Gly Leu
    1370                1375                1380

Val Ser  Ala Gln Arg Ala Leu  Ser Phe Glu Arg Asp  Asp Thr Leu
    1385                1390                1395

Leu Asn  Asn Ala Gly Gly Arg  Ile Asn Gly Gly Ser  Leu Leu Leu
    1400                1405                1410

Lys Gly  Ala Ser Leu Asp Asn  Ser Asp Gly Gln Leu  Ile Ser Gln
    1415                1420                1425

Gly Arg  Leu Asp Ala Ile Leu  Gly Gly Ala Leu Val  Asn Thr Gly
    1430                1435                1440

Ala Ala  Arg Leu Ala Ser Gly  Gly Asp Leu Leu Leu  Arg Ser Ala
    1445                1450                1455

Ser Val  Asp Asn Arg Gly Gly  Lys Leu Val Ser Gln  Gly Leu Leu
    1460                1465                1470

Glu Ile  Ser Ala Gly Ser Leu  Asp Asn Ser Ala Ser  Gly Thr Leu
    1475                1480                1485

Ala Ser  Gln Ala Gly Met Ser  Leu Arg Leu Gly Gly  Gly Ala Leu
    1490                1495                1500

Arg Asn  Gln Gln Asp Gly Leu  Ile Phe Ser Gln Ala  Gly Ala Leu
    1505                1510                1515

Asp Val  Gln Ala Gly Ser Leu  Asp Asn Arg Gln Gly  Thr Leu Gln
    1520                1525                1530
```

-continued

```
Ala Gln  Gly Asp Asn Arg Leu  Arg Ile Gly Gly Ala  Leu Asp Asn
    1535                 1540                 1545

Gln Gly  Gly Arg Leu Asp Ser  Arg Ala Gly Asn Leu  Asp Leu Gln
    1550                 1555                 1560

Ser Gly  Ser Leu Asp Asn Gly  Ala Gly Gly Val Leu  Asn Ser Ala
    1565                 1570                 1575

Lys Gly  Trp Leu Lys Leu Val  Thr Gly Leu Phe Asp  Asn Ser Ala
    1580                 1585                 1590

Gly Val  Thr Gln Ala Gln Ser  Leu Glu Ile Arg Ala  Gly Gln Gly
    1595                 1600                 1605

Val Arg  Asn Gln Gln Gly His  Leu Ser Ala Leu Gly  Gly Asp Asn
    1610                 1615                 1620

Arg Ile  Val Thr Ala Asp Phe  Asp Asn Gln Gly Gly  Gly Leu Tyr
    1625                 1630                 1635

Ala Ser  Gly Leu Leu Ser Leu  Asp Gly Gln Arg Phe  Leu Asn Gln
    1640                 1645                 1650

Gly Ala  Ala Ala Gly Gln Gly  Gly Lys Val Gly Ala  Gly Arg Ile
    1655                 1660                 1665

Asp Phe  Ser Leu Ala Gly Ala  Leu Ala Asn Arg Phe  Gly Gln Leu
    1670                 1675                 1680

Glu Ser  Glu Ser Glu Leu His  Leu Arg Ala Ala Ala  Ile Asp Asn
    1685                 1690                 1695

Ser Gly  Gly Ser Leu Arg Ala  Leu Gly Arg Ser Gly  Ser Thr Arg
    1700                 1705                 1710

Leu Val  Ala Gly Gly Leu Asn  Asn Ala Tyr Gly Val  Leu Glu Ser
    1715                 1720                 1725

Ala Asn  Gln Asp Leu Asp Leu  Gln Leu Gly Ser Leu  Ala Asn Ala
    1730                 1735                 1740

Gly Gly  Arg Ile Leu His Thr  Gly Asn Gly Thr Phe  Gly Leu Asp
    1745                 1750                 1755

Ser Gly  Gln Val Ile Arg Ala  Gly Gly Glu Leu Thr  Thr Asn Gly
    1760                 1765                 1770

Leu Leu  Asp Ile Arg Ala Ser  Glu Trp Thr Asn Ser  Ser Val Leu
    1775                 1780                 1785

Gln Ala  Gly Arg Leu Asn Leu  Asp Ile Gly Thr Phe  Arg Gln Thr
    1790                 1795                 1800

Ala Glu  Gly Lys Leu Leu Ala  Val Gln Ser Phe Thr  Gly Arg Gly
    1805                 1810                 1815

Gly Asp  Trp Ser Asn Asp Gly  Leu Leu Ala Ser Asp  Gly Ser Phe
    1820                 1825                 1830

Arg Leu  Asp Leu Ser Gly Gly  Tyr Arg Gly Asn Gly  Arg Ala Thr
    1835                 1840                 1845

Ser Leu  Gly Asp Phe Ala Leu  Asn Ala Ala Ser Leu  Asp Leu Gly
    1850                 1855                 1860

Asn Ala  Ala Ser Leu Ala Gly  Gly Ala Asn Val Thr  Leu Gly Ala
    1865                 1870                 1875

Gly Asn  Leu Leu Val Asn Arg  Gly Arg Ile Thr Ala  Ala Gly Asp
    1880                 1885                 1890

Leu Val  Ala Ser Ala Ala Ser  Leu Asn Asn Tyr Gly  Thr Leu Gly
    1895                 1900                 1905
```

-continued

```
Gly Gly  Gly Asn Leu Arg Leu  Asn Ala Pro Ala Leu  Leu Asn Glu
    1910                 1915                 1920

Arg Gly  Leu Leu Phe Ser Gly  Ala Asp Met Thr Leu  Arg Ala Gly
    1925                 1930                 1935

Asp Ile  Thr Asn Leu Tyr Gly  Asp Val Tyr Ser Leu  Gly Arg Leu
    1940                 1945                 1950

Asp Ile  Ala Arg Asp Asp Ala  Gly Asn Arg Ala Ala  Ser Leu Arg
    1955                 1960                 1965

Asn Leu  Ser Gly Val Ile Glu  Ser Gly Lys Asp Phe  Ser Leu Arg
    1970                 1975                 1980

Ala Ser  Leu Ile Glu Asn Arg  Arg Ala Val Leu Glu  Ser Lys Ser
    1985                 1990                 1995

Gly Leu  Tyr Thr Ala Lys Met  Glu Gln Thr Ala Cys  Ile Glu Gly
    2000                 2005                 2010

Val Asn  Ala Gly Asp Cys Ser  Gly Lys Arg Asn Ala  Ile Trp Thr
    2015                 2020                 2025

Ile Thr  Gln Arg Asp Lys Thr  Glu Val Thr Ala Ser  Ser Ala Met
    2030                 2035                 2040

Gly Gln  Leu Leu Ala Gly Gly  Asp Phe Ala Ile Asp  Gly Gly Thr
    2045                 2050                 2055

Leu Asn  Asn Leu Ser Ser Leu  Ile Gly Ser Gly Gly  Asn Leu Thr
    2060                 2065                 2070

Ala Asn  Leu Glu Val Leu Asp  Asn Gln Gly Leu Glu  Thr Gly Glu
    2075                 2080                 2085

Leu Glu  Thr Ile Arg Val Leu  Arg Thr Ala Arg Gly  Gly Asp Ile
    2090                 2095                 2100

Gly Gly  Ile Asp Gln Lys Ser  Arg Asn Phe Thr Asn  Leu Tyr Trp
    2105                 2110                 2115

Tyr Gln  Ser Ala Asn Phe Asp  Pro Ala Arg Ala Gly  Glu Ile Pro
    2120                 2125                 2130

Ala Ala  Leu Asn Ala Ile Leu  Ser Asp Trp Ser Phe  Glu Tyr Glu
    2135                 2140                 2145

Phe Pro  Ser Lys Gly Pro Thr  Pro Ile Ser Ser Gly  Asp Gln Ser
    2150                 2155                 2160

Tyr Ala  Ala Val Ile Gln Ala  Ala Gly Asp Val Thr  Val Asn Ala
    2165                 2170                 2175

Ser Thr  Arg Ile Asp Asn Gly  Val Thr Arg Pro Gly  Tyr Thr Phe
    2180                 2185                 2190

Val Gly  Ser Gly Arg Gln Val  Gly Asp Ser Ala Val  Gly Gly Ser
    2195                 2200                 2205

Gly Val  Ser Val Val Val Pro  Leu Thr Ser Gln Leu  Pro Pro Asp
    2210                 2215                 2220

Leu Ala  Arg Arg Gln Val Asn  Pro Val Thr Leu Pro  Gly Phe Ser
    2225                 2230                 2235

Leu Pro  Gln Gly Asp Asn Gly  Leu Phe Arg Leu Ser  Ser Arg Phe
    2240                 2245                 2250

Ala Glu  Asp Gly Asn Gly Ser  Ala Ala Leu Gly Ala  Gly Ala Asp
    2255                 2260                 2265

Arg Thr  Gln Gly Gly Ser Gly  Val Ser Val Gly Gln  Gln Gly Ala
    2270                 2275                 2280

Gly Asn  Ala Ala Gly Thr Trp  Gln Gly Gln Gly Val  Arg Val Asp
```

-continued

```
    2285                 2290                 2295

Gly Leu  Ala Gly Ala Ala Asn  Val Gln Gly Gln Gly  Gly Ser Thr
    2300                 2305                 2310

Leu Gly  Gly Ser Leu Pro Gly  Val Ala Arg Val Gln  Gly Val Pro
    2315                 2320                 2325

Gly Asn  Ala Thr Pro Ser Ala  Ser His Lys Tyr Leu  Ile Glu Thr
    2330                 2335                 2340

Asn Pro  Ala Leu Thr Glu Leu  Lys Gln Phe Leu Asn  Ser Asp Tyr
    2345                 2350                 2355

Leu Leu  Ser Gly Leu Gly Met  Asn Pro Asp Asp Ser  Lys Lys Arg
    2360                 2365                 2370

Leu Gly  Asp Gly Leu Tyr Glu  Gln Arg Leu Ile Arg  Asp Ala Val
    2375                 2380                 2385

Val Ala  Arg Thr Gly Gln Arg  Tyr Ile Asp Gly Leu  Ser Ser Asp
    2390                 2395                 2400

Glu Ala  Leu Phe Arg Tyr Leu  Met Asp Asn Ala Ile  Ala Tyr Lys
    2405                 2410                 2415

Asp Gln  Leu His Leu Gln Leu  Gly Val Gly Leu Ser  Ala Glu Gln
    2420                 2425                 2430

Met Ala  Ala Leu Thr His Asp  Ile Val Trp Leu Glu  Glu Val Glu
    2435                 2440                 2445

Val Asn  Gly Glu Lys Val Leu  Ala Pro Val Val Tyr  Leu Ala Gln
    2450                 2455                 2460

Ala Glu  Gly Arg Leu Ala Pro  Asn Gly Ala Leu Ile  Gln Gly Arg
    2465                 2470                 2475

Asp Val  Lys Leu Val Ser Gly  Gly Asp Leu His Asn  Val Gly Thr
    2480                 2485                 2490

Leu Arg  Ala Arg Asn Asp Leu  Ser Ala Thr Ala Asp  Asn Leu Asp
    2495                 2500                 2505

Asn Ser  Gly Leu Ile Glu Ala  Gly Lys Arg Leu Asp  Leu Leu Ala
    2510                 2515                 2520

Gly Asp  Ser Ile Arg Asn Arg  Gln Gly Gly Val Ile  Ala Gly Arg
    2525                 2530                 2535

Asp Val  Ser Leu Thr Ala Leu  Thr Gly Asp Val Ile  Asn Glu Arg
    2540                 2545                 2550

Ser Val  Thr Arg Tyr Asp Ser  Ala Leu Asp Gly Arg  Thr Trp Glu
    2555                 2560                 2565

Arg Ser  Phe Ala Asp Ser Ala  Ala Arg Val Glu Ala  Ala Asn Ser
    2570                 2575                 2580

Leu Asn  Val Gln Ala Gly Arg  Asp Ile Ala Asn Leu  Gly Gly Val
    2585                 2590                 2595

Leu Gln  Ser Arg Gly Asp Leu  Ser Leu Asp Ala Gly  Arg Asp Val
    2600                 2605                 2610

Thr Val  Ala Ala Val Glu Asp  Arg Gln Gly Gln Thr  Arg Trp Ser
    2615                 2620                 2625

Thr Ser  Arg Leu Gln Ser Val  Thr Gln Leu Gly Ala  Glu Val Ser
    2630                 2635                 2640

Ala Gly  Arg Asp Leu Asn Val  Ser Ala Gly Arg Asp  Leu Thr Ala
    2645                 2650                 2655

Val Ala  Ser Thr Leu Glu Ala  Arg Arg Asp Ile Ala  Leu Ser Ala
    2660                 2665                 2670
```

-continued

```
Gly Arg  Asp Val Thr Leu Ala  Ala Ala Ala Asn Glu  Glu His Ala
    2675                 2680                 2685

Tyr Ser  Lys Thr Arg Lys Val  Thr Tyr Gln Glu Asp  Lys Val Ala
    2690                 2695                 2700

Gln Gln  Gly Thr Arg Val Asp  Ala Gly Gly Asp Leu  Ala Ile Asn
    2705                 2710                 2715

Ala Gly  Gln Asp Leu Arg Leu  Ile Ala Ser Gln Ala  Ser Ala Gly
    2720                 2725                 2730

Asp Glu  Ala Tyr Leu Val Ala  Gly Asp Lys Leu Glu  Leu Leu Ala
    2735                 2740                 2745

Ala Asn  Asp Ser Asn Tyr Tyr  Leu Tyr Asp Lys Lys  Lys Lys Gly
    2750                 2755                 2760

Asp Phe  Gly Arg Lys Glu Thr  Arg Arg Asp Glu Val  Thr Asp Val
    2765                 2770                 2775

Lys Ala  Val Gly Ser Gln Ile  Ser Ser Gly Gly Asp  Leu Thr Leu
    2780                 2785                 2790

Leu Ser  Gly Gly Asp Gln Thr  Tyr Gln Gly Ala Lys  Leu Glu Ser
    2795                 2800                 2805

Gly Asn  Asp Leu Ala Ile Val  Ser Gly Gly Ala Val  Thr Phe Glu
    2810                 2815                 2820

Ala Val  Lys Asp Leu His Gln  Glu Ser His Glu Lys  Ser Lys Gly
    2825                 2830                 2835

Asp Leu  Ala Trp Asn Ser Ala  Lys Gly Lys Gly Gln  Thr Asp Glu
    2840                 2845                 2850

Thr Leu  Arg Gln Thr Gln Ile  Val Ala Gln Gly Asn  Leu Ala Ile
    2855                 2860                 2865

Lys Ala  Val Glu Gly Leu Lys  Ile Asp Leu Lys His  Ile Asp Gln
    2870                 2875                 2880

Lys Thr  Val Ser Gln Thr Ile  Asp Ala Met Val Gln  Ala Asp Pro
    2885                 2890                 2895

Gln Leu  Ala Trp Leu Lys Glu  Ala Glu Gln Arg Gly  Asp Val Asp
    2900                 2905                 2910

Trp Arg  Met Val Gln Glu Val  His Asp Ser Trp Lys  Tyr Ser Asn
    2915                 2920                 2925

Ser Gly  Met Gly Pro Ala Thr  Gln Ile Ala Val Ala  Ile Ala Ala
    2930                 2935                 2940

Ala Ala  Ile Gly Gly Met Ala  Ala Ala Gly Ala Leu  Ser Gly Ala
    2945                 2950                 2955

Gly Val  Gly Ala Ser Ser Phe  Ala Met Gly Ala Gly  Val Gly Ala
    2960                 2965                 2970

Ala Gly  Ser Leu Ser Gly Thr  Ala Ala Val Ser Leu  Ile Asn Asn
    2975                 2980                 2985

Lys Gly  Asp Leu Gly Lys Val  Leu Lys Asp Ser Phe  Ser Ser Asp
    2990                 2995                 3000

Ser Leu  Lys Gln Ile Ala Ile  Ala Ser Leu Thr Gly  Gly Leu Thr
    3005                 3010                 3015

Ala Glu  Tyr Phe Asp Gly Ile  Leu Gln Thr Lys Thr  Asp Pro Leu
    3020                 3025                 3030

Thr Gly  Lys Val Thr Val Asp  Leu Ser Ser Leu Ser  Gly Val Gly
    3035                 3040                 3045
```

-continued

```
Arg Phe  Ala Ala Asn Gln Ala  Met Gln Asn Ala Thr  Ser Thr Val
    3050                  3055                 3060

Leu Ser  Gln Ala Leu Gly Gln  Gly Gly Ser Leu Asn  Glu Ala Leu
    3065                  3070                 3075

Lys Ser  Ala Leu Tyr Asn Ser  Phe Ala Ala Ala Gly  Phe Asn Phe
    3080                  3085                 3090

Val Gly  Asp Ile Gly Gln Glu  Tyr Ser Leu Lys Pro  Gly Asp Pro
    3095                  3100                 3105

Ser Met  Val Thr Met His Ala  Leu Met Gly Gly Leu  Ala Ala Gln
    3110                  3115                 3120

Val Ser  Gly Gly Asp Phe Ala  Thr Gly Ala Ala Ala  Ala Gly Ala
    3125                  3130                 3135

Asn Glu  Ala Leu Val Ala Lys  Leu Asp Gln Ala Phe  Lys Ser Leu
    3140                  3145                 3150

Ser Pro  Glu Asn Arg Glu Ala  Met Val Thr Met Gly  Ser Gln Leu
    3155                  3160                 3165

Val Gly  Val Leu Ala Ala Ala  Val Arg Asp Pro Asp  Val Thr Gly
    3170                  3175                 3180

Lys Ala  Leu Glu Ser Ala Ala  Trp Val Ala Lys Asn  Ser Thr Gln
    3185                  3190                 3195

Tyr Asn  Phe Leu Asn His Gln  Asp Val Ala Asp Leu  Asp Asn Ala
    3200                  3205                 3210

Leu Gln  Lys Cys Lys Ser Gln  Gly Asn Cys Arg Gln  Val Glu Glu
    3215                  3220                 3225

Glu Phe  Lys Ala Arg Ser Asp  Glu Asn Arg Arg Arg  Leu Asn Gly
    3230                  3235                 3240

Cys Val  Ala Val Gly Asn Cys  Ala Glu Ile Arg Ala  Glu Ile Asp
    3245                  3250                 3255

Ala Gly  Ser Thr Ala Leu Asn  Glu Leu Val Ala Arg  Gln Glu Thr
    3260                  3265                 3270

Ala Asn  Pro Gly Gly Ser Asp  Ser Asp Ile Ala Tyr  Gly Phe Leu
    3275                  3280                 3285

Met Gly  Arg Asn Val Val Asp  Trp Thr Thr Ala Gly  Gln Leu His
    3290                  3295                 3300

Leu Glu  Gln Thr Ala Asn Leu  Trp Trp Asn Gly Asn  Pro Gln Trp
    3305                  3310                 3315

Gln Lys  Glu Val Gly Ala Tyr  Leu Asp Gln Thr Gly  Phe Asn Pro
    3320                  3325                 3330

Phe Gly  Ile Gly Val Pro Ala  Met Gly Gly Ala Ala  Gly Lys Val
    3335                  3340                 3345

Thr Ala  Lys Ala Leu Met Asn  Ala Leu Lys Ala Gly  Glu Leu Pro
    3350                  3355                 3360

Lys Gly  Glu Val Ala Pro Gly  Lys Ala Asn Leu Pro  Thr Ile Gly
    3365                  3370                 3375

Ala Leu  Ala Asp Ala Glu Ala  Gly Met Pro Tyr Thr  His Pro Val
    3380                  3385                 3390

Lys Leu  Ala Ala Lys Ala Thr  Gly Thr Ala Gly Lys  Ile Lys Ile
    3395                  3400                 3405

Glu Ala  Gly Ala Ile Pro Asp  Ala Asn Glu Val Arg  Ala Gly Gln
    3410                  3415                 3420

Gly Leu  Ser Gly Leu Gly Tyr  Asp Val Thr His Gln  Thr Thr Ala
```

-continued

```
    3425                 3430                 3435

Ser Ala  Lys Gly Ile Gln Gly  Gln Arg Thr Ala Asp  Leu His Val
    3440                 3445                 3450

Asp Gly  Leu Gly Ser Ile Asp  Val Tyr Thr Pro Lys  Asn Leu Asp
    3455                 3460                 3465

Pro Thr  Lys Ile Val Arg Ala  Ile Glu Lys Lys Ser  Asn Gln Ala
    3470                 3475                 3480

Gly Gly  Val Leu Val Gln Ala  Asp Leu Pro Ser Thr  Asp Met Ser
    3485                 3490                 3495

Ser Ile  Ala Ala Arg Met Trp  Gly Lys Thr Asn Ala  Gln Ser Ile
    3500                 3505                 3510

Lys Thr  Ile Phe Phe Gln Lys  Pro Asp Gly Ser Leu  Val Arg Phe
    3515                 3520                 3525

Asp Arg  Pro Ala Gly Gly Gly
    3530                 3535


<210> SEQ ID NO 30
<211> LENGTH: 5627
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 30

Met Asp Ile Arg Ser Pro Leu Asn Gln Cys Ile Ala Leu Ser Leu Ala
1               5                   10                  15

Gly Ile Leu Phe Leu Asn Pro Ile Val Ala Ala Ala Ala Gly Leu Ala
            20                  25                  30

Leu Asp Lys Ala Ala Gly Gly Asn Thr Gly Leu Gly Gln Ala Gly Asn
        35                  40                  45

Gly Val Pro Ile Val Asn Ile Ala Thr Pro Asn Gly Ala Gly Leu Ser
    50                  55                  60

Asn Asn His Phe Arg Asp Tyr Asn Val Gly Ala Asn Gly Leu Ile Leu
65                  70                  75                  80

Asn Asn Ala Thr Gly Lys Thr Gln Gly Thr Gln Leu Gly Gly Ile Ile
                85                  90                  95

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

Gln Val Thr Gly Gly Asn Arg Ser Thr Leu Ala Gly Tyr Thr Glu Val
        115                 120                 125

Ala Gly Gln Ser Ala Arg Val Ile Val Ala Asn Pro His Gly Ile Thr
    130                 135                 140

Cys Gln Gly Cys Gly Phe Ile Asn Thr Pro Arg Ala Thr Leu Thr Thr
145                 150                 155                 160

Gly Lys Pro Ile Met Asp Gly Gln Arg Leu Glu Arg Phe Gln Val Asp
                165                 170                 175

Gly Gly Asp Ile Val Val Glu Gly Ala Glu Leu Asn Val Gly Asn Leu
            180                 185                 190

Glu Gln Phe Asp Leu Ile Thr Arg Ser Ala Lys Leu Asn Ala Lys Leu
        195                 200                 205

Tyr Ala Lys Asn Leu Asn Ile Val Thr Gly Arg Asn Asp Val Gln Ala
    210                 215                 220

Asp Ser Leu Gln Ala Thr Pro Arg Ala Ala Asp Gly Ser Glu Lys Pro
225                 230                 235                 240
```

-continued

```
Gln Leu Ala Ile Asp Ser Ser Ala Leu Gly Gly Met Tyr Ala Gly Ala
                245                 250                 255

Ile Arg Leu Val Gly Thr Glu Gln Gly Val Gly Val Lys Leu Ala Gly
            260                 265                 270

Asp Met Ala Ala Ser Gly Gly Asp Ile Arg Ile Asp Ala Ser Gly Lys
        275                 280                 285

Leu Ser Leu Ala Gln Ala Ser Ser Gln Gly Asp Leu Lys Ile Ala Ala
    290                 295                 300

Gln Ala Val Glu Leu Asn Gly Lys Thr Tyr Ala Gly Gly Ser Ala Glu
305                 310                 315                 320

Ile Arg Ser Ala Glu Glu Leu Val Asn Arg Gln Ser Leu Ala Ala Arg
                325                 330                 335

Glu Arg Ile Ala Leu Glu Ala Ala His Ile Asp Asn Ala Gly Val Ile
            340                 345                 350

Glu Ala Gly Val Glu Pro Asp Glu Arg Arg Asn Ala Arg Gly Asp Leu
        355                 360                 365

Glu Leu Arg Ser Gly Thr Leu Arg Asn Ala Gly Ser Leu Val Ala Ser
    370                 375                 380

Arg Ala Leu Glu Ala Lys Ala Ser Gln Ala Leu Asp Asn Gln Gly Gly
385                 390                 395                 400

Ser Leu Lys Gly Ala Thr Val Arg Val Asp Gly Gly His Leu Asp Asn
                405                 410                 415

Arg Gly Gly Lys Leu Leu Ala Glu Gly Glu Leu Arg Val Glu Ala Ser
            420                 425                 430

Ser Leu Asp Asn Arg Gln Asp Gly Leu Leu Gln Ser Arg Asp Arg Ala
        435                 440                 445

Val Val Lys Thr Arg Gly Asp Leu Asp Asn Arg Gly Gly Gln Val Val
    450                 455                 460

Gly Leu Asn Glu Leu Gln Val Gln Ala Ala Ala Leu Asp Asn Arg Ser
465                 470                 475                 480

Ala Gly Leu Leu Ser Ser Lys Gly Asp Met Asp Ile Glu Phe Ala Arg
                485                 490                 495

Leu Asp Asn Ser Ala Gly Gly Lys Leu Val Ser Glu Arg Arg Thr Leu
            500                 505                 510

Leu Lys Ala Asp Arg Leu Asp Asn Arg Ser Gly Arg Ile Val Ala Gly
        515                 520                 525

Gln Asp Leu Asp Leu Ser Ser Arg Leu Ile Asp Asn Arg Ala Gly Asp
    530                 535                 540

Ile Ser Ser Thr Ser Arg Val Val Ala Ser Ala Arg Glu Gln Leu Asp
545                 550                 555                 560

Asn Arg Gly Gly Lys Ile Val Gly Asp Ser Gly Leu Asp Ile Thr Thr
                565                 570                 575

Pro Arg Met Leu Asn Gln Asp Lys Gly Val Leu Ala Ser Arg Asp Gly
            580                 585                 590

Leu Arg Leu Ser Ala Thr Glu Leu Phe Asn Gly Ala Gly Gly Leu Leu
        595                 600                 605

Ser Ser Gln Lys Gly Ile Asp Val Ser Leu Ala Gly Ala Phe Asp Asn
    610                 615                 620

Gln Ala Gly Ser Leu Asp Ser Arg Gly Phe Leu Thr Val Lys Ser Ala
625                 630                 635                 640

Trp Leu Asp Asn Gln Gly Gly Thr Leu Ser Ser Ala Gly Ala Leu Ala
```

-continued

```
                645                 650                 655

Val Thr Ser Gln Gly Ala Leu Asn Asn Gln Gly Gly Arg Leu Ala Ser
            660                 665                 670

Asp Ala Gly Leu Ser Leu Ser Ser Ala Ser Leu Asp Asn Ser Gln Ala
        675                 680                 685

Gly Ala Ile Ser Gly Lys Gly Ala Val Glu Ile Arg Thr Gly Asn Leu
    690                 695                 700

Asn Asn Ser Arg Lys Ala Ser Ile Gly Ser Asp Ala Gly Leu Thr Leu
705                 710                 715                 720

Val Ala Ala Arg Val Asp Asn Ser Gln Ala Gly Arg Ile Ala Ala Lys
                725                 730                 735

Gly Val Ile Asp Ala Asp Leu Gln Gly Leu Asp Gln His Asp Arg Gly
            740                 745                 750

Asn Leu Val Ser Asp Thr Gly Ile Thr Leu Asp Leu Asn Lys Gly Ser
        755                 760                 765

Leu Val Asn Arg Ala Gln Gly Leu Ile Ala Thr Pro Gly Thr Leu Leu
    770                 775                 780

Leu Arg Gln Leu Gly Val Val Asp Asn Ser Gly Gly Glu Ile Ser Ser
785                 790                 795                 800

Asp Arg Ala Phe Thr Leu Ala Thr Ser Ala Leu Asn Asn Gln Gly Gly
                805                 810                 815

Arg Leu Leu Ser Gly Gly Ala Leu Thr Leu Arg Ile Ala Gln Ala Leu
            820                 825                 830

Asp Asn Ser Leu Glu Gly Ile Val Ser Gly Ala Gly Gly Leu Asp Ile
        835                 840                 845

Gln Ala Phe Val Leu Asp Asn Arg Ser Gly Ser Ile Gly Ser Lys Gly
    850                 855                 860

Ala Ile Asp Ile Gly Val Thr Arg Leu Glu Asn Asp Ala Gly Thr Leu
865                 870                 875                 880

Ile Ala Glu Arg Gly Leu Lys Leu Val Ala Asp Glu Ala Asn Ser Ser
                885                 890                 895

Lys Gly Arg Ile Ala Ala Asn Gly Ser Leu His Ala Lys Val Gly Thr
            900                 905                 910

Leu Ser Gln Lys Gly Gly Glu Leu Thr Ser Gln Asp Ser Leu Thr Leu
        915                 920                 925

Asp Leu Gly Ile Leu Asn Asn Asn Ala Gly Arg Ile Ala Gly Asn Gln
    930                 935                 940

Gly Val Asp Ile Thr Ala Arg Gln Val Asp Asn Ser Val Gly Glu Ile
945                 950                 955                 960

Ala Ser Gln Gly Val Val Ala Leu Asn Leu Thr Glu Gln Leu Asp Asn
                965                 970                 975

Arg Gly Gly Lys Ile Val Gly Asp Ser Gly Leu Gly Ile Thr Ala Pro
            980                 985                 990

His Val Leu Asn Gln Asp Lys Gly  Val Leu Ala Ser Arg  Asp Gly Leu
        995                 1000                 1005

Arg Leu  Ser Ala Thr Glu Leu  Phe Asn Gly Ala Gly  Gly Leu Leu
    1010                 1015                 1020

Ser Ser  Gln Lys Gly Ile Asp  Val Ser Leu Ala Gly  Ala Phe Asp
    1025                 1030                 1035

Asn Gln  Ala Gly Ser Leu Asp  Ser Arg Gly Phe Leu  Thr Val Lys
    1040                 1045                 1050
```

-continued

```
Ser Ala  Trp Leu Asp Asn Gln  Gly Gly Thr Leu Ser  Ser Ala Gly
    1055                 1060                 1065

Ala Leu  Ala Val Thr Ser Gln  Gly Ala Leu Asn Asn  Gln Gly Gly
    1070                 1075                 1080

Arg Leu  Ala Ser Asp Ala Gly  Leu Ser Leu Ser Ser  Ala Ser Leu
    1085                 1090                 1095

Asp Asn  Ser Gln Ala Gly Ala  Ile Ser Gly Lys Gly  Ala Val Glu
    1100                 1105                 1110

Ile Arg  Thr Gly Asn Leu Asn  Asn Ser Arg Lys Ala  Ser Ile Gly
    1115                 1120                 1125

Ser Asp  Ala Gly Leu Thr Leu  Val Ala Ala Arg Val  Asp Asn Ser
    1130                 1135                 1140

Gln Ala  Gly Arg Ile Ala Ala  Lys Gly Ala Ile Asp  Ala Ala Leu
    1145                 1150                 1155

Gln Gly  Leu Asp Gln His Asp  Arg Gly Ser Leu Val  Ser Asp Thr
    1160                 1165                 1170

Gly Ile  Thr Leu Asp Leu Asn  Lys Gly Ser Leu Val  Asn Arg Ala
    1175                 1180                 1185

Gln Gly  Leu Ile Ala Thr Pro  Gly Thr Leu Leu Leu  Arg Gln Leu
    1190                 1195                 1200

Gly Val  Val Asp Asn Ser Gly  Gly Glu Ile Ser Ser  Asp Arg Ala
    1205                 1210                 1215

Phe Thr  Leu Ala Thr Ser Ala  Leu Asn Asn Gln Gly  Gly Arg Leu
    1220                 1225                 1230

Leu Ser  Gly Gly Ala Leu Thr  Leu Arg Ile Ala Gln  Ala Leu Asp
    1235                 1240                 1245

Asn Ser  Leu Glu Gly Ile Val  Ser Gly Ala Gly Gly  Leu Asp Ile
    1250                 1255                 1260

Gln Ala  Phe Val Leu Asp Asn  Arg Ser Gly Ser Ile  Gly Ser Lys
    1265                 1270                 1275

Gly Ala  Ile Asp Ile Gly Val  Thr Arg Leu Glu Asn  Asp Ala Gly
    1280                 1285                 1290

Thr Leu  Ile Ala Glu Arg Gly  Leu Lys Leu Ala Ala  Asp Glu Ala
    1295                 1300                 1305

Asn Asn  Ser Lys Gly Arg Ile  Val Ala Lys Asp Glu  Leu Arg Ala
    1310                 1315                 1320

Lys Leu  Gly Ala Leu Val Gln  Asn Gly Gly Glu Leu  Thr Thr Gln
    1325                 1330                 1335

Gly Ala  Leu Ala Leu Asp Ala  Asp Lys Val Asp Asn  Gly Ala Gly
    1340                 1345                 1350

Arg Ile  Ala Gly Asn Arg Gly  Val Val Ile Asp Ala  Arg Gln Val
    1355                 1360                 1365

Asp Asn  Arg Ala Gly Glu Ile  Ala Ser Gln Gly Val  Ala Thr Leu
    1370                 1375                 1380

Asn Leu  Thr Glu Gln Leu Asp  Asn Arg Gly Gly Lys  Val Val Ala
    1385                 1390                 1395

Asp Ser  Gly Leu Gly Ile Thr  Ala Pro Arg Val Leu  Asn Gln Asp
    1400                 1405                 1410

Lys Gly  Val Ile Ala Ser Arg  Asp Gly Leu Arg Leu  Ser Gly Thr
    1415                 1420                 1425
```

-continued

```
Glu Leu  Phe Asn Gly Asn Ala  Gly Leu Leu Ser Ser  Gln Arg His
    1430                 1435                 1440

Ile Glu  Val Thr Leu Asp Gly  Val Leu Asp Asn Gln  Gly Lys Gly
    1445                 1450                 1455

Ala Leu  Leu Ser Asp Gly Thr  Leu Thr Val Ser Ala  Gly Arg Ile
    1460                 1465                 1470

His Asn  Gln Asp Ala Thr Leu  Ser Ser Ala Gly Ala  Leu Arg Leu
    1475                 1480                 1485

Ser Ser  Gln Glu Ala Val Asp  Asn Arg Gly Gly Lys  Leu Val Thr
    1490                 1495                 1500

Asp Ser  Ser Leu Arg Leu Thr  Ser Ala Ser Leu Asp  Asn Ser Arg
    1505                 1510                 1515

Ser Gly  Ile Ile Ser Ala Asn  Ala Ala Ala Glu Ile  His Thr Gly
    1520                 1525                 1530

Val Leu  Asn Asn Ser Gln Lys  Gly Asn Leu Gly Ser  Asn Asp Gly
    1535                 1540                 1545

Leu Gly  Leu Ile Ala Thr Glu  Val Asp Asn Ser Gln  Glu Gly Arg
    1550                 1555                 1560

Ile Thr  Ala Lys Gly Met Ile  Asp Ala Asn Ile Lys  Gly Leu Asp
    1565                 1570                 1575

Gln Gln  Gly Lys Gly Arg Leu  Val Ser Asn Ala Gly  Ile Ile Leu
    1580                 1585                 1590

Asp Leu  Asn Glu Gly Thr Leu  Ala Asn Gly Ala Gln  Gly Leu Ile
    1595                 1600                 1605

Ala Thr  Pro Gly Thr Leu Leu  Leu Arg Gln Leu Gly  Met Val Asp
    1610                 1615                 1620

Asn Ser  Gly Gly Glu Ile Ser  Ser Asp Arg Ala Phe  Thr Leu Thr
    1625                 1630                 1635

Thr Ser  Ala Leu Thr Asn Gln  Gly Gly Arg Leu Arg  Ser Gly Gly
    1640                 1645                 1650

Val Leu  Thr Leu Arg Ile Ala  Gln Ala Leu Asp Asn  Ser Leu Glu
    1655                 1660                 1665

Gly Val  Leu Ser Gly Thr Gly  Gly Leu Asp Ile Arg  Ala Leu Ala
    1670                 1675                 1680

Leu Asp  Asn Arg Ser Gly Ser  Ile Gly Ser Lys Gly  Ala Val Asp
    1685                 1690                 1695

Ile Asp  Val Ser Arg Leu Glu  Asn Asp Asp Gly Asp  Leu Leu Ser
    1700                 1705                 1710

Glu Gly  Arg Leu Lys Leu Thr  Ala Glu Arg Ala Asn  Ser Val Arg
    1715                 1720                 1725

Gly Arg  Ile Ala Ala Arg Gly  Asp Leu His Ala Ser  Val Thr Ala
    1730                 1735                 1740

Phe Asn  Gln Ala Gly Gly Glu  Leu Ser Ser Glu Gly  Ala Leu Met
    1745                 1750                 1755

Leu Glu  Ala Asp Ser Leu Asp  Asn Arg Ser Gly Gly  Leu Val Ser
    1760                 1765                 1770

Ala Asp  Gly Asn Leu Thr Val  Ser Ala Arg Arg Ile  Asp Asn Arg
    1775                 1780                 1785

Ala Gly  Glu Ile Ala Ser Pro  Gly Gln Val Thr Leu  Asp Val Ala
    1790                 1795                 1800

Glu Gln  Leu Asp Asn Arg Gly  Gly Lys Ala Ile Gly  Asp Ser Gly
```

-continued

```
    1805                1810                1815

Leu Arg  Leu Ala Ala Pro Arg  Val Leu Asn Gln Asp  Gly Gly Val
    1820                1825                1830

Leu Ala  Ser Arg Asp Gly Leu  Arg Leu Asn Gly Ala  Glu Leu Phe
    1835                1840                1845

Asn Gly  Asn Gly Gly Leu Leu  Ser Ser Gln Gln Ser  Ile Asp Val
    1850                1855                1860

Ile Leu  Asp Gly Val Leu Gly  Asn Gln Ala Gly Ser  Leu Ser Ser
    1865                1870                1875

Gln Gly  Arg Leu Ser Val Lys  Ser Gly Arg Leu Asp  Asn Gln Gly
    1880                1885                1890

Gly Ala  Val Ser Ser Ala Gly  Thr Leu Ser Leu Ser  Ser Gln Gly
    1895                1900                1905

Ala Leu  Asn Asn Gln Gly Gly  Arg Val Val Thr Asp  Ala Gly Ala
    1910                1915                1920

Val Leu  Arg Ser Ala Ser Leu  Asp Asn Ser Gln Gly  Gly Ile Val
    1925                1930                1935

Ser Ala  Lys Gly Ala Ala Glu  Ile Arg Thr Gly Ser  Leu Asn Asn
    1940                1945                1950

Ser Gln  Lys Gly Gly Ile Gly  Ser Gly Ala Gly Leu  Ala Leu Val
    1955                1960                1965

Ala Asp  Leu Val Asp Asn Ser  Gln Asn Gly Arg Ile  Thr Ala Lys
    1970                1975                1980

Gly Ala  Ile Asp Ala Asn Leu  Lys Gly Leu Asp Gln  Gln Gly Ser
    1985                1990                1995

Gly Arg  Leu Val Ser Asp Thr  Ala Ile Ala Leu Asp  Leu Arg Gly
    2000                2005                2010

Gly Glu  Leu Val Asn Arg Ala  Gln Gly Leu Ile Ala  Thr Pro Gly
    2015                2020                2025

Ala Leu  Leu Leu Arg Gln Leu  Gly Val Val Asp Asn  Ser Gly Gly
    2030                2035                2040

Gly Glu  Ile Ser Ser Asp Arg  Ser Phe Thr Leu Ala  Ala Thr Ala
    2045                2050                2055

Leu Ser  Asn Arg Gly Gly Arg  Val Ile Ser Gly Asp  Ser Leu Thr
    2060                2065                2070

Leu Arg  Ile Ala Gln Ala Leu  Asp Asn Ser Leu Gln  Gly Val Leu
    2075                2080                2085

Ser Ala  Ser Gly Gly Leu Asp  Val Ala Ala Leu Val  Phe Asp Asn
    2090                2095                2100

His Ser  Gly Ile Val Ala Ser  Lys Gly Asp Thr His  Ile Gly Val
    2105                2110                2115

Asn Arg  Leu Glu Asn Glu Ala  Gly Arg Val Val Ser  Glu Gly Ala
    2120                2125                2130

Leu Asp  Leu Thr Ala Lys Gln  Val Ser Ser Ala Lys  Gly Arg Ile
    2135                2140                2145

Ala Ala  Lys Gly Asp Leu Gln  Val Thr Val Gly Thr  Leu Glu Gln
    2150                2155                2160

Gln Gly  Gly Glu Leu Ala Ser  Gln Gly Thr Leu Thr  Leu Asp Ala
    2165                2170                2175

Asp Ser  Leu Asp Asn Arg Asn  Gly Gly Leu Val Ser  Ala Asp Gly
    2180                2185                2190
```

-continued

```
Gly Val  Thr Ala Glu Ala Arg  Gln Ile Asp Asn Arg  Gly Gly Glu
    2195                 2200                 2205

Ile Ser  Ser Val Ala Lys Val  Ala Leu Ala Val Arg  Glu Gln Leu
    2210                 2215                 2220

Asp Asn  Arg Gly Gly Lys Val  Ile Gly Asp Ser Glu  Leu Ser Leu
    2225                 2230                 2235

Thr Val  Gln Arg Leu Leu Asn  Gln Ala Lys Gly Val  Leu Ala Ser
    2240                 2245                 2250

Arg Asp  Gly Leu His Leu Asp  Gly Ala Glu Leu Leu  Asn Gly Asp
    2255                 2260                 2265

Gly Gly  Leu Leu Ser Ser Gln  Arg Leu Val Asp Val  Thr Leu Ser
    2270                 2275                 2280

Gly Ala  Leu Asp Asn Gln Gly  Ser Gly Ala Leu Val  Ser Glu Glu
    2285                 2290                 2295

Ser Leu  Thr Val Lys Ala Asp  Gln Val Asn Asn Gln  Ala Gly Thr
    2300                 2305                 2310

Phe Ser  Ser Ala Gly Ser Leu  Leu Val Thr Ser Arg  Gly Glu Leu
    2315                 2320                 2325

Asn Asn  Gln Gly Gly Arg Leu  Val Thr Asp Ala Gly  Ala Thr Leu
    2330                 2335                 2340

Asn Ser  Thr Gly Phe Asp Asn  Ser Arg Ala Gly Leu  Val Ser Ala
    2345                 2350                 2355

Lys Gly  Ala Val Ala Ile Arg  Thr Gly Ala Leu Asn  Asn Ser Gln
    2360                 2365                 2370

Lys Gly  Ser Ile Gly Gly Asn  Thr Gly Val Thr Leu  Val Ala Gly
    2375                 2380                 2385

Leu Val  Asp Asn Gly Arg Glu  Gly Arg Ile Ser Thr  Lys Gly Thr
    2390                 2395                 2400

Leu Asp  Ala Asn Leu Lys Gly  Leu Leu Gln Gln Gly  Gly Gly Ser
    2405                 2410                 2415

Leu Val  Gly Glu Arg Gly Val  Thr Leu Asp Leu Asn  Gly Gly Thr
    2420                 2425                 2430

Leu Asp  Asn His Asp Leu Gly  Leu Val Ser Thr Pro  Gly Ala Leu
    2435                 2440                 2445

Leu Leu  Arg Gln Leu Gly Met  Val Asp Asn Ser Val  Gly Gly Glu
    2450                 2455                 2460

Ile Ser  Ser Asp Arg Ala Phe  Thr Leu Ala Ala Asn  Thr Leu Asn
    2465                 2470                 2475

Asn Gln  Gly Gly Arg Leu Ile  Ser Ser Glu Ala Leu  Thr Leu Arg
    2480                 2485                 2490

Ile Ala  Lys Thr Leu Asp Asn  Ser Leu Lys Gly Gln  Val Leu Ala
    2495                 2500                 2505

Thr Asp  Gly Leu Ala Ile Glu  Ser Gln Val Leu Asp  Asn Arg Ala
    2510                 2515                 2520

Gly Thr  Ile Gly Ser Lys Gly  Asp Ala Arg Ile Ser  Val Thr Ser
    2525                 2530                 2535

Leu Asp  Asn Ala Glu Gln Gly  Ser Leu Val Ser Glu  Gly Arg Leu
    2540                 2545                 2550

Glu Leu  Val Ala Asp Gln Val  Ser Asn Gly Asn Gln  Gly Arg Ile
    2555                 2560                 2565
```

-continued

```
Ala Ala  Arg Gly Val Leu Glu  Ala Ala Val Gly Thr  Leu Leu Gln
    2570                 2575                 2580

Gln Gly  Gly Glu Leu Val Ser  Gln Gly Ser Leu Asp  Leu Arg Ala
    2585                 2590                 2595

Asp Thr  Leu Asp Asn Ser Gln  Ser Gly Leu Ile Ala  Ala Asn Gly
    2600                 2605                 2610

Gly Ile  Ala Ile Glu Ala Arg  Gln Val Asp Asn Arg  Ala Gly Glu
    2615                 2620                 2625

Ile Ser  Ser Thr Ser Lys Val  Ala Val Asn Ala Arg  Glu Gln Leu
    2630                 2635                 2640

Asp Asn  Arg Gly Gly Lys Val  Ile Gly Asp Ser Gly  Leu Arg Leu
    2645                 2650                 2655

Thr Val  Gln Arg Leu Leu Asn  Gln Ala Lys Gly Val  Leu Ala Gly
    2660                 2665                 2670

Arg Asp  Gly Leu Ser Leu Asp  Gly Gly Glu Leu Phe  Asn Gly Asp
    2675                 2680                 2685

Gly Gly  Arg Leu Asp Ser Gln  Asn Ser Leu Ser Val  Ser Leu Gly
    2690                 2695                 2700

Gly Val  Leu Asp Asn Gln Gly  Gly Ala Leu Val Ser  Glu Gly Ser
    2705                 2710                 2715

Leu Thr  Ala Arg Ala Ala Arg  Leu Asp Asn Arg Gly  Gly Thr Phe
    2720                 2725                 2730

Ser Ser  Ala Gly Ala Leu Ala  Leu Thr Ser Gln Ala  Val Leu Asp
    2735                 2740                 2745

Asn Gln  Gly Gly Arg Leu Leu  Ser Asp Ala Gly Val  Thr Leu Lys
    2750                 2755                 2760

Gly Ala  Ser Leu Asp Asn Ser  Arg Ser Gly Val Ile  Ser Ala Lys
    2765                 2770                 2775

Gly Ala  Val Asp Ile Arg Thr  Gly Val Leu Asp Asn  Ser Arg Asn
    2780                 2785                 2790

Gly Gly  Ile Gly Ser Asn Ala  Gly Ile Thr Leu Val  Ala Ala Arg
    2795                 2800                 2805

Leu Asp  Asn Gly Gln Gln Gly  Arg Val Ser Ala Lys  Gly Leu Leu
    2810                 2815                 2820

Asp Ala  Asn Leu Lys Gly Leu  Asp Gln Arg Gly Gly  Gly Val Leu
    2825                 2830                 2835

Val Ser  Glu Thr Gly Val Thr  Leu Asp Leu Asn Gly  Gly Thr Leu
    2840                 2845                 2850

Val Asn  Arg Asp Gly Gly Leu  Ile Ala Thr Pro Gly  Ala Leu Leu
    2855                 2860                 2865

Leu Arg  Gln Leu Gly Ala Val  Asp Asn Gly Ala Gly  Gly Glu Ile
    2870                 2875                 2880

Ser Ser  Asp Arg Ala Phe Thr  Leu Ala Ala Ala Ser  Leu Asp Asn
    2885                 2890                 2895

Arg Gly  Gly Arg Leu Ile Gly  Ala Asp Ser Leu Thr  Leu Arg Ile
    2900                 2905                 2910

Ala Gln  Ala Leu Asp Asn Ser  Leu Ala Gly Val Ile  Ser Gly Ala
    2915                 2920                 2925

Ala Gly  Leu Asp Ile Ala Ala  Ala Arg Leu Asp Asn  Ser Ala Lys
    2930                 2935                 2940

Gly Thr  Leu Ala Ser Arg Ala  Gly Ile Asp Leu Arg  Val Asp Gly
```

-continued

```
    2945                2950                2955

Ala Leu  Asp Asn His Ala Glu  Gly Thr Val Ser Gly  Ala Arg Leu
    2960                2965                2970

Thr Leu  Ala Ser Ala Ser Leu  Asp Asn Ser Gly Lys  Gly Leu Leu
    2975                2980                2985

Ser Gly  Asn Ala Gly Leu Ser  Val Ala Thr Gly Ala  Leu Asp Asn
    2990                2995                3000

Ala Glu  Gly Gly Gln Leu Ile  Ser Gln Gly Val Leu  Asp Val Ser
    3005                3010                3015

Ser Ala  Asp Leu Asp Asn Arg  Gly Gly Ala Leu Ser  Gly Lys Gln
    3020                3025                3030

Ser Leu  Arg Leu Ser Ala Ala  Asn Leu Asp Asn Arg  Gly Gly Leu
    3035                3040                3045

Leu Thr  Ser Asp Gly Glu Leu  Glu Leu Thr Ala Gly  Arg Val Asp
    3050                3055                3060

Ser Ala  Asp Gly Gly Glu Ile  Ser Ala Arg Gly Asp  Leu Arg Leu
    3065                3070                3075

Thr Val  Glu Arg Leu Val Gln  Arg Gln Gly Arg Leu  Ile Gly Glu
    3080                3085                3090

Arg Gly  Val Ser Leu Asp Leu  Arg Gly Gly Asp Leu  Asp Asn Gln
    3095                3100                3105

Gly Gly  Leu Ile Ser Ala Arg  Gly Pro Leu Ser Ile  Glu Arg Leu
    3110                3115                3120

Asn Val  Leu Asp Asn Arg Gln  Gly Gly Glu Ile Tyr  Ser Gln Gln
    3125                3130                3135

Gly Phe  Glu Leu Leu Ala Arg  Arg Ile Asp Asn Gly  Gln Gln Gly
    3140                3145                3150

Arg Ile  Ile Ser Ala Gly Lys  Leu Arg Leu Asp Ala  Asp Ala Leu
    3155                3160                3165

Gly Asn  Ala Gly Ala Gly Leu  Leu Ser Gly Trp Gln  Gly Leu Thr
    3170                3175                3180

Val Thr  Gly Gly Ser Leu Asp  Asn Ser Ala Gly Gly  Thr Leu Ser
    3185                3190                3195

Ser Lys  Asp Gly Glu Leu Ala  Ile Ser Leu Gly Gly  Ala Leu Asp
    3200                3205                3210

Asn His  Gly Gln Gly Ala Leu  Val Ser Lys Gly Ala  Gln Arg Ile
    3215                3220                3225

Asp Ala  Ala Ser Leu Asp Asn  Ala Gln Gly Ile Val  Ser Gly Glu
    3230                3235                3240

Ser Asp  Val Thr Leu Ser Ile  Ala Gly Lys Leu Asp  Asn Gly Gln
    3245                3250                3255

Gly Gly  Leu Val Ser Ala Gln  Arg Ala Leu Ser Phe  Glu Arg Asp
    3260                3265                3270

Asp Thr  Leu Leu Asn Asn Ala  Gly Gly Arg Ile Asn  Gly Gly Ser
    3275                3280                3285

Leu Leu  Leu Lys Gly Ala Ser  Leu Asp Asn Ser Asp  Gly Gln Leu
    3290                3295                3300

Ile Ser  Gln Gly Arg Leu Asp  Ala Ile Leu Gly Gly  Ala Leu Val
    3305                3310                3315

Asn Ala  Gly Ala Ala Arg Leu  Ala Ser Gly Gly Asp  Leu Leu Leu
    3320                3325                3330
```

-continued

```
Arg Ser  Ala Ser Val Asp Asn  Arg Gly Gly Lys Leu  Val Ser Gln
    3335                 3340                 3345

Gly Leu  Leu Glu Ile Ser Ala  Gly Ser Leu Asp Asn  Ser Ala Ser
    3350                 3355                 3360

Gly Thr  Leu Ala Ser Gln Ala  Asp Met Ser Leu Arg  Leu Gly Gly
    3365                 3370                 3375

Gly Ala  Leu Arg Asn Gln Gln  Asp Gly Leu Ile Phe  Ser Gln Ala
    3380                 3385                 3390

Gly Ala  Leu Glu Val Gln Ala  Gly Ser Leu Asp Asn  Arg Gln Gly
    3395                 3400                 3405

Thr Leu  Gln Ala Gln Gly Asp  Asn Arg Leu Arg Ile  Gly Gly Ala
    3410                 3415                 3420

Leu Asp  Asn Gln Ala Gly Arg  Leu Asp Ser Arg Ala  Gly Asn Leu
    3425                 3430                 3435

Asp Leu  Gln Ser Gly Ser Leu  Asp Asn Gly Ala Gly  Gly Val Leu
    3440                 3445                 3450

Asn Ser  Ala Lys Gly Trp Leu  Lys Leu Val Thr Gly  Leu Phe Asp
    3455                 3460                 3465

Asn Ser  Ala Gly Val Thr Gln  Ala Gln Ser Leu Glu  Ile Arg Ala
    3470                 3475                 3480

Gly Gln  Gly Val Arg Asn Gln  Gln Gly His Leu Ser  Ala Leu Gly
    3485                 3490                 3495

Gly Asp  Asn Arg Ile Val Thr  Ala Asp Phe Asp Asn  Gln Gly Gly
    3500                 3505                 3510

Gly Leu  Tyr Ala Ser Gly Leu  Leu Ser Leu Asp Gly  Gln Arg Phe
    3515                 3520                 3525

Leu Asn  Gln Gly Ala Ala Ala  Gly Gln Gly Gly Lys  Val Gly Ala
    3530                 3535                 3540

Gly Arg  Ile Asp Phe Ser Leu  Ala Gly Ala Leu Ala  Asn Arg Phe
    3545                 3550                 3555

Gly Gln  Leu Glu Ser Glu Ser  Glu Leu His Leu Arg  Ala Ala Ala
    3560                 3565                 3570

Ile Asp  Asn Ser Gly Gly Ser  Leu Arg Ala Leu Gly  Arg Ser Gly
    3575                 3580                 3585

Ser Thr  Arg Leu Val Ala Gly  Asp Leu Asn Asn Ala  Tyr Gly Val
    3590                 3595                 3600

Leu Glu  Ser Ala Asn Gln Asp  Leu Asp Leu Gln Leu  Gly Ser Leu
    3605                 3610                 3615

Ala Asn  Ala Gly Gly Arg Ile  Leu His Thr Gly Asn  Gly Thr Phe
    3620                 3625                 3630

Gly Leu  Asp Ser Gly Gln Val  Ile Arg Ala Gly Gly  Glu Leu Thr
    3635                 3640                 3645

Thr Asn  Gly Leu Leu Asp Ile  Arg Ala Ser Glu Trp  Thr Asn Ser
    3650                 3655                 3660

Ser Val  Leu Gln Ala Gly Arg  Leu Asn Leu Asp Ile  Gly Thr Phe
    3665                 3670                 3675

Arg Gln  Thr Ala Glu Gly Lys  Leu Leu Ala Val Gln  Ser Phe Thr
    3680                 3685                 3690

Gly Arg  Gly Gly Asp Trp Ser  Asn Asp Gly Leu Leu  Ala Ser Asn
    3695                 3700                 3705
```

-continued

```
Gly Ser  Leu Arg Leu Glu Leu  Ser Gly Gly Tyr Arg  Gly Asn Gly
    3710                 3715                 3720

Arg Ala  Thr Ser Leu Gly Asp  Phe Ala Leu Asn Ala  Ala Ser Leu
    3725                 3730                 3735

Asp Leu  Gly Asn Ala Ala Ser  Leu Ala Gly Gly Ala  Asn Val Thr
    3740                 3745                 3750

Leu Gly  Ala Gly Asn Leu Leu  Val Asn Arg Gly Arg  Ile Thr Ala
    3755                 3760                 3765

Ala Gly  Asp Leu Val Ala Ser  Ala Ala Ser Leu Asn  Asn Tyr Gly
    3770                 3775                 3780

Thr Leu  Gly Gly Gly Gly Asn  Leu Arg Leu Asn Ala  Pro Ala Leu
    3785                 3790                 3795

Leu Asn  Glu Arg Gly Leu Leu  Phe Ser Gly Ala Asp  Met Thr Leu
    3800                 3805                 3810

Arg Ala  Gly Asp Ile Thr Asn  Leu Tyr Gly Asp Val  Tyr Ser Leu
    3815                 3820                 3825

Gly Arg  Leu Asp Ile Ala Arg  Asp Asp Ala Gly Gly  Trp Ala Asn
    3830                 3835                 3840

Arg Leu  Glu Asn Ile Ser Gly  Asn Leu Glu Ser Thr  Gly Asp Met
    3845                 3850                 3855

Arg Phe  Ser Val Ser Ser Leu  Leu Asn Arg Arg Glu  Thr Leu Glu
    3860                 3865                 3870

Ile Glu  Gly Asp Leu Gln Asn  Ser Ala Ile Gly Val  Arg Cys Thr
    3875                 3880                 3885

Gly Cys  Gln Leu Ser Glu Arg  Trp Gly Lys Thr Arg  Ser Ser Ser
    3890                 3895                 3900

Glu Leu  Val Trp Ile Arg Glu  Tyr Lys Ser Thr Leu  Gly Asp Ser
    3905                 3910                 3915

Ser Ala  Ala Ala Ser Ile Thr  Ala Gly Arg Asp Leu  Leu Val Val
    3920                 3925                 3930

Gly Ala  Ser Leu Gln Asn Ile  Ala Ser Asn Ile Ser  Ala Val Arg
    3935                 3940                 3945

Asp Ala  Thr Leu Ser Leu Ser  Asn Phe Glu Asn Lys  Gly Tyr Ala
    3950                 3955                 3960

Leu Gly  Glu Tyr Ala Val Arg  Gly Val Tyr Ser Pro  Pro Ser Lys
    3965                 3970                 3975

Phe Gly  Glu Glu Leu Leu Met  Arg Ile Leu Ala Tyr  Asn Ala Val
    3980                 3985                 3990

Asn Asp  Pro Ser Tyr Gly Glu  Gly Tyr Ala Ser Thr  Gly Gly Arg
    3995                 4000                 4005

Leu Pro  Asn Ile His Tyr Phe  Asp Lys Asn Phe Asn  Glu Lys Val
    4010                 4015                 4020

Ser Pro  Leu Glu Val Ile His  Gly Asn Gly Lys Asn  Gly Gly Pro
    4025                 4030                 4035

Gly Trp  His Leu Tyr Phe Gly  Thr Leu Asp Val Glu  Tyr Pro Asp
    4040                 4045                 4050

Thr Asp  Arg Trp Asn Lys Ala  Ile Gly Arg Ile Pro  Ala Pro Asn
    4055                 4060                 4065

Tyr Ser  Ser Lys Lys Thr Asp  Ala Ile Pro Asp Leu  Leu Lys Gly
    4070                 4075                 4080

Leu Ala  Pro Leu Asp Glu Leu  Thr Ile Asn Lys Gly  Ala Asn Ser
```

-continued

4085 4090 4095

Thr Val Gly Ala Val Val Gln Ala Gly Gly Arg Val Thr Val Asn
4100 4105 4110

Ala Ala Glu Ser Phe Asn Asn Ser Val Leu Gln Gly Phe Gln Ala
4115 4120 4125

Val Gln Glu Thr Gln Leu Pro His Gln Asp Ile Ala Val Ser Ser
4130 4135 4140

Thr Thr Ser Ala Val Val Thr Leu Lys Ser Gln Leu Pro Ala Asp
4145 4150 4155

Leu Ala Arg Gln Gln Ile Asn Pro Leu Thr Leu Pro Gly Phe Ser
4160 4165 4170

Leu Pro Gln Gly Gln Asn Gly Leu Phe Arg Leu Ala Ser Gln Gly
4175 4180 4185

Ala Gln Val Asn Gln Ala Ser Gly Ala Leu Lys Ser Ala Ser Asp
4190 4195 4200

Leu Thr Gln Ser Gly His Gly Val Ser Val Ser Ala Gln Thr Gly
4205 4210 4215

Ser Gly Ala Ser Gly Trp Ser Thr Gln Ala Arg Arg Val Gly Asp
4220 4225 4230

Asp Arg Val Thr Ser Leu Ala Gly Ser Ala Tyr Gln Gly Arg Val
4235 4240 4245

Ala Glu Ala Ile Asp Ala Leu Arg Ala Ser Ala Pro Ile Ser Gly
4250 4255 4260

Asp Gly Gly Asn Thr Gly Arg Phe Gln Ala Gly Glu His Gln Ala
4265 4270 4275

Thr Thr Gly Leu Gly Gly Leu Val Glu Gly Asn Ala Ser Gly His
4280 4285 4290

Ser Gly Asn Gly Val Ile Leu Ala Asp Leu Arg Gly Gly Leu Pro
4295 4300 4305

Ser Phe Ser Ser Leu Pro Ala Ser Asp His Val Gln Gly Thr Val
4310 4315 4320

Pro Gly His Asp Gly Asn Gly Thr Ile Leu Ala Asn Trp Gln Gly
4325 4330 4335

Ala Gln Ala Thr Val Gln Ala Ser Pro Ser Thr Val Arg Val Glu
4340 4345 4350

Gly Val Val Ser Ser Pro Gly Gly Asn Gly Ser Ile Leu Ala Asp
4355 4360 4365

Leu Pro Ala Glu Gln Ser Ser Val Gln Ala Leu Pro Ser Ala Val
4370 4375 4380

Arg Ala Gln Gly Ser Leu Pro Arg Leu Glu Glu Arg Ser Ala Leu
4385 4390 4395

Leu Ala Glu Pro Pro Val Gly Gln Pro Ala Leu Gln Thr Leu Pro
4400 4405 4410

Ser Val Ala Arg Val Glu Gly Val Pro Ser Asn Ala Thr Pro Ser
4415 4420 4425

Asn Ser His Lys Tyr Leu Ile Glu Thr Asn Pro Ala Leu Thr Glu
4430 4435 4440

Leu Lys Gln Phe Leu Asn Ser Asp Tyr Leu Leu Gly Gly Leu Gly
4445 4450 4455

Ile Asn Pro Asp Asp Ser Lys Lys Arg Leu Gly Asp Gly Leu Tyr
4460 4465 4470

-continued

```
Glu Gln  Arg Leu Val Arg Glu  Ala Ile Val Gln Arg  Thr Gly Gln
    4475                 4480                 4485

Arg Phe  Ile Ala Gly Leu Asn  Ser Asp Glu Ala Met  Phe Arg Tyr
    4490                 4495                 4500

Leu Met  Asp Asn Ala Ile Ala  Ser Lys Asp Val Leu  Gly Leu Thr
    4505                 4510                 4515

Pro Gly  Val Thr Leu Ser Ala  Ala Gln Val Ala Ala  Leu Thr His
    4520                 4525                 4530

Asp Ile  Val Trp Leu Glu Glu  Val Glu Val Asn Gly  Glu Lys Val
    4535                 4540                 4545

Leu Ala  Pro Val Val Tyr Leu  Ala Gln Ala Glu Gly  Arg Leu Gly
    4550                 4555                 4560

Pro Asn  Gly Ala Leu Ile Gln  Gly Arg Asp Val Asn  Leu Ile Thr
    4565                 4570                 4575

Gly Gly  Asp Leu Arg Asn Ala  Gly Thr Leu Arg Ala  Gln Asn Asp
    4580                 4585                 4590

Leu Ser  Ala Thr Ala Gly Asn  Ile Asp Asn Ser Gly  Leu Ile Glu
    4595                 4600                 4605

Ala Gly  Asn Arg Leu Asp Leu  Leu Ala Ser Gly Ser  Ile Arg Asn
    4610                 4615                 4620

Asp Gln  Gly Gly Ile Ile Ala  Gly Arg Glu Val Ser  Leu Ser Ala
    4625                 4630                 4635

Leu Thr  Gly Asp Val Ile Asn  Glu Arg Thr Val Thr  Gln His Gln
    4640                 4645                 4650

Ser Ser  Tyr Arg Gly Thr Gly  Thr Thr Glu Ala Phe  Ala Asp Ser
    4655                 4660                 4665

Ala Ala  Arg Ile Glu Ala Ala  Gln Lys Leu Thr Val  Ser Ala Gly
    4670                 4675                 4680

Arg Asp  Val Ala Asn Ile Gly  Gly Val Ile Asp Ser  Lys Gly Asp
    4685                 4690                 4695

Leu Ala  Leu Gln Gly Gly Arg  Asp Val Leu Val Ser  Ala Ala Val
    4700                 4705                 4710

Ala Glu  Arg Gly Trp Thr Ala  Gly Ser Gln Ala Tyr  Gln Thr Gln
    4715                 4720                 4725

Thr Thr  Gln Met Gly Ala Glu  Val Val Ala Gly Arg  Asp Ile Ser
    4730                 4735                 4740

Val Ser  Ala Gly Arg Asp Ile  Ser Val Val Gly Ser  Arg Ile Asp
    4745                 4750                 4755

Ala Arg  Arg Asp Val Thr Phe  Glu Ala Gly Arg Asp  Val Gly Leu
    4760                 4765                 4770

Val Ala  Ala Ala Asn Glu Glu  His Ala Tyr Gly Lys  Thr Lys Lys
    4775                 4780                 4785

Val Thr  Phe Gln Asp Asp Lys  Ile Thr Gln Gln Ala  Thr Arg Val
    4790                 4795                 4800

Asp Ala  Gly Gly Asp Leu Ala  Ile Asn Ala Gly Gln  Asp Leu Arg
    4805                 4810                 4815

Leu Val  Ala Ser Gln Ala Ser  Ala Gly Asp Glu Ala  Tyr Leu Val
    4820                 4825                 4830

Ala Gly  Asp Lys Leu Glu Leu  Leu Ala Ala Asn Asp  Ser Ser Tyr
    4835                 4840                 4845
```

-continued

```
Tyr Leu  Tyr Asp Lys Lys Ser  Lys Gly Ser Phe Gly  Ser Lys Lys
    4850                 4855                 4860

Thr Arg  Arg Asp Glu Ile Thr  Asp Val Thr Ala Val  Gly Ser Gln
    4865                 4870                 4875

Ile Ser  Ser Gly Gly Asp Leu  Thr Leu Leu Ser Gly  Gly Asp Gln
    4880                 4885                 4890

Thr Tyr  Gln Gly Ala Lys Leu  Glu Ser Gly Asn Asp  Leu Ala Ile
    4895                 4900                 4905

Val Ser  Gly Gly Ala Val Thr  Phe Glu Ala Val Lys  Asp Leu His
    4910                 4915                 4920

Gln Glu  Ser His Glu Lys Ser  Lys Gly Asp Leu Ala  Trp Gln Ser
    4925                 4930                 4935

Ser Lys  Gly Lys Gly Gln Thr  Asp Glu Thr Val Arg  Gln Ser Gln
    4940                 4945                 4950

Ile Val  Ala Gln Gly Asn Leu  Ala Ile Lys Ala Val  Glu Gly Leu
    4955                 4960                 4965

Lys Ile  Asp Leu Lys His Ile  Asp Gln Lys Thr Val  Ser Gln Thr
    4970                 4975                 4980

Ile Asp  Ala Met Val Gln Ala  Asp Pro Gln Leu Ala  Trp Leu Lys
    4985                 4990                 4995

Gln Met  Glu Gln Arg Gly Asp  Val Asp Trp Arg Arg  Val Gln Glu
    5000                 5005                 5010

Leu His  Asp Ser Trp Lys Tyr  Ser Asn Ser Gly Leu  Gly Val Gly
    5015                 5020                 5025

Ala Gln  Leu Ala Ile Ala Ile  Val Val Ala Tyr Phe  Thr Ala Gly
    5030                 5035                 5040

Ala Ala  Ser Ala Ala Leu Gly  Ser Met Ala Gly Val  Gly Ala Gly
    5045                 5050                 5055

Ser Gly  Ser Met Met Ala Ala  Ala Gly Ser Thr Ala  Met Val Gln
    5060                 5065                 5070

Ala Gly  Thr Ala Val Gly Thr  Ala Ala Ala Gly Trp  Ala Asn Ala
    5075                 5080                 5085

Ala Gly  Thr Ala Val Ala Met  Gly Met Ala Ser Asn  Gly Ala Ile
    5090                 5095                 5100

Ser Thr  Ile Asn Asn Arg Gly  Asn Leu Gly Asp Val  Val Lys Asp
    5105                 5110                 5115

Val Thr  Ser Ser Asp Ala Leu  Arg Gly Tyr Val Val  Ala Gly Thr
    5120                 5125                 5130

Thr Ala  Gly Leu Thr Ala Gly  Val Tyr Asp Lys Trp  Thr Ser Thr
    5135                 5140                 5145

Gln Thr  Gly Thr Ser Thr Ala  Leu Pro Asn Thr Gly  Ala Val Ala
    5150                 5155                 5160

Pro Ala  Ala Gly Leu Gly Thr  Trp Gln Gly Val Gly  Gln Phe Thr
    5165                 5170                 5175

Ser Asn  Gln Leu Leu Gln Asn  Gly Thr Ser Val Leu  Leu Asp Arg
    5180                 5185                 5190

Ala Leu  Gly Gly Lys Gly Ser  Leu Gly Asp Ala Leu  Gln Asn Ser
    5195                 5200                 5205

Leu Ala  Asn Ala Phe Ala Ala  Tyr Gly Phe Lys Leu  Ile Gly Asp
    5210                 5215                 5220

Thr Thr  His Gly Val Leu Asp  Asp Gly Ser Leu Gly  Lys Ile Gly
```

-continued

```
    5225                5230                5235

Leu His  Ala Leu Met Gly Gly  Leu Ala Ala Glu Ala  Val Gly Gly
    5240                5245                5250

Asp Phe  Arg Thr Gly Ala Leu  Ala Ala Gly Val Asn  Glu Ala Leu
    5255                5260                5265

Val Asp  Ser Leu Ala Lys Gln  Tyr Ala Ser Leu Pro  Ile Asp Asp
    5270                5275                5280

Lys Lys  Gly Leu Leu Ile Met  Ser Ser Gln Leu Ile  Gly Val Leu
    5285                5290                5295

Ala Ala  Ser Thr Gln Gly Asp  Ala Asp Ala Lys Ser  Leu Gln Thr
    5300                5305                5310

Gly Ala  Trp Val Ala Gly Asn  Ala Thr Gln His Asn  Tyr Leu Ser
    5315                5320                5325

His Trp  Gln Glu Glu Lys Lys  Arg Gln Glu Val Asp  Gly Cys Lys
    5330                5335                5340

Asp Lys  Gln Leu Cys Lys Thr  Gly Ile Glu Ala Lys  Trp Ala Ile
    5345                5350                5355

Ile Ser  Ala Gln Gln Asp Val  Gly Ile Val Val Gly  Val Gly Gly
    5360                5365                5370

Gly Ile  Gly Leu Ser Thr Ala  Glu Thr Ala Val Gly  Val Tyr Glu
    5375                5380                5385

Leu Val  Lys Asn Trp Arg Glu  Thr Tyr Ala Ala Leu  Glu Gln Leu
    5390                5395                5400

Ala Thr  Ser Pro Glu Phe Arg  Gln Gln Phe Gly Asp  Asn Tyr Leu
    5405                5410                5415

Lys Gly  Leu Glu Glu Arg Ala  Ala Phe Leu Thr Gln  Ala Tyr Glu
    5420                5425                5430

Asp Ala  Gly Trp Gln Gly Ser  Val Thr Ala Gly Val  Glu Gly Gly
    5435                5440                5445

Arg Phe  Ala Ala Glu Leu Val  Gly Val Leu Thr Ala  Val Lys Gly
    5450                5455                5460

Gly Ala  Gln Ile Thr Ala Lys  Leu Pro Thr Ala Ala  Lys Asn Leu
    5465                5470                5475

Val Asn  Ala Ile Ala Glu Ser  Pro Val Ser Gly Ser  Met Ser Ser
    5480                5485                5490

Gln Leu  Gly Ala Val Gly Asp  Leu Gly Arg Leu Gly  Gly Gly Gly
    5495                5500                5505

Lys Gly  Tyr Val Asp Ile Leu  Ser His Glu Ala Lys  Gln His Ile
    5510                5515                5520

Leu Tyr  Gly Asp Lys Pro Gly  Ser Gly Gly His Leu  Trp Pro Gly
    5525                5530                5535

Gln Ala  Gly Lys Thr Val Phe  Pro Gln Asn Trp Ser  Ala Asp Lys
    5540                5545                5550

Ile Val  His Glu Val Gly Asp  Ile Ala Thr Ser Pro  Ser Thr Lys
    5555                5560                5565

Trp Tyr  Ala Gln Thr Gly Thr  Gly Gly Val Tyr Thr  Ser Lys Gly
    5570                5575                5580

Asp Pro  Ala Lys Trp Val Ala  Tyr Glu Val Arg Asp  Gly Val Arg
    5585                5590                5595

Met Arg  Val Val Tyr Gln Pro  Ala Thr Gly Lys Val  Ile Thr Ala
    5600                5605                5610
```

-continued

```
Phe Pro  Asp Asn Ala Pro Ile  Pro Pro Tyr Lys Pro  Ile Lys
    5615                 5620                 5625
```

<210> SEQ ID NO 31
<211> LENGTH: 201
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 31

```
atgagtcagg aaccccacgt acacggcccg aactgcaacc acgaccacga tcatcatcac      60

gatcatggcc atggtcatgt ccatggtccg cactgcaacc acagccacga gccggtgcgc     120

aatccgctca aggccgtagg ccgcaacgat ccctgcccct gcggcagcga gaagaaattc     180

aagaagtgcc acggcgcctg a                                               201
```

<210> SEQ ID NO 32
<211> LENGTH: 237
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 32

```
atgaaaaaga ccgtaactct tgccctgctg ctcgctgcca gccttggcct ggccgcttgc      60

gacaagaaag aggaagacaa ggcagcggcc ccggcagctc cggctaccga gacccagccg     120

agcgctccgg ctactccccc tgccgagccc agcgccccgg cgccgtcgag cgacactccg     180

gcaaccccgc agactccggc accgactccg gagcaaccgc aacagaacca gcaataa        237
```

<210> SEQ ID NO 33
<211> LENGTH: 315
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 33

```
atgaaaaaga tttccctcgc ttcttccgtc gtcggcgctg ctctgctcgg cgtagccagt      60

gtcggcgcgc atgccgcgca gaatcccttc gccgtgcagg agctgagcag cggctacagc     120

gtggctgccg ccgagaaagc caaggaaggt tcctgcggcg aggccaagtg cggtgccgac     180

aagggcaagc gcgaagcctc caaggccggt catgaaggca gctgcggtgc ggatcgcaag     240

gccaaggaag gttcctgcgg tggcgagaag aaggccggcg aaggcaactg cggcgccgac     300

aagaagaagt cgtaa                                                      315
```

<210> SEQ ID NO 34
<211> LENGTH: 468
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 34

```
atgtccgttt tcgattcgcg tcaaaagact tccgccagcc tgctcggtgc cgtactggtg      60

gggggaatgc tgctcggcgg ttcggcgttc gccgtcgagc cgctgggcca ggggctgcaa     120

gtggcggcgg cgagcgccgg cgaaggcaag tgcggagaag gcaagtgtgg tagcggcggc     180

tccgcgaaga ccccggccaa ggccggcgcc gagggcaagt gcggggaggg caagtgcggc     240

gacgcctcct ttgcccgaac cgacaccgat cacgatggca aggtctcgcg cgccgagttc     300

ctcgcggtgg ccaaggaccg tgccggtgag ttcgacagca tcgatagcga ccatgacggc     360
```

-continued

ttcatttccg aagccgaggc ctacgaacac ctgcgcaaga cctacgaggc caacggcaag 420

ccgatgcccg ccgggctgtt cagcaagctg gagcaaggcc agcactga 468

<210> SEQ ID NO 35
<211> LENGTH: 540
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 35

atgcgttccc tgtccctcct tctcctcctc tcgctggcgt ccacctgcga ggccgctgcg 60

gtattccgct gcgaagacgc cagcggccat gtcagcttca cccaactcgg ttgccccgcc 120

gggcaggccg gcgagaccgt cgtggcggac aacccgccgc cgggaggcag gagcgtcacg 180

ccgatggccg agacgaagac gaaaaaggcg tccatcggcc ggaaaagcgt gccgctcgcg 240

gtgatcggag aaagagaaga tcgctgcggc agacgcctgg acgagaagga acgccgcaag 300

gcgatcgtgg agcagcggat aatggcggga atgacccgct ccgatgtgga gcgggcgctg 360

ggcaagccgg accgggtcag cgggaacaat gcggaggtgc gttatcagta caaggccgac 420

aagcgacggg gagcgagaag cgtgagcttc gatcaggagg gatgtgtgaa gggaagagaa 480

ggtaccgggt ggagcgagtc gatcccggga gctaaggccg ggccgtcctc ataccgatga 540

<210> SEQ ID NO 36
<211> LENGTH: 915
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 36

atgagccaac ccagcgaaaa ccgtttgatc acctcggcgc gctacgcgct ctgcctgttg 60

accgccagcg gcgtgctgct cagcggctgc gccagcagcg gcgtcggctc ggtcgcccag 120

accacccgcg cggaatacta cccgtcctgc tacgagccgg tgtcgcacct gcgcagcacc 180

gataacgcag tgcgcaattc ggccatcacc ggcgccatta ccggcggcct cctgggcggc 240

ctggccggcg gcctggccag cgacgagaac cgcggccgca atgccgccct cgctgccgca 300

ggcggcgccc tggccggcgg cgcggcgggc tactacatgg agaagcagaa gcagatcagc 360

gatgaccgcg cgcgcatcgg ctcctacggt accgacgtcg accgcagcac cgtcgagatc 420

aaccgtagcg tggcctacgc caagtcggcg caaagctgct accagagcca gttcaaggct 480

ctgctcgacg gtcgcaagaa caagtcgatc aacgaagccg aagggcgcaa gcgcctggcc 540

gagatcgtca gcggcctgca ggagaccaac gccttgctgg tcgccgccaa cggccgtgcc 600

ggcgagaaca tcagcaacta cacccaggcc tacgagaaag acctgcagca ggtcggcgta 660

ccgcgcgccg aggtgaccaa ggtcgccgag gccgagaacc gcgccagcac tacgaaaggc 720

ggcagcaagc ccaagaccgg cagcaatccc aaggtgccga aggaagcggt cgccaccgag 780

cagaccatcc gcaaggccca ggacgcgcaa agcgaaggca acaaggtggc ctcccagggc 840

cagggcatga tccgggaagt ctgcaacagc ccggacatgg gcgactgggc gccgccgagc 900

tgcgccaagg cctga 915

<210> SEQ ID NO 37
<211> LENGTH: 930
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

-continued

<400> SEQUENCE: 37

atggctggca agaagaagag cgaaaaagag tccagttgga tcggcgagat cgagaaatac 60

tcgcggcaga tctggctggc tggtctgggg gcctactcga aggtcagcaa ggacggcagc 120

aagctgttcg agaccttggt gaaagacggc gagaaggctg aaaaagaagc gaagtccgat 180

gtggacgcgc aggtcggtgc ggcgaaggct tccgcccgct ctgcgaagag caaggtcgac 240

gaggttcggg accgtgcgct cggcaagtgg agcgagctcg aggaagcttt cgacaagcgc 300

ctgaacagcg ccatctcgcg tctcggcgtg ccgagccgca acgaggtgaa ggagctgcac 360

agcaaggtcg atacgctgac caagcagatc gagaaactca ccggcgtcag cgtcaagccg 420

gcggcgaagg cagcggccaa gcctgcggcg aaaccggctg ccaagcccgc ggcgaaaacc 480

gcagcggcca agccggcagc taaaccggca gccaaggccg ccgccaagcc tgcggcgaaa 540

cccgcggcga aaaaaaccgc ggcgaaaacc gcggccgcca agccggcagc caagcccgcc 600

gccaaaccga ctgcgaaggc cgcagcgaaa ccggcgacca agccggcagc caaggccgcg 660

gcgaagcctg ctgcgaaacc tgccgcagcc aagcctgccg cgaagccggc agccaagccg 720

gccgctgcga ccgccgccaa gcccgcggcg aaacctgccg ccaagccggc tgcgaaaaag 780

cctgcggcga agaagccggc agccaagccc gccgcggcga aaccggccgc tcccgccgcg 840

tcttcgagcg cgcccgctgc ccccgccgcc acaccggctg ccagcgctcc ggcagcgaac 900

gctccggcga cgccgagcag ccagggctga 930

<210> SEQ ID NO 38
<211> LENGTH: 1023
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 38

atgaaagcga ctatggtcct gaccccgctg gccctggcaa tggctgcagt gctgtcggta 60

tcggcctacg ccggaaacga aggtggctgg cacccgccga aacccaaccc gcagtcgaac 120

aacaagggcg gagccacggc cctggtggtg gatacgcagc agaactacaa caacaaggtc 180

agcaacttcg gcacgctgaa caatgcctcg gtgagcggct cgatcaagga tgcctcgggc 240

aacgtcgggg tcaacgtcgc cgccggcgac aacaaccagc aggccaacgc cgccgcgctg 300

gccagcgccg acgccagctt cgtgttcggc accgcgaccg ccagcaccag cgtgctgcag 360

agcggctacg gcaatacgct gaacaactac tccaacccca acaccgcatc gctgagcaac 420

tcggccaaca acgtctcggg caacctgggc gtgaacgtcg ccgccggcaa cttcaaccag 480

cagaagaacg acctggccgc cgccgtctcc aacggccagt acagcactgc cggtagcgcc 540

gcgtcgcaga cctccaccgg caacaccacc gtcaacagcg ccaactacgc ctatggcggc 600

acctacgtgt cgctgaagct gaacgccgac ggcagctaca agggcacctc cgaccagatc 660

ggcgacgtct acctcgacac ctgggaaggc cagacccatc cgggcggcag caataccggc 720

cacatcgacg tggacagcca ggcccagggc gccaaggacc tgaaccacga cggcggcgcg 780

ttcgccttca aggaaaaggg cgacgtcgac ctgaaaggca cggtgtccgg cttcatcccg 840

gcgatcgtcg gcttcaagac cccggtcacc aacaacgcca gcctgagcaa ctcgttgcag 900

aacgtctcgg gcaacgtcgg ggtgaacatc gccgccggtg gcggcaacca gcagagcaac 960

tccctgtcca tcgccgccgg ttgcagcagc tgcccggccg gtggcgagag ccttggcttc 1020

-continued

tga 1023

<210> SEQ ID NO 39
<211> LENGTH: 1044
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 39

atgaagcaac agttcgaacg ctcgccttcc gagagttatt tctggcccgt cgtcctggcg 60

gtggtcctgc acgttctgat cttcgccatg ctgttcgtca gctgggcgtt tgctccggag 120

cttcctccct ccaagccgat cgtgcaggcc acgctctacc agctcaagtc gaagagccag 180

gcgacgacac agaccaacca gaagatcgct ggcgaggcga agaagaccgc ctccaagcaa 240

tacgaagtcg agcagctcga acagaagaag ctcgagcagc agaaactcga gcaacaaaag 300

ctggaacagc agcaggtcgc tgctgcgaaa gcggcggaac aaaagaaggc tgacgaggct 360

cgaaaggccg aggcccagaa agccgccgag gcgaaaaagg ccgatgaagc caagaaagct 420

gccgaggcca aggccgccga acagaagaag caggctgaca tagccaagaa gcgcgccgag 480

gacgaggcca agaaaaaggc cgctgaggac gccaagaaaa aggcagccga ggacgcgaag 540

aagaaagcgg ccgaggaggc caagaagaag gctgctgcgg aagcggcgaa gaagaaagcc 600

gccgtcgagg ccgccaagaa aaaggccgcc gccgctgccg cggcagcccg caaggctgcc 660

gaggacaaga aggcgcgggc attggccgag ttgctttcgg atacgaccga gcgccagcag 720

gccctggccg acgaggtggg cagcgaggtc accggcagtc tcgacgacct gatcgtcaac 780

ctggtgagcc agcagtggcg gcgtcctcca tcggcgcgta atggaatgag cgtagaagta 840

ctgatcgaaa tgctgccgga cggtaccatc accaatgcca gcgtcagccg ttcgagtggc 900

gacaagcctt tcgacagttc ggcggtggcg gcggtgcgca acgtcggccg tattcccgag 960

atgcagcaat tgccgcgggc taccttcgac agcctgtatc gtcagcgccg catcatcttt 1020

aaaccggagg atttgagtct gtga 1044

<210> SEQ ID NO 40
<211> LENGTH: 1059
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 40

atgtcggcca acaagaagcc cgtcaccacc cccttgcacc tgttgcagca actttcccac 60

agccttgtcg agcacctgga aggtgcgtgc aaacaagcgc tggtcgattc ggaaaagctc 120

ctggccaaac ttgaaaagca acgtggcaaa gcccaggaaa agctgcacaa ggctcgcacc 180

aagctgcagg atgctgccaa ggccggcaag accaaggcac aggccaaggc gcgcgagacc 240

atcagcgacc tggaagaggc gttggatacc ctgaaggccc ggcaggcgga cacccgtacc 300

tacatcgtcg gcctcaagcg tgacgtacag gaaagcctca agctggcgca gggtgtcggc 360

aaggtgaagg aagctgctgg caaggctctg gagagccgca aggcgaaacc cgcgaccaaa 420

cctgctgcga aggcggcagc caagcctgcg gtgaaaaccg tagcggcgaa gcctgcggcc 480

aagccggctg cgaagcctgc tgcgaaaccg gcggccaagc ctgcggcgaa aaccgcggca 540

gcgaagcccg cagccaagcc gacggcgaag cctgctgcga aaccggcggc caagcccgcg 600

gcgaaaaccg cagccgcgaa gcccgcagcc aagccggcgg cgaagcctgt ggcgaaaccg 660

-continued

gcggccaagc ctgcggcgaa aaccgcagcc gcgaagcccg ccgccaagcc ggcagcgaag 720

cctgtcgcga aaccgacggc caagcccgcg gcgaaaaccg cagccgcgaa gcccgcagcc 780

aagccagctg cgaagcctgc ggcgaaaccg gcggccaagc ctgtggcgaa atccgcggcc 840

gcgaagcctg cagccaagcc ggctgcgaag cctgcggcga aaccggcggc caagcctgcg 900

gcgaaacccg tagccgcgaa acctgccgca accaagcccg ccaccgctcc tgctgcgaag 960

cctgcggcga ctcccagcgc cccggcagcc gcctccagcg ctgcttcggc aacgcctgcc 1020

gcgggcagca acggcgccgc cccgaccagc gcctcctaa 1059

<210> SEQ ID NO 41
<211> LENGTH: 1263
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 41

atgtggggtc ttacgatgaa gtttgcgagc ctgattctga tgcttctctt tgccacggtg 60

gcgagggctg aggattacta ctggaaaatt cagtcactgc ctgaacgctt ttcttcgccc 120

tcggcagctt gcgcggcgtg ggccaaagcc acgggacgcc ctggggagtt caccttcacc 180

gggtctatga aagcccgtga ccagacctcg ttttggtgcg agttcacgaa caacgaaacc 240

ggcaagactg ctgccgggta tggtcctgcc ggacgctatg gcgatagctg tcccgagggg 300

acggaatacg ataaggcgac cggggtttgt aagtcgcctc cgcaagaatg caaggaaggc 360

gaactgttcc cggccaaagg cccggactct cccgtggtta cctcgggagg ccgtaactat 420

gtcggtgacg gcggcgcccc gaccgcctgc tatcaaagct gtgagtatgg cggcaatccc 480

agcccggcca gttgctatct ggtcaaaggc tccaccacga ccggcttctg caattacatc 540

ctcaagggca ccggacagaa ttgcggtgcc gattcctaca ccttctccca gaccggcgat 600

tcgctgaacc cgcccgacac tccgaacacc gatccttccg acccgaacga ccccggctgc 660

ccgcccggct ggtcgtggtc gggaactacc tgcgtcaagg ccccgaccga tcccacggat 720

ccaaccgacc cgaccacgcc gggcagtgac ggcggcggcg atggcaatgg cggtggaaac 780

aataacggcg gcggcaatga cggcggcacc ggcaatggcg gcgacggcag cgggggaggg 840

gacggcaacg gcgggggcga tggtagcggc gacggtgacg gcagcggcac gggcggcgat 900

ggcaacggca cctgcgaccc ggcgaaagag aactgctcca ccggccccga aggccccggc 960

ggcgaactca aggagcccac gcccggcacc tgggatgacg ccatcgccac ctgggaaaag 1020

aaggtcgagg acgccaagca agaactcaag accaaggtga aggccaacgt cgatcagatg 1080

aagggcgcct tcgacctcaa cctggcggaa ggcggcgggc aactgccctg cgagtccatg 1140

accatttggg gcaagtccta ctccctctgt atctccgact acgccggcca actctccagc 1200

ctgcgcgtgg cgctgctgct gatggccgcg ctgatcgccg ccctcattct gctgaaggac 1260

tga 1263

<210> SEQ ID NO 42
<211> LENGTH: 1284
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 42

atggccgtcg cccctggtgt gttgttgccg ccgacgcctg atgtaaagcc caaggccgct 60

-continued

gcgccgaaga gccagcagaa aacgcctgag cccagtaacg acaagacttc cagcttctcc 120

gacatgtatg ccaaggagac cgcgaagaag cccgccgagc gcgccgacgg tcccgcgaag 180

ggttcgcggg acaagccacg ggacgccggc aaggacgccg ccgaagcgca gccgacggat 240

gccgtcaggc agccggccgt tgccgaagac ggcaagcctt tgccggccga cggccaggcc 300

aaggccgacg gcgaagataa agtcgaaacg ccggtcgatc cgctgcaatt gctcggcctc 360

ggcggtgccg taccgttgct cgacgagaat acccaggcga ctttgctgcc accggccgtg 420

ccgacggcca gcagtgctcc ggccagcctt accgaagcca gcagcgaccc gaccctggtc 480

aagctcaacg gcgtgccggc ggtgaacatg gccctggagc agggcgccca ggacgccgcg 540

cagacggcga aaggcgggcc ggcgaagagc gccgatcccc gccaggcgaa cctcggcgat 600

gcccttgccg gcctgacctc ggattccttg accaaggccg tcgacggcaa ggcgctcgag 660

gcccagttgc agcagaccgc cgagccggcc gtcgccagcg ccgcctccga gagcctgctg 720

gagagcaagg cggaaccccg cggtgaacct ttcgcggcca agctcaacgg gctgacccag 780

gccatggcgc aacaggccct gaccaaccgt ccggtgaacg gcacggtgcc cggccagccg 840

gtggcgatgc agcagaacgg ctggagcgag gcggtggtgg accgggtgat gtggatgtcc 900

agccagaacc tgaagtcggc ggagatccag ctcgaccccg ccgagctggg acgcctggac 960

gtgcgcatcc acatgaccgc cgaccagacc caggtgacct tcgccagtcc caacgccggc 1020

gttcgcgacg ccctggaaag ccagatgcac cggctgcgcg acatgttcag ccagcagggc 1080

atgaaccagc tcgacgtgaa cgtctccgac cagtcgctgg cgcggggctg gcagggccag 1140

cagcagggcg agggcggatc ggcgcgcgga cgcggcttgg ccggcgaggc ctcgggcgat 1200

gaggaaaccc tcgccggagt cagcgagatc cgcagccggc cgggtgcgtc ggcggcgcgc 1260

ggtctggtcg actactacgc ctga 1284

<210> SEQ ID NO 43
<211> LENGTH: 1287
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 43

atgctccgcc tccttcctct cctgctatcc ctcgcctgtc tcgctccggc cttcgccgac 60

gagcgcgccg acacccaacg ccagctggaa cagacgcaga aggacatcgg cgagctgaag 120

aagctgctgg acggcatcca gcaggaaaag agcggcgtgc agaagcagct gaagtccacc 180

gagaccgaga tgggcgacct ggaaaaacag atcaaggccc tgcaggacga gctggacaag 240

agcgaagccg agctgaaacg gctggatggg gagaaaaaaa aactccagga cgcgcgcatt 300

gagcagcagc gcctcctcgc catccaggcc cgcgcggcct accagagtgg acgcgaggaa 360

tacctgaagc tgctgctgaa ccaggaacac ccggaaaaat tcagccgcac cctcacctac 420

tacgactaca tcaacaaagc ccgtctcgaa cagctcgcca gcttcaacga aaccctccgc 480

cagctggcca acgtcgagca ggacatctct gcgcagaaag ccgaacaact gagcaagcaa 540

ggcgagctgg acagccgccg cgaggcgctg gcagcgaccc gcaaggagcg ccagcaagcc 600

ctggccaagc tgaacagcga ctaccgcgaa cgcgaccaga agctcaagtc ccgccaacag 660

gaccaggccg agctggccaa ggtactgcgg accatcgagg aaaccctggc ccgccaggcc 720

cgcgaagccg ccgccgcggc ggagcgcgag cgccagcgcg cgctggccgc cgaacgcgag 780

-continued

cgtgcgcgcc agcagcaggc cgcccccgga cgagtcacca gcccgccgcg cgaacctgcg 840

ccgggcccgc tggtctcaag cactggcgcg gtctacggcg gcgcgttcgg ctcggcccgc 900

ggcaagctgc cgtggccggt gaatggccgc gtcgtggcgc gcttcggcag ccagcgcggc 960

gacgatccgc gggcgaaatg ggacggcgta ctgatttcgg cgagcgccgg cagcaccgtc 1020

cgcgcggtgc acggcggacg cgtggtattc gccgactggt tgcgcggagc cggcctgttg 1080

gtcatcctcg accacggtgg cggctacctc agcctttatg gccataatca aagcctgctg 1140

aaagacgccg gcgacaccgt gaaggccgga gacccgatcg ccaccgttgg aaccagcggc 1200

ggccagagta gcccggccgt gtacttcgcc attcgccatc agggccgccc ggcggaccct 1260

actacctggt gccgcgcaca gggatag 1287

<210> SEQ ID NO 44
<211> LENGTH: 1707
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 44

atgcaaagac tgtcgcgtat cggccgcaac accctcgccg tctccgtttc caccttgctc 60

ctcagcgcct gcaaccaggg cgacgatgcg ccgaagcctg cggcagtcgc gccgcaaccg 120

gccgcaccga gcatggctgc actgagcatc ccgctatgcc tcaacggcca gtgcgcggtg 180

atcgaccagg acgccaagct gctcgtgccg ttcgacaacg actacgacaa tatcgtcgcc 240

agcgcctacc agggcaccct gatggcggcg cgcgaggagc gctggaacct gatccaggcg 300

aaggacggca aggtgttgcg cgacgatatc ggcgaagccc tgtcgctgct cacccccaac 360

ctctatggct tcgtccgcga tggcaagtac ggcgtggtcg acggccaggg caaggaagtc 420

caggcgccgc gtttcgacga catctacccc aacagtgcca acgaattcat catctacgag 480

atcgatggca agcgcggcat cctcgatgcc aagggcaagc agctcaccga ggcgctctac 540

gacaccaccc tggtcaacgg cagcgtcgcc gaacacggtg gcttgatcag cgccgagcgt 600

ggcgaggaga agtggatcat caacctcgct accggcgaac agaaggccgt ggcctacgag 660

agcctgggcg acctccacga cggcgtgatg agcgccagcg tcatcggcaa gggctcccaa 720

ctggtggatg ccaagggcga cgtggtcggt gacggcaaga gctacgatta cctgggcacc 780

ccggccaacg gcctggtcgc gttccgcgag aagtacgaca gcccctgtgg ctacctcgac 840

taccagggca aggtggcgat cgccgcccag ttcgccggtt gcggcgcctt cggcaagcag 900

ggcgggctgg cccagcagcg catggaagat ggctcgtcgg gcaagtacgg cctgatcgat 960

cgcagcggcg cctggaaggt gcagccgcag tacgattcgg ccgacagcgc cggcctcacc 1020

gcgcttggct acaccgtcga cgtgcccggc ctggctgccg tcggcgtgag caccggcctg 1080

ttcagcgccg acttcggcat cttcaacctc gacgaaggca gcgagtgggt gaagccgggt 1140

tatgcgcaga tcggcgcgct gggcaacgac ctgttcgtcg tggcgaagaa gggcgggccg 1200

cagaagaccg tcagcttcat gggttcggaa agccaggtgc cggtggtggg cctgatggac 1260

cgcagcggca agatgctgct ggagccggac gaactgatca gcatccagtc tgcttatgac 1320

ggtcgtttcc tggaaggtct cgacggtatg gacaacgctg cccacaccgt gttgctcgat 1380

cgccagggac gcacgctggt tccagcgctc tggcagaagc tggaggtgaa tccgcagcag 1440

ggttacatcc tgggctacga agtcagcggc actggcgacg aggcgacgga aaccttgcgc 1500

-continued

gcactgtacg acctgaacgg caagccgcgc ttcaccgtgg ccaccaccga ttgcggcgcc 1560

gaacagttgc tcgacggcaa tggcaaggcg atctggccgc aggacccgac cccgtattgc 1620

cagtcggacg acgagcagga cgacgaaggc gagccggagc aggagccggc gcccgtcgaa 1680

gagagcgagg aaaccagcga gagctga 1707

<210> SEQ ID NO 45
<211> LENGTH: 1740
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 45

atgcttcgcc ccgccaggtc tctctcgctc tgctccgccc tggtcatcct gctcgccgcc 60

tgtggcgagg gcgaaccgct gctcccggcc gatgcgcgcc tgcctgacgg cgcgcgctat 120

cgcggcgagc tggtggacgg gcgcctggaa ggccagggcc ggctggacta cgacaacggc 180

gcctggtacg ccggccgctt cgagcatggc ctgctgcacg gccatggcac ctggcagggc 240

gccgacggca gccgctacag cggtggcttc gcggccggcc tgttcgacgg tcagggacgc 300

ctggcgatgg ccgatggcag cgtctaccag ggcggtttcc gccagggcct gttcgatggc 360

gaaggcagcc tggaacaaca gggcactcgc taccgcggcg gtttccgcaa gggcctgtac 420

agcggccagg gcacgctgga cggcagcgat ggcagccgct accagggcag cttccgccag 480

ggccgcctgg aaggcgaagg cagcttcagc gacagccagg gcaaccagta cgccggtacc 540

ttccgcgacg ggcaactgaa cggcaagggg cgctggagcg ggcccgatgg cgaccgctac 600

gtcggccagt tcaaggacaa ccagttccat ggccaggggc gctacgaaag cgccagcggc 660

gatgtctgga tcggccgctt cagcgaaggc gcgctgaacg gccccggcga gcttctcggc 720

gccgacggca gccgctaccg cggcggtttc cagttctggc gcttccatgg ccagggcctg 780

ctcgaacaac tggacggcac ccgctacgaa ggcggcttcg ccgccggcgc ctatgccggc 840

caaggcaccc tggaccgcgc cgacggcagc cgtgagcagg gactctgggc cgacggcaag 900

cgcatccgcg acgccgccgg caaggccctg cccgacactc tggaagtcgg cctgttggcc 960

cagggtcgcc tgctcgacga agaactgcgc aagatcccgg cctcgacgcc ggccagcgaa 1020

ctctatgccc tgagcctggg cggcgatggc cgccagggcg tgttcctgcg cgaggccgat 1080

tacgccggcg acctgctcgg ccagcgtttc gccgctcgtg gcgtgattcg cctggtcaac 1140

caccgcgacc acttcggcga ccgcccgctg gctacccggg aaagcctgtc ccgcgccgtg 1200

cgcaccctgg ccgaacgcag cgggccggaa gacctggtct tcatctacct gaccagccac 1260

ggctccagcg accaccagtt ggccctggac atgcccggcc tgaacctcgg cgacctgccg 1320

gccgcggaac tggccgaact gctcgcgccg ctgcgccagc gcgacaaggt gctggtggta 1380

tcggcctgct acagcggggg cttcatcccg ccgctgaaag acgaacgtac cctgatcctg 1440

accgccgcgc gtgccgaccg ggtctcgttc ggctgttccg acgacgccga cttcacctat 1500

ttcggccgcg ccttgctggc caatgcgctg aaccgcaccg acgatctgtc caaagcgttc 1560

gaactggcga aagaggaagt gcgtcaaagg gagaaggagg aaggtttcga agcttcggaa 1620

ccgcaagcct ggttaccgga acgcgtgctc gcgcactggc ggacgctgcg ggggcagcaa 1680

gccgagcgcg cgctcgcgtc ccgggaagga aaaaccggcg agggcgcggc gggcaaatag 1740

<210> SEQ ID NO 46

<211> LENGTH: 1866
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 46

atgctgcaga acatcaggga taattcccag ggctggatcg ccaagaccat cattggcgtg 60

atcatcgttc tcctgtcgct gaccggcttc gacgcgatca tccgggccac cgaccactcc 120

aacgtggccg ccaaggtcaa cggcgacgat atcagtctca atgaagtcca acaggccgtg 180

gacatgcagc gtcgccagct gctgcaacgc ctgggcaagg atttcgatcc atccatgctg 240

gatgacaagc tgctcaagga agcggccctg aaggggctga tcgagcgtac cctgctgctc 300

caggccgcca aggacgacaa gttcgccttc tccgaccagg cgctggacca gttgatcctg 360

caaactcccg agttccaggt cgacggcaag ttcaacgcgg atcgcttcga ccaggtcatc 420

cgccagatga actacagccg catgcagttc cgccagatgc tcggccagga aatgctcatc 480

ggccagcttc gcgccggcct ggcgggcacc ggtttcgtca ccgacaacga attgcagtcc 540

ttcgctcgcc tcgagaagca gacccgcgac ttcgccaccc tggcgatcaa ggccgacgcc 600

tccaagagca gcgtgagcga cgacgaggtg aaggccttct acgaaggcca caagagcgag 660

ttcatgactc ccgagcaggt ggtcgtcgaa tacgtggagc tgaagaagtc ctccttcttc 720

gaccaggtca aggtgaagca ggaagacctc gaggcgctgt accagaagga aatcgccaac 780

ctttccgagc agcgcgatgc cgcccacatc ctgatcgagg tgaacgacaa ggtcggcgac 840

gagcaggcca aggcgaagat cgacgagatc aaggctcgcc tggccaaggg cgaggatttc 900

gccgcgctgg ccaaggagtt ctcccaggat atcggctcgg ccgccaccgg cggcgacctg 960

ggctacgccg gtcgcggcgt gtacgacccc gcgttcgagg aggcgctgta tgcgctgaag 1020

caaggtgagg tatccgcccc ggtgaagact ccgtacggct accacctgat caagctgctg 1080

ggcgtgcagg cgccggaagt accgagcctg gaaagcctca agccgaagct cgaggacgaa 1140

ctgaagaaac agatggtcga gcagcgcttc gtcgaggcta ccaaggacct ggaaagctcc 1200

gcctacgaag ccgccgacct gagccagccg gcgcaggaaa tgggcctgaa ggtccagacc 1260

agccagccgt tcggacgttc ggggggcgac ggcatcgctg ccaaccgcca gatcgtgcag 1320

accgcgttca gcgccgaggt gctggaagaa gccgccaaca gtggcgccat cgagctggat 1380

ccggacaccg tggtggtgct gcgggtcaag gaacacaaca agccgaagga gcaaccgctg 1440

gagcaggtcg cggcgaacat ccgcgagcgc ctggccgccg aaaaggccgc cgaggaggcg 1500

cagaagcgtg gcgaggccct gatcgcagag ctgcgtgaag gccgtacctc ttccgcagcg 1560

ggtgagtcgt ggaaagtggt cgaggcggcc tcccgcggcc acgaaggcgt cgatccgaaa 1620

ctgctccagg cggtgttccg catgcagcgt ccggaggcca aggacaagcc ttcgttctct 1680

ggcgtgaccc tggccaatgg cgattacgtg gtgatccgcc tgaatggcgt cagcgagccg 1740

gaggaggcta tctccgacga cgagaaggcc atgtaccgcc gcttcctggc ttcgcgcagc 1800

ggacaggcag acttcgccgc cttccgccgt cagttgcagg acaaggcgga agtcgagaaa 1860

tactga 1866

<210> SEQ ID NO 47
<211> LENGTH: 2067
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

-continued

<400> SEQUENCE: 47

atggatatga cgtcgctgat gcccctcctg ctgggagtgg gcctggtcgt tctgctggtc 60

gtgggcctgc tggccctgtt caaggccttc tacatcaagg tcccgcaagg caccgcgctg 120

atcgtcaacg acatgtcgtc gacgcccaag gtgcatttca ccggtgcgct ggtctatccg 180

gtgatccacc tgaaggagtt catgcgcatc tcgctgatca ccctggaggt cgaccggcgc 240

ggcaaggacg gcctgatctg ccgcgacaac atgcgcgcgg acatcaccgt tgccttctac 300

ctgcgggtca acgagaccca ggacgacgtg ctcaaggtgg ccaaggccat cggcgtcgac 360

cgtgcttccg accgttcggc ggtgaacgag ctgttcaatg ccaagttctc cgaggcgctg 420

aagaccgtcg gcaagcagtt cgacttcgtc cagctgttcg agaatcgcca ggacttccgt 480

gaccgcatca tcgaggtgat cggcaacgac ctgaacggct acgtcctgga agacgtcgcc 540

atcgactacc tggagcagac cgcgaagaac tcgctggacc cgagcaacat ccttgatgcc 600

gagggcatcc gcaagatcac cgagctgacc gccacccaga acgtcatcac caacgaactg 660

gagcgcaacg aagagctggc gatcaagaag aagaacgtcg agacccgcga ggcggccctg 720

gccctggagc gccagcaggc tgacgccgag gcccggcaga agcgcgagat cgagaccatc 780

cgtgcccgcg aggaagcgga aaccgcgcgg gtcaaggaag aggagcggct gaaggccgag 840

caggcgcgga tccaggcgca gcaggaaatc gacgtgcgca ccgagaacca ccagcgcgag 900

gtcgaggtgg cgcagcagaa ccgccagcgc gcggtggtca tcgaggtgga gaaggtcacc 960

cgcgccaagg acctggagat cgtcgcccgc gagcgtgagg tggagctgca gaagatcgag 1020

aaggaaaagg cgctggaaga gcagcgcaag aacattgcca atgtgattcg cgagcgcgtc 1080

gcggtggaaa agaccgtggc ccaagaggag gagcggatca aggaggtgcg cgaggtttcc 1140

gaggccgagc gggtcaagca ggtgatactg ctgcaggccc aggcggaagc cgagcaggag 1200

ctggtacgcc aggtcaagca ggcggaagcc gacgaggccc gctccaagca caaggcggtg 1260

gaaatcaaca ccatggcgca ggccgagctg gaggcggcgt cgaagcaggc cgaggcgaag 1320

aagcgtctgg ccgagggcat cgaggccgag cgcgcagcgc cgggcctggc cgatgcgcgg 1380

gtgctggaag tcaccgccgc ggcgaaggaa aaggatggct tggcagcggc gcgggtacgt 1440

gccgaacaac tgatcgccga agccaggggc gacgaagagc gcggcctggc cgacgcccgg 1500

gtgctcgagg cgcaggccgc ggccaaggag aaggacggcc tggccgaagc caaggtgctg 1560

gccgagaagc tcggcgccca ggcgcgcggc gaggagcagc tcggcgcggc caaggccaag 1620

gccaccaagg accagggcag cgcggaagcg gaagtactgc tgcagcgcct gaatgccgag 1680

gccgaggggc ttggcaagaa gttcggcgcc ctggatgccc tcagcgacag cgctcgccag 1740

cacgaagagt tccgcatgca gctggagaag agcttcgagg aggccatggc ggccatcgcc 1800

gcgaacaagg acatcgccaa ggaccaggcc gaggtgctcg ccaccgcgct gggcaaggcg 1860

aacatcgaga tcgtcggcgg cgagggcgac ttcttcaact ccttcgccaa gtcgctgtcg 1920

gtgggcaagg ccatcgaagg tgtggtcggc aagagcccgg tggtgcagga cgtcctcgcc 1980

cgcctgctca acggccgtgg cgcagccgct gcggtgatgc cggaacgcaa gagcggccac 2040

gagaacgagc cggcggcgga agtctga 2067

<210> SEQ ID NO 48
<211> LENGTH: 2229
<212> TYPE: DNA

-continued

<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 48

atgtaccccc aattccgtcg cggccatctc gccgctgccg tccttttcgc ttcatcgagc 60

ctgctgggcg ggcaggccct ggccgaggac gagcgcctgg aagaactgga cgaacgcgcc 120

gaatcggtgg tccagctggg tgacgaggtg gtgctgggca ccgccgaaca ggagctcaag 180

caggcaccgg gggtatccat catcaccgcc gaggacatca ggaagcgccc gccggtgaac 240

gatctctccg agatcatccg caccatgccc ggggtcaacc tcaccggcaa cagttccagc 300

ggccagcgcg gcaacaaccg gcagatcgac atccgcggca tggggccgga gaacaccctg 360

atcctggtcg acggcaaacc ggtcagctcg cgcaactcgg tgcgctacgg ctggcgcggc 420

gaacgcgaca cccgcggcga cagcaactgg gtgccgccgg aggaggtcga gcgcatcgag 480

gtcctccgtg ggcccgcggc ggcacgctac ggttccggcg cggcgggcgg ggtagtcaac 540

atcatcacca agcgcccgac cgatcgtttg cgtggttcca tgacggtgtt caccaacatt 600

ccggaaagct ccaaggatgg cgccacgcgc cgcgccaact tcagccttag cgggccgctg 660

accgaagcct tgagcttccg cgcgtacggc agcgcgaaca agaccgattc ggacgatacc 720

gacatcaacc tcggacatac cgtcaacccg agccgtaccg tggccggacg cgaaggggta 780

cgcaatcgcg atctcagcgg gatgctgtcg tggcaggtga cccccgacca ggtcgtcgat 840

ttcgaagcgg gcttcagccg acagggcaat atctatgccg gcgataccca gaacaacaac 900

ggcaccgcca atacccaggg actcgccgac gacggtgcgg agaccaaccg catgtatcgc 960

gagaactacg ccatcaccca caacgggacc tggtcgttcg gtacttccag gttcgtcgcc 1020

cagtacgact ccacccgcaa caaccgtctg gaggaggggc tggccggttc cgtcgagggg 1080

cagatcggcg ccgaccgttc gttcagcgcc agcaagctgg agaactatcg cctcagcggc 1140

gaactcaacc ttccgttgca tgcgttgttc gagcaggtgc tgacggtggg cgcggagtgg 1200

aacaaggaaa ccctcaacga cccgtcctcg ctcaagcagg gcttcgtggg aagcgatagc 1260

ttgccgggga cccccgcggc cggctcgcga agcccgaaaa gcaaggcgga gatccgcgcg 1320

ctgtacgtgg aagacaatat cgaactgcgc cccggcacca tgctcacccc cgggctgcgc 1380

ctggacgatc acagcgactt cggcctgaac tggagcccga gcctgaacgc ttcccaaacg 1440

ctcggcgaat acttcacggt caaggccggt atcgcacggg ccttcaaggc gcccaacctg 1500

taccagagca acccgaacta cctgctctat acccgtggca acggttgccc gatccagact 1560

agcagcggcg gctgctacct ggtcggcaac gagaacctgg acgccgagac cagcgtaaac 1620

aaggaactgg gcatcgagtt ccggcgcgat ggctgggtcg ccgggctcac ctacttccgc 1680

aacgactaca agaacaagat cgtcgcgccg ctggatgtca tgggacagac cgggaccggc 1740

aacaacatcc tgcaatggag caacgcgaag aaagcagtgg tcgagggcct ggaaggcaac 1800

ctgctggtcc ccctgcacga ggacctgagc tggagcacca acctgaccta tatgctgcaa 1860

tccaaggaca aggacaccgg caacccgctt tcggtgatcc ccgagtacac cctgaactcg 1920

accctggact ggcaggccag cgagcgtctt tccacccaac tgaccagcac catctacggc 1980

cgccaggagc cgccgaagca tggcaccagc cgcaacacgc cggtggtctc gcgaaaagag 2040

gtgggtacct atggcatctg gggcgtcagc gccggctaca ccttcagcga gaacctgagc 2100

gtacggggcg gggtaagcaa cctcttcgac aagcgcctgt accgccaggg caactccttc 2160 gacgccggcg cggcaaccta caacgagccg ggtcgcgcct actacgtttc gatgaccacc 2220

tcgttctga 2229

<210> SEQ ID NO 49
<211> LENGTH: 2241
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 49

atgtcctcac gcgcccttcc cgccgttccc ttcctgctgc tgtccagttg cctgctcgcc 60

aacgccgtac acgccgccgg ccagggcgac ggctccgtca tcgagctggg cgagcagacc 120

gtggtcgcca ccgcccagga ggaaaccaag caggcgccgg gggtttccat catcaccgcc 180

gaggacatcg ccaagcgacc gccgagcaac gacctgtcgc agatcatccg gaccatgccg 240

ggggtcaacc tgaccggcaa cagctccagc ggccagcgtg gaaacaaccg gcagatcgac 300

atccgcggca tgggcccgga gaacaccctg atcctggtcg acggcaagcc ggtcagctcg 360

cgcaactcgg tgcgctacgg ctggcgcggc gagcgcgaca gccgcggcga caccaactgg 420

gtgccggccg accaggtcga gcgcatcgaa gtgatccgcg gcccggcggc ggcgcgctac 480

ggcaacggcg cggcgggcgg cgtggtgaac atcatcacca agcaggccgg cgcggaaacc 540

cacggtaatc tcagcgtcta cagcaatttc ccgcaacaca aggccgaagg cgccagcgaa 600

cggatgagct tcggtctcaa cgggccgctc acggaaaacc tcagctaccg cgtctacggc 660

aacatcgcca agaccgactc ggacgactgg gacatcaacg ccggccacga atccaaccgt 720

accggcaagc aggccggcac cctccccgcc ggtcgcgaag gcgtgcgcaa caaggacatc 780

gacgggctgc tcagctggcg cctgacgccc gagcagaccc tcgagttcga ggccggcttc 840

agccgccagg gcaacatcta caccggcgac acgcagaaca ccaacagcaa caactacgtg 900

aagcagatgc tcggccacga gaccaaccgc atgtaccgcg agacctactc ggtcacccat 960

cgcggcgaat gggacttcgg cagctcgctg gcctacctgc agtacgagaa gacccgcaac 1020

agccggatca acgaaggcct ggccggcggc accgaaggta tcttcgaccc caacaacgcc 1080

ggcttctaca ccgccaccct gcgcgacctg accgcccacg gcgaggtcaa cctgccgctg 1140

cacctgggct acgagcagac cctgaccctc ggcagcgagt ggaccgagca gaagctcgac 1200

gaccccagct ccaacaccca gaacaccgag gaaggcggct cgatccccgg tctcgccgga 1260

aagaaccgca gcagcagttc ctcggcgcgg atcttctcgc tgttcgccga ggacaacatc 1320

gagctgatgc ccggcaccat gctcacccca ggcctgcgct gggaccacca cgacatcgtc 1380

ggcgacaact ggagcccatc gctgaacctg tcccacgcgc tcaccgagcg ggtcaccctg 1440

aaggccggta tcgcccgcgc ctacaaggcc cccaacctgt accagctgaa ccccgactac 1500

ctgctctaca gccgtggcca gggttgctac gggcaaagca ccagttgcta cctgcgcggc 1560

aacgacggcc tcaaggccga gaccagcgtg aacaaggaac tgggcatcga gtacagccac 1620

gacggcctgg tagcggggct gacctacttc cgcaacgact acaagaacaa gatcgaatcc 1680

ggcctgtcac cggtcgacca cgccagcggc ggcaagggcg actacgccaa cgcggcgatc 1740

taccagtggg agaacgtgcc caaggcggtg gtcgagggcc tcgaaggcac cctgaccctg 1800

cccctggccg acggcctgaa gtggagcaac aacctcacct acatgctgca atcgaagaac 1860

aaggaaaccg gcgacgtgct ctcggtgacg ccgcgctaca ccctcaactc gatgctcgac 1920

-continued

tggcaggcca ccgacgacct ctcgctgcaa gccacggtca cctggtacgg caagcagaag 1980

ccgaagaaat acgactatca cggcgaccgt gtcaccggca gcgccaacga ccagctctcg 2040

ccctacgcca tcgccggcct cggcggcacc tatcggttga gcaagaacct gagcctcggc 2100

gccggcgtcg acaacctgtt cgacaagcgc ctgttccgcg ccggcaatgc ccagggcgtg 2160

gtcggcatcg acggggccgg cgcggcgacc tacaacgagc ccggacggac cttctatacc 2220

agcctgaccg cgtcgttctg a 2241

<210> SEQ ID NO 50
<211> LENGTH: 2355
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 50

atgtccccgt cacgcgccct gtcgccgctc agccgcgccc tgctcctcgc ctgcctcggc 60

ggtcccgtcc tggtttccgc cggcagcgcc tgcgccgccg agatccgcac cgatgcccgc 120

cagtactacc gcctgcctgc cgagccgctg gagcaggcgc tgaaccacct aggccgccag 180

gccggcgtgc tgatcgcctt cagcccggaa cagaccgccg cgcgacgcag ccaggcgctg 240

gacggcgagt acaccctgga ggaagccctg gccgccctgc tcgtcggctc cggcctggag 300

gcgcgcgccc gcggcgacgg cgcctacacc ctggaagcgc tgccggtgga agacccggcc 360

aacctgcagg cgctcaccgt ggtcggcgac tggctggccg acgccagcgc cgccgacgtc 420

ttcgagcatc ccggtgcgcg cgacgtggtc cgccgcgagc agttccaggc ccaaggcgcg 480

gccagcaccc gcgaagtgct ggagcgcatt cccggggtca gcgcgccgct caacaacggc 540

accggcagcc acgacctggc attgaacttc ggcattcgcg gcctcaaccc gcgcctggcg 600

tcgcgctcga cggtgctgat ggacggcatc ccggtgccct tcgcccccta cggccagcca 660

cagttgtcgc tggcgccggt gtccatcggc aacatggacg cggtggacgt ggtccgcggc 720

ggcggcgcgg tgcgctacgg gccgcagaac gtcggcggca tcgtcaactt cgtgacccgg 780

gcgatccccg aggacttcgc caccaagctc gacgtgcaca gcgaactcag ccccagctcc 840

agccaggacg gcctgaagac cacccacaac gtgctgatcg gcggcaccgg cgccaacggc 900

ctcggcggcg ccctgctcta ctccggcacc cgcggcggcg attggcgcga gcacagcgat 960

acgcggatcg acgacctgat cctcaagggc cgcttccagc ccagcgacga acacacgttt 1020

tcggcgatga cccagtacta cgacggcgag gccgacatgc ccggcggcct cggcaccgcg 1080

gcctaccacg acgacccgta ccagtcgacc cgtccctacg acaagttctg ggccgccgt 1140

accctggcca gcgccagcta cgaatacacc cccaacgcca gccagaagct caacgtcacc 1200

ggcttcttca ccaagaccct gcgcagcggc tacctcgacc agggccgcaa cctcaccctg 1260

tcgccgcgcg aatactgggt gcgaggcctg gaaacccgct tcagccaggg cttcgagctg 1320

ggcgaaagtc gccacgaagt gggcatcggc caccgctacg tcaacgaagc cagccacgag 1380

ctgcgctact ggacccgcgc cgacagcggc cagctaccca gcaccggcag ccgcaacgac 1440

cgcgacaccc gcggcagcac cgaagccaac gcgttctaca tcgacgatcg catcgacatc 1500

ggcaactgga ccatcacccc cggcatccgc tacgagaaga tcgattccga acagaagaac 1560

ctgctgaaga acagcaagga cagcggccgc tacaacgcct cgctgccggc gctcaacgtg 1620

atctaccacc tcacgccgag ctggaacctc tacgccaaca ccgagggctc gttcggcacc 1680

-continued

gtgcagtaca gccagatggg caaggcggtg cgcagcggcg acatcgagcc ggagaaggcc 1740

cgcacctggg aactcggcag ccgctacgac gacggcatcc tgcgcgccga actgggcgcc 1800

ttcctgatca acttcgacaa ccagtacgag agcaaccagc agaccgacag cgtgaccgcc 1860

cgcggcaaga cccggcacaa gggcatcgag gcggcgatcg cctacgacct ggccgatctc 1920

gacccgctgc tctccggctt cgacgtctat gccagctacg cctacgtcga cgcgagcatt 1980

cgcgaagacg ggccgaacaa gggcaaccag gtgccgttct cctcgaagca caagggcacc 2040

cttggcgcca actaccgcac cggcgcctgg agctacaacc tcgacggcag cttccagacc 2100

agccagtacg ccgacaacgc caacaccgag agcgaaagcg ccgacggcag caccgggcgg 2160

atcgccggct ggatggtctg gagcgcgcgc ggcacctacg acttcggccc gcaactgaac 2220

gacctcaagc tcggcctggg ggtgaagaac ctgttcgatc gccgctacta cacccgctcg 2280

ttcgacgaca acaacaaggg cctctacgtc ggccagccgc gcaccctgta cgtacaggcc 2340

tcggtcggtt tctga 2355

<210> SEQ ID NO 51
<211> LENGTH: 2556
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 51

atgaccttgc ctttcacccg cgccgcctgg cgcccgctgt gttccgccgc cgtgctcggc 60

gccgcgttgt gggccgccgg cgccagcgct gccgaacgac gcttcgacct gccggcgcag 120

ccgctggccg cctcgctgtc gcgcctggcg cagcaggcgc aggtccaggt gctgttcgac 180

gagtcgctcc tgcggggcct gcgcgctccg gcgctgagcg gcagctacgg ggtgcgcgag 240

gcgctggagc ggttgctggt cggttccgag ctggagctgg tggaggcggg cggcggctac 300

gtggtgcgcc ggcgccaggt cgacgcctac agcgacaacg cgctgcaact ggacgcgcag 360

accatcgtcg gcaacggtcg cgaagtggac gccagcaacg tcggccgttc gaccctgacc 420

cggcgggata tcgaacgcca gcaggcggac aacatcccca gcctgctgca gaccctgccc 480

ggagtgacca tgggcggctc gcccaagccg ggcggacaga ccaccaacat ctggggcctg 540

ggcgacgccg aggacgtgcc ctataccctg gacggcgcgc agaagagcgg cttcgagcgc 600

taccagcagg gcaccgtgtt catcgaaccg gaaatgatca agcgcatcga ggtggagaag 660

ggaccgcact cggtgttcac cggcaatggc ggcttcggcg gcaccgtgca catggagacc 720

aaggacgcgc cggacctgct gcgcgaaggc cgcgacgtcg gcgccatgct caagtacggc 780

tatcactcca acgaccagca gaagatctac tccggcgccg tgttcggtcg cagcgaagac 840

cgcccgcgtcg atgccctgct ctatctcaac ggtcgcgacg gccgcgacat gaagctggcc 900

gacaacctgc cgctgtcgcc caccgactac ccgatcaacc ccaagcgcct gcccaacagc 960

gcccaggacg agaagaccgg cctgttcaag ctcaacctgc accccaccga ggagcacgac 1020

ctgggtttca cctacctgcg ctcgaaaagc tcgcgctgga cgccgttctc cgccagcagc 1080

tacccgaccc cgccgagcca gtggaccatc gaccgctacg gctacgagct gggcctgacc 1140

cgcctgctgg cccaccgcga taccaccgac accacctgga ccggcaagta caactaccat 1200

ccgctggaca acccctggat cgacctgcaa ctgagctatt ccgacgcccg caccgagcaa 1260

ctcgaccgtc gcgaggacac cgccttctac cagctcgcca ccggtggcaa gcggatgcgt 1320

-continued

accgagtacc aggacaaggt cctggaactg cgcaacacca gccgtttcga taccggagcg 1380

ctacagcacg agctgaccct gggcgcggcg ctgcacaagc acaagcgcga catcctcatg 1440

cacatgccgg gcaagaccta cgagaccccg cgctacaatt acggctggct gcaaccggca 1500

ttcatgccgg ccggcaagca ggacacgcag agcttctaca tccaggacgc gatcacctac 1560

ggcagcctga ccgtcacccc atcgatgcgc ttcgacagcg tgcgcaacga cggccaggcc 1620

aacctggcgc cgatctacga caatcccaag ctcggccatg actatcgcgc ccagacctac 1680

tccggctggt caccgcggct gtcggtgttc tggaccgcga cgccgaacct ggcgttcttc 1740

gccgactaca ccgagacctg gcgagcgccg gtgatcgacg agcagtacga agtgcagaac 1800

agttcgacca tcggtggcag cagccgcgac ctggacgccg agcgcatcca tgcgatccgt 1860

ggcggcagcg tgatcaacct gccggacctg ctggtcgccg gcgacagcct gcagatccgc 1920

accacgttgt tccagaaccg catcaaggac gagatattcc gcacccgcag cgtcggctgc 1980

cgccagcagt cgatcgacaa cggcagtatc ggtggtagct gcggcgacat gctgccgctg 2040

agcaactacc gcaacttgcc gggcctgacc atcaagggct tcgagatcga gagcttctac 2100

gacagccagc ggctgttcgg cagcctgtcc tactcgtgga tgaccggcaa gcacgatggg 2160

gcctacagca atccctgggg accgaacgtg tgggcgcgcg acatcccgcc gccgaagtgg 2220

gtggccatgc tcggcctgaa ggttccggaa tgggatgcca agctcggctg gcagggcgag 2280

ttcgtgcgca agaccgaccg cctgcccagc gatcgctaca gcggcgggat gggtaccggt 2340

tccggcgata tctactggga tcacgcggcc aacgacagct acgacactca tcggctgttc 2400

gccgagtggg tcccggccaa gctgggcctg aaggacaccc gcatcgactt caccgtggac 2460

aacctgttca accgctccta tcgccagccg ctgggcggcg acctggtcta cagccaggga 2520

cgcaacgcca agatcagcgt cacccagttc ttctga 2556

<210> SEQ ID NO 52
<211> LENGTH: 2643
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 52

atgcaccgat cgctccacac cgacgcgccg ctgggcgccg ccctgctgct ggccctgcag 60

ctcgctcccg gcagcgccgc cgcggcggag gaacaggcgc ctgtcgaccc gcccacggtc 120

cagttgcaac gaatcgaggt gaccggcagc gcgatccgcc gggtcgatgc ggaaaccgcg 180

gtgccgatca gcgtcctgcg cgccgaggag ctgcgccaac agggcgtgac cagcaccgag 240

gaactgatcg gccggctttc cggcaaccag ggcgtataca actccagtcg ctcggtcggc 300

agcgccaccg gcggcgcctc gttcgccgac ctgcgcggaa tcggcgcgaa caagaccctg 360

gtgctgctca acggccggcg cctggcgaac aatgccatcg acggctccgc ggtggatctc 420

aacaccattc ccttcgccgc catcgaccgg gtcgaggtgc tgcgcgacgg cgcctccgcg 480

ctgtacggca ccgatgccat cggcggggtg atcaacttca tcacccgcaa gagcctgaac 540

gaaggccgct tcgacagcgg ctacgcctcc cccacccacg acggcggcgg caaccagcgc 600

aacgtcagcg ctagctgggg cttcggcgag ctggaggagg atcgcttcaa tgtcttcgcg 660

gtggccaact acgacaagca ggagcgcctc ggcgccaagg accgcggcta cacctacaac 720

taccagccgg gacgcggcct cgactacagc tccggcaccg ccttccccgg caactggagc 780

-continued

cagggcgcca acgccagcaa tccgctggcc gccggcggtt gcaagggcgc cgacctgatt 840

ccgcgcaacg gcatctgccg gcagagcctg tggcgctacc tcgacctggt gccggaaacc 900

gagaagacct cggtgttcag ccgcgccacc ggcaagctgg ccgacgagca caacgtcagc 960

ctggagtact tctggtcgcg cagcgacaac gctacccagg tcggcccagg gaccctcacc 1020

ggcctgcaga tcgatcccgg caccgccttc tatcccggca acggcatcac tcccggaccc 1080

ggcggcttcg tcctcgaccc gagccggccg gtggaggtca actggcgaca gagcgtgctc 1140

gggccgcgcc tgcaatcctc gcagaacacc ggccagcgcc tgctgctcgg cttcgacggc 1200

cagttcgccg gctgggacta cgatatcggc gcctcgtaca accagaacaa ggtggtcgac 1260

catatccaca gcggctacgt cgatgatcgc gccgccgccc tcggcatcgc caacgggacg 1320

ctgaacccgt tcgggccgca gaccgacgcc ggcctcgcct acctcggcag ccatgccctg 1380

agcggcgact tccgtacctc ggtcggccgc gtcaagggcc tggacgcccg cgccagccgg 1440

gagatcggcg actggttcgg cgccgggccg gcggccctgg cgctgggcgg cgagttccgc 1500

aaggaagcgt tccaccagga catccaggac ttcgccggca acgtgcagag cctcggcgtc 1560

gatcccgccg ccacggtcag cggcgagcgc aacctgaagg cgcagtacgc cgaactcaac 1620

gtgccggtgc tggacagcct ggaactcagc gcggcgatcc gccacgacaa gtacagcgac 1680

ttcggcagca ccagcaaccc gaaatattcg ttccgcttcc agccgttccg ccagttggtc 1740

ctgcgcggcg cctacagcga aggtttccgt gcgccgtcgc tgtacgaact gtacaacccg 1800

accttcacca cctataccag cgccaactac gacgacccgc gcctgtgcgc cggcggccag 1860

ccgagccagg gcggcatcgc caaccgcgac tgcgcccagc agttctacaa cgccaccggc 1920

ggcaataccg acctgcgacc ggaaaccgcg cgcaacgtta ccctgggcct ggtctaccag 1980

ccgctgcgcg acctttccgt cggcctggac ttctggtgga tcaggatcgc caaccagatc 2040

gccgagtttc ccgaagcggc gatcttcgcc gacccgcagg cctacgccgg acgcatcgtg 2100

cgcaaggccg acggctcgat cgatcacgtc gtcaccggac tggccaacct cggcaaagtg 2160

aagaccagcg gcgtcgacct gagcctcgat tatcgtttcc cggccagccg ctacgggcag 2220

ttcgggctcg acctgcaagg cacctacgtg tcccgctacg acttccagca gcagatcggc 2280

ggccagtacc tggacaacgt cggcgacttc cagggcgtcg gcgtgatcgc ccgctggaag 2340

cacgtcgcca acgccacctg gagccgcgac gcctggcagg ccaccctgag caaccgctac 2400

accagcggct acaacgacta cgaccgcgcc agccacggca aggtcggctc gtggaacctc 2460

tgggacctgg ccggcagcta ccgcctcagc cacgcgctgg ggctgaccct cggggtgaag 2520

aacctgttcg accgcgaacc gccgttcagc aaccagacct acaccttcca gagcggctac 2580

gacccgcgct acaccgatcc ctacgggcgc atcctgttcg gccgcctcag ctacagcttc 2640

tga 2643

<210> SEQ ID NO 53
<211> LENGTH: 2760
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 53

atggttcggc ttcgtacact ggttcgggca atcgcggcgg cctcggtcct gacttccggc 60

atggcgcatg gattgggact gggggaaatc accctgaagt cggcgttgaa ccaaccgttg 120

-continued

gatgccgaga tcgagctgct cgaagttcgt gacctgggtt cgggcgaggt gatcccgagc 180

ctggcgtcgc cggaagagtt cagcaaggcg ggcgtcgatc gcctgtacta cctcaccgac 240

ctgaagttca cgccggtggt gaagcccaac ggcaagagcg tcattcgcgt gacctcgtcg 300

aagccggtgc aggagcccta cctgaacttc ctggtccagg tgctctggcc gaacggccgc 360

ctgctgcgcg agtacaccgt cctgctggat ccgccgctgt actccccgca ggccgcggca 420

agcgctccgc aagcgccggt cagcgcgccg cgcgcgaccg gcgccccgcg agccccgcag 480

gctccggctc cggtgcgtac caccgcgccg gcaggcagcg acacctatcg caccgtttcc 540

aacgacacgc tctgggagat cgcccagcgc aaccgtaccg atcgcgtttc cgtaccccag 600

gcgatgctcg cgttccagga gctgaatccg ggcgccttcg tcgatggcaa catcaaccgg 660

ctgaagagcg gccaggtcct gcgcattccc accgaacagc agatgctgga gcgctcgccg 720

cgcgaggcgc tgtcccaggt gcaggcgcag aaccagagct ggcgcggcag ccgcaatccg 780

gccgcgggca gcgctggcgc caggcagttg gatgcgaccc agcgcaatgc cgccgggtcg 840

gcgccatcca aggtcgacgc cacggacaat ctgcgcctgg tgtctggcga gggcaaggcc 900

agcaagggtg ccgacaaggg cggaaagggc gacagcaagg cgatcgccga taccctggcg 960

gtgaccaagg aaagcctcga cagcactcgc cgcgagaacg aagaactgca gagtcgcatg 1020

caggatctgc agagccagtt ggacaagctg cagaagttga tccagctgaa ggacgcccag 1080

ttggccaagc tgcaagggca gttgggcgcc gaaggccagg gcgcagccca gccgaacgca 1140

gccctgccgg atgcgtccca gcccaatgcg gccgcgcagg cgccggctca gcccgggact 1200

cctgctgcgg cagcgccgac tcctgctcca gccggagaag cacccgccgc tccggcgcag 1260

cctccggtgg cgccgccgcc cgcgccagct gccgagaagc ctccggcacc tgccgttccg 1320

gcgcccgctc cggtacaggc ggcagagcag ccggcaccga gcttcctcga cgaactgctg 1380

gccaacccgc tgtggttggc ggtgatcggc ggtagcgcac tgctggcgtt gctggtgctg 1440

ctgatgatcc tgtcgcggcg caatgcgcag aaagagaagg aagaagccca ggctttcgcc 1500

gcggataccg gcgaggaaca ggaggatgcg ctggacctgg gaaaggacgg cttcgacgac 1560

ctgaccctcg acgagcctga gccgcaggtc gcagccgtcg ctccgcaggt cgagaagacc 1620

accgcgcaga cttccgatgc gctgggcgag gccgacatct atatcgccta cgggcgtttc 1680

aaccaggccg ccgaactgtt gcagaacgcc atctacgacg agccgcagcg caccgacctg 1740

cgcctcaagc tgatggaagt ctatgccgag atgggcgatc gcgaaggttt cgctcgccag 1800

gaaaacgagc tgcgcgaaat cggcggcgca cagccgcagg tcgagcagct caagtcgcgc 1860

tatccggcaa tggtcgcggt cgccgcggtt gccggcctgg ccggcgccaa gctggcgcag 1920

gacgagctgg atagcttcag ccttgacgac ctgtcgctcg acgacagcgg tcacgcggcc 1980

aagccggatg cggcaggaca ggatctcgac gacgccttcg acctgagcct ggacgacctg 2040

ggcggcgacg acgtgcaggc cgacctcaag tccgacagcg ggcgctggga cgacctgacc 2100

ctggacagcg atctggacct ggcggcctcg accccggcgg acaagcctgt cgacgatctc 2160

gacttcggcc tggatttcgc ggagttggca gagactccga gccaacccaa gcatgacgac 2220

ctgggcgatt tctccctgga tctcgacgcg ccggaagaca agctttcgga cgacgacttc 2280

ctgctttcgc tgaacgacga agtgcccgcc gcggcgcctg ccgacaacga attcaccctc 2340

gataccgagg ctgccgaaga gccggcgttg tccctgccgg acgacttcga cctgtcgctg 2400

-continued

```
gccgacgagc cgacggagcc ggccgctccg gagaagggcg aggacagttt cgccgcccag   2460

ttggacgagg tgagtgcgca gttggacgag ttggccagca accttgacga gccgaagagc   2520

gcgacgccga gtttctccgc cgaagatgca gcggtcgcct ccgccctgga cggagacgcc   2580

gacgatgact tcgacttcct ctccggtgcc gacgaagcgg cgaccaagct ggatctggct   2640

cgcgcctaca tcgacatggg cgatagcgaa ggcgcgcgcg atatcctcga cgaagtcctg   2700

gccgaaggta atgacagcca gcaggcggaa gcccgcgagt tgctggagcg cctggcctga   2760


<210> SEQ ID NO 54
<211> LENGTH: 2988
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 54

atgaccgacg accactcctt ccgccctcgc cccacctcgt tgtcagccgc cctgctgctg     60

ggcgcctgga tcgcacagcc ggccacggcc gcctatgtcg aagccggtcg gcccggcgat    120

ccggccagtt ggcgctccgc cgaataccag caggactggg gcctggaacg gatgcgggcc    180

gaccaggcct atgccgccgg catcgacggc cagggcgtga agatcggcga gatggactcc    240

ggtttcgacc cgagccatcc ggatactccc gcctcgcgct accagccggt gacggccagc    300

ggcacctatg tcgacggcac gccgttcagc gtcagcggcg cgatgaacgg caacaacgac    360

tcccacggta cccacgtcgg cggcaccctc ggcgcctcgc gcgacggcgt cggcatgcac    420

ggggtggcct acgcggcaca ggtgtatgtc gccaacacca accagaacga cagcttcctg    480

ttcggcccga cgcccgaccc gaactatttc aaggccgcct accaggcgct ggccgacgcc    540

ggggtgcggg cgatcaacaa cagttggggc agccagccca aggacgtcag ctacgagacc    600

ctcgacggcc tgcacgccgc ctatgcccag cactacgggc gctccacctg gctggacgcc    660

gccgccggcg tctcccgcca gggcgtgatc aacgtcttca gcgccggcaa cagcggctac    720

gccaacgcca gcgtgcgctc cgccctgccc tacttccagc cggacctgga aggccactgg    780

ctggccgtgt ccggcctcga ccagcagaac ggccagcgct acaaccgctg cggcatcgcc    840

aagtactggt gcatcaccac gcccggccgc ctgatcaaca gcaccatgcc cggcggcggc    900

tacgccaaca agtccggtac ctcgatggcc gcgccccacg ccaccggcgc gctggccctg    960

gtcatgcagc gctatccgta cctgaacaac gagcaggcgc tgcaggttct gctgaccacc   1020

gccacccagc tcgacggcac gccgaccggc gcccccaccg acaccgtcgg ctggggcgtg   1080

ccggatctcg gtcgggcgat gcatgggcct ggacaattgc tcggccgctt cgaggccaac   1140

ctcccggccg gcctgcgcga cgaatggagc aacccgattt ccgatagcgc cctgctccag   1200

cgccaggccg aggacgccgc cgagcacgcg gcctggcagc ggacgctgaa ggacaagggc   1260

tgggaaaacg gcttgccggc cggtgccagc cagcaggaac gcaccgacta tgccatcggc   1320

atggcccgcg accaggccgc cgcccagcgc cagtaccagg gcagcctggt caaggccggt   1380

gccggcagcc tggtcctgag cggcgacagc acctatcgcg ggccgaccct ggtcgatggc   1440

gggctgctca gcgtcgacgg ttcgctgctg tccgccgtcg aagtcaatgc cggcggcacc   1500

ctcggcggca gcggcaggat cggcggcctg ctggcgcgct ccggcggcac ggtggccgcg   1560

ggcaactcca tcggcaccct ggaggtcgcc ggggacctgc gcttcgaatc cggctcgacc   1620

tacgcggtgg agctttcgga aagcgccagc gaccggatcg tcgccagcgg caaggcgagc   1680
```

-continued

atcgcgggcg gcaacgtcac cctggccatg gaaaacagcc ccgacctgct cagccagtcc 1740

caggtcgaga gcctggtcgg ccgccgctac gacatcctcg acgccgccgg cggcatcgac 1800

gggcgcttcg acgcggtatt gccgaactac ctgttcctcg gcggcaccct ggactacgcg 1860

gccaacgcca tccgcctgga tatcggacgc aacggcacga ccctcgccag cgtcgcgcag 1920

acgcccaacc aggcggcggt cgctggggcc gtggaaacgc tcggcgccgg caacccggtc 1980

tacgaaagcc tgctcctgtc ggaaaacgcc gcaaccgccc aacgggcctt ccagcaattg 2040

tccggggaaa tctacccggc gctcgccggc ctgttgctca acgacagccg ctatctgcgc 2100

gacagcgtcg gcgaacgcct gcgccagacc agcgacggcg aggccggcgg ggaggctccc 2160

gaaggctggt tcaaggcgct cggctcctgg ggcaagagcg ccgatggcag ccacggtagc 2220

gaaggctacc ggcattcggt cggcggcttc ctgctcggcg tcgacagcca ggtcgccagc 2280

gacacgcgcc tcggcctggt ggccggctac agcaacagct cgctgaacat ggacagcagc 2340

ctgcaatcct ccgccagcat cgacagctac cacctcggcg cctacctcgg ccggcaattg 2400

cagcaatggc gcctgagcct cggcgcagcg cacgcctggc accgcgccga ggtcaagcgc 2460

gacctgcaat acggcgccgt ggccggcaag cagaaggcca agctcgacgc acagagcagc 2520

cagttgttcg ccgaggccgc ctacgcgctg ggttggcgca gcctggagct ggaacccttc 2580

gccgggctgg cctacgtgca cgtcgccagc gatgacttcc gcgaacgcgg tagcgccgcg 2640

gccctggagg gtggcgacga caacctggac gccgccttca ccaccctggg cctgcgcgcg 2700

aaacggcatt tcgagctgga tgccggacgc cgcctggcgc tctccggcac cctcggctgg 2760

cgccacaacc tgagcgacac caccccgcaa cgccacctgg cgttcgccag cggcagccag 2820

ccattcagcg tggaaagcgt ggccctgtcc cgcgacgccg cgctgctcgg cgtcgacgcc 2880

agcctcgcgg tgaatcgcga agtgagcgtg cggctgggct acaacggcct gctgggcagc 2940

cgcgagaagg accatggcgt cggactggcc gtcgactggc gtttctga 2988

<210> SEQ ID NO 55
<211> LENGTH: 3174
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 55

atgaaaagaa tgctgatcaa cgcgactcaa cccgaggagt tgcgtgttgc actggtcgac 60

ggccaacgcc tgttcgacct cgacatcgag tcgggcgccc gcgagcagaa gaaggccaac 120

atctacaaag gccgcatcac tcgcgtcgaa cccagcctcg aagccgcctt cgtcgacttc 180

ggcgccgaac gccacggctt cctccccctc aaagaaatct cccgcgaata cttcaagaaa 240

tcccccgaag gccggatcaa catcaaggaa gtcctgagcg aaggccagga agtcatcgtc 300

caggtcgaga aggaagagcg cggcaacaag ggcgccgccc tgaccacctt catcagcctg 360

gccggccgtt acctggtgct gatgccgaac aacccgcgcg ccggcggcat ctcccgccgt 420

atcgaaggcg aagagcgcaa cgagctgcgc gaggccctga acggcctcaa cgcaccggcc 480

gacatgggcc tgatcgtgcg caccgccggc ctcggccgca gcaccgagga actgcagtgg 540

gacctcgact acctgctgca actgtggagc gcgatcaagg aagcgtccgg cgaacgtggc 600

gcgcccttcc tgatctacca ggaaagcaac gtcatcatcc gcgccatccg cgactacctg 660

cgccaggaca tcggcgaagt gctgatcgac agcatcgacg cccaggaaga agccctgaac 720

-continued

ttcatccgcc aggtgatgcc gcagtacgcc agcaaggtga agctgtacca ggacagcgtt 780

ccgctgttca atcgcttcca gatcgagagc cagatcgaga ccgctttcca gcgcgaagtg 840

aagctgccgt ccggcggctc catcgtcatc gacccgaccg aggccctggt ttccatcgac 900

atcaactcgg cgcgcgccac caagggcggc gacatcgagg aaaccgccct gcagaccaac 960

ctggaagcgg ccgaggaaat cgcccgccag ctgcgcctgc gtgacatcgg cggcctgatc 1020

gtcatcgact tcatcgacat gaccccggcg aagaaccagc gcgccgtgga agagcgtgtc 1080

cgcgaagccc tcgaggccga ccgcgcgcgc gtccaggtcg gtcgcatctc gcgcttcggc 1140

ctgctggaaa tgtcccgcca gcgcctgcgt ccgtccctcg gcgagaccag cggcatcgtc 1200

tgcccgcgct gcaacggcca gggcatcatc cgcgacgtcg agtcgctgtc gctggccatc 1260

ctgcgcctga tcgaggaaga agccctgaag gaccgcaccg cggaagtccg cgcccgcgtg 1320

cccttccagg tcgccgcctt cctgctcaac gagaagcgca acgccatcac caagatcgaa 1380

ctgcgtaccc gcgcgcgcat cttcatcctg ccggacgatc atctggaaac cccgcatttc 1440

gaagtccagc gtctgcgcga tgacagcccc gaactggttg ccggccagac cagctacgaa 1500

atggccaccg tcgagcacga agaagcccag ccggtcagct cgacccgcac cctggtccgc 1560

caggaagcag cagtcaagac cgtcgctccc cagcagcccg caccgcaaca caccgaagca 1620

ccggtcgagc cggccaagcc gatgcccgag ccgagcctgt tccagggcct ggtgaagtcc 1680

ctggtcggcc tgttcgcagg caaggatcaa cctgccgcca agcctgctga aaccagcaag 1740

ccggctgccg agcgccaaac ccgccaggac gagcgtcgca acggccgcca gcagaaccgc 1800

cgccgcgatg gccgcgatgg caatcgccgc gacgaagagc gcaaaccgcg cgaggagcgt 1860

gcagagcgtc aaccgcgcga agagcgcgcc gaacgcccga accgcgaaga gcgcagcgaa 1920

cgtcgccgcg aagagcgcgc cgagcgcccg gctcgcgagg agcgccagcc gcgcgaaggc 1980

cgtgaagagc gcgccgagcg gacaccccgc gaagagcgcc agccgcgcga aggccgcgaa 2040

ggtcgcgagg aacgcagcga acgccgccgc gaagagcgcg ccgaacgccc ggcccgcgaa 2100

gagcgccaac cccgcgaagg ccgtgaagaa cgcgccgagc gcccggcccg cgaagagcgc 2160

cagccgcgcg aggatcgcca ggctcgcgac gccgcggccc tggaagccga ggcattgccg 2220

aacgacgaga gcctggagca ggacgagcag gacgataccg atggcgagcg cccgcgccgc 2280

cgctcccgcg gccagcgtcg tcgcagcaac cgccgcgaac gccagcgcga ggtcagcggc 2340

gagctggaag gcagcgaggc gaccgataac gccgccgcgc cgctgaacac cgtcgcagcc 2400

gccgccgctg ccggtatcgc tgtcgccagc gaagccgtag aagcaaacgt ggagcaagcc 2460

ccggccacta ccagcgaggc tgccagcgaa accacggcaa gcgatgagac cgacgcgtcg 2520

accagcgaag ccgtcgaaac ccagggcgcg gacagcgagg ccaataccgg cgaaaccgcc 2580

gacatcgaag cgccggtgac cgtcagcgtg gtccgggacg aagccgacca gagcaccctg 2640

ctggtcgcgc aagccactga agaagctccc ttcgccagcg aaagcgtgga aagccgcgaa 2700

gacgccgaga gcgccgtgca accggcaacg gaagcggccg aagaagttgc cgctccggtg 2760

cccgtcgaag tagcagcccc tagcgagccc gcagccaccg aggagccgac cccggccatc 2820

gcggcggtgc cggccaacgc gactggccgt gccctcaacg acccacggga aaaacgtcgc 2880

ctgcaacgcg aagccgagcg tctggcacgc gaagccgcag cagcagccga agcggcagct 2940

caggccgctc ccgccgtcga ggagatcccg gctgtagcga gcgaggaagc gtcggcccag 3000

-continued

gaggaacctg ctgcacccca ggctgaagaa atcacccagg ccgacgttcc gtcccaggcg 3060

gacgaagccc aggaagcggt acaggccgag cctgaagctt ccggcgaagg cgccgccgac 3120

acggagcacg cgaaaaagac cgaggaaagc gaaacctcgc gcccgcatgc ctga 3174

<210> SEQ ID NO 56
<211> LENGTH: 3486
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 56

atgaaatcgg tactccacca gatcggcaag acctcgctgg cagccgcgct cagcggcgcc 60

gtcctgctct ccgcccagac cacccacgcc gccgccctgt cggtcagcca gcagccgctg 120

atgctgatcc agggcgtcgc ccccgaacatg ctggtgactc tcgacgactc gggcagtatg 180

gcgttcgcct atgcgccaga cagcatttcc ggctatggaa actatacgtt cttcgcgtcg 240

aacagcttca acccgatgta cttcgatccg aacacgcaat acaagcttcc gaagaaactc 300

acactggtga acggacaggt acagatccag gattatccgg cccccaactt ctcctctgcc 360

tggcgcaatg gcttcactcg cagcgggagt atcaatctgt cgaacagcta caaggtcacc 420

atcgagtacg gcaggggata tgataaggag tcgacgataa aagccgacgc tgcctactac 480

tatgacttca cgggctcatc cagttgcaac cgcaccaatc aggcatgcta cacccgccgt 540

tatgtgagca cagagcaaag gcagaacttc gccaactggt attcgttcta ccgcacccgc 600

gcccttgcca ctcagaccgc cgccaacctg gcgttctaca gcctgcctga aaacgctcgg 660

gtgagctggc aattgctgaa cgactcgaac tgcaaccaga tgggcagcgg ctccagctcc 720

ggcaactgtt tcagcaacta tctacgggac ttcaccggtc aacaccgggt gaacttcttc 780

aattggctgg aaaaactttc ggtcaatggt ggtacgccac tgcgccaggc gatgacccgg 840

gcaggcgagt ttctcaagaa gaccggcgtc aacggtccct atgcctatcg cccagggacc 900

cagaccgcgc ccgagtacag ttgccggggc agctatcata tcctgatgac cgacggtctc 960

tggaacaacg actcggccaa cgtaggcaat gccgacagca ccgctcgtaa cctccccgac 1020

gggaagagct atagcagcca gacaccctac agggacggta cgttcgatac cctggccgac 1080

caggccttcc attactgggc caccgatgcc cggccggata tcgacgacaa tatcaaaccg 1140

tacattccct acccggacca ggccaatccc tcggcggaat actggaatcc ccgcaacgat 1200

ccggcaacct ggcaacacat ggtgacctac accctgggcc tgggcctgac caccagcctc 1260

accagtccga gatgggaagg ctccaccttt tccggtggct acaacgatat cgtggctggc 1320

aacctgagct ggccccgcgc gtcgaacaac gactccaaca acgtctacga tctgtggcac 1380

gccgcagtga actcccgggg cgagttcttc agcgccgact cgccggacca actggtcgcg 1440

gccttccagg acatcctcaa ccgaatttcg ggcaaggacc tgccggcatc ccgccccgcc 1500

atcagctcgt ccctgcagga agacgacact ggcgacaagc tgacccgctt cgcctaccag 1560

accagcttcg ccagcgacaa gaactgggct ggcgacctga cccgctacag cctgaccacc 1620

caggacaagg ccaccgtgca gaccaagctg tggagcgcgc agagcatcct cgacgcgatg 1680

cccaacggtg gagctggccg caagatcatg atggccggat ccggtacctc gggcctcaag 1740

gagttcacct ggggcagcct cagcgccgac cagcagcggc agttgaaccg cgatccggac 1800

cgcaacgatg tcgccgacac caagggccag gaccgcgtgg ccttcctgcg cggcgatcgc 1860

-continued

cgcaaggaga acagcgacaa cttccgcacc cgcaactcga tcctcggcga tatcatcaac 1920

tcctcgccgg cgacggtcgg caaggcccag tacctgacct acctggccca gccgatcgag 1980

cccagcggta actactccac gttcgcagaa gcacagaaaa cccgtgcccc gcgggtatac 2040

gtcggcgcca acgacggcat gctgcacggt ttcgataccg acggtaacga gaccttcgcc 2100

ttcatcccaa gcgcggtctt cgagaagctc cacaagttga ccgcccgcgg ctaccagggc 2160

ggcgcccacc agttctacgt cgacggttcg ccggtggtcg ccgacgcctt cttcggcggc 2220

gcctggcata ccgtgctgat cggcagcctg cgcgccggcg gcaagggcct gttcgccctc 2280

gacgtgaccg atcccgccaa catcaagctg ctctgggaaa tcggcgtgga ccaggagccc 2340

gaccttggct acagcttccc caaacccacg gtcgcccggc tgcacaacgg caagtgggcc 2400

gtggtcaccg gaaacggtta ttccagcctg aacgacaagg ccgcgctgct gatcatcgac 2460

ctggagaccg ggggccatcac ccgcaaactg gaagtcaccg gcaggaccgg cgtacccaac 2520

ggcctatcca gccctcgcct ggcagacaac aacagcgacg gcgtagccga ctacgcctac 2580

gccggcgacc tgcaaggcaa cctctggcgc ttcgacctga tcgccggcaa ggtcaaccag 2640

gacgatccgt tcagccgagc caacgacggc ccggcggtgg cctcgagctt cagggtgtct 2700

ttcggtggcc agccgctcta ttcggcagtc gactccgccg gcgcggcgca agcgatcacc 2760

gccgcgccct cgctggttcg ccatccgaca cgcaagggct acatcgtgat cttcggtacc 2820

ggcaagtatt tcgagaacgc cgacgcccgg gccgatacca gccgcgccca gacgctctac 2880

ggcatctggg accagcaaac caagggcgaa gccgcgggca gcacaccccg actgacgcgc 2940

ggcaacctgc agcagcagac cctggacctc caggccgact cgaccttcgc ctcgaccgct 3000

cgcaccattc gcatcgccag tcagaacccg gtcaactggc tgaacaatga cggcagcacc 3060

aagcagtccg gctggtatct ggacttcatg gtcaacggca ccctgaaggg cgagatgctg 3120

atcgaggaca tgatcgccat cggccaggtg gtgctgctgc aaaccatcac cccgaacgat 3180

gacccctgtg ccgacggcgc cagcaactgg acctatggcc tcgatcccta taccggcggt 3240

cgcaccagct tcaccgtgtt cgacctggca cgccagggcg tcgtggactc gaaatccgac 3300

tacagctaca acaagcagaa cgtcgcggta tccggtaccg agcagaaagg cctgggaggc 3360

ttgacgctga gcaccaacga acagggcaat ccggaagtct gctcctcggg cgaatgcctg 3420

accgtgaacc ccggtccgaa cacccgtggc cgccagaact ggcgccccat cgaaggaaag 3480

aactga 3486

<210> SEQ ID NO 57
<211> LENGTH: 3636
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 57

atgaagattc tcgccatccg cctgaagaac ctcgcctccc tcgctggcga gcaggaaatc 60

gacttcaccc gcgaaccgct gtccagcgcc ggcctgttcg ccatcaccgg tccgaccggc 120

gccggcaaga gcaccgtgct ggacgccctg tgcctggccc tgttcggcag cacgccgcgg 180

ctggaaagca cttcggccag cagcaaggtt cccgatggcc ggaacgagct gtccagcaac 240

gacgaacgca acctgctgcg ccgcggttgc gccagcggct acgccgaagt ggatttcgtc 300

ggcatcgacg gccaccgcta tcgcgcccgc tgggaaaccc ggcgctcccg ggacaaggcg 360

-continued

gacggcgcct tgcaaaagag ccagcagagc ctccaggacc tggagaccca gcaaatgctg 420

gcagcgaaca agaaaagcga gttccgcgaa cagctggagc agaagctcgg cctcaatttc 480

gcccagttca ctcgcgccgt gctgctggcc cagagcgaat tcagcgcctt cctcaaggcc 540

agcgacaacg accgcggcgc attgctggag aaactcaccg acaccggcct gtacagccaa 600

ttgagcaaag ccgcctatca gcgcgccagc caggccgacg agcagcgcaa gcaactcgag 660

caacgcctgg aaggcagcct gcccctggcc gagcaggccc gggccgggct cgaggcggcg 720

ctggaatccc acgcccaggc gcgtctccag gagcaacagg cactgcaacg tctggaaggc 780

cagcaacaat ggttcaccga ggagcagcgg ctgctgcaat cctgcgagca cgcacaaggc 840

caactggccg aggccaggca ggcctgggac gccctggcga cggagcggga aaccctgcaa 900

tggctggagc gcctggctcc ggttcgcgga ctgatcgaac gcctgaagca actcgagcag 960

gaactccggc actccgagca gcagcagcgg cagcgcaccg agcagcaagc cgcgggcacc 1020

gagcgcttgc aaggattgca ggcccgcttg caggaggcgc gcgagcgcca ggcccaggcc 1080

gacaaccatc tgcgtcaggc ccaggcgccg ttgcgcgagg ctttccagct ggagagcgag 1140

gccaggcgcc tggagcgaac gctggccgag cgacaggaac tccatcggca atcgaaccag 1200

cgccacgccc agcaaagcga cgccgctcgg caactggata tggagcagca gcgccatgtc 1260

gcggaacagg cgcaactgca ggcggcattg cgcgacagcc aggctctcgc cgcgctcggc 1320

gacgcctggg tgacccacca gggccagctc gccaccttcg tgcaacgtcg ccagcgcgcg 1380

ctcgaaagcc aggcgcagct ccccgagctg gaaaaatccc tggcccacgc cggggaaccg 1440

ctcgaacgct tgcaggcgca atggaccgcc ctccatggca gcgagccgga cgacctggcg 1500

gcacgcctgg tcgaattgcg ccggcagacc gatagcctgg aacgacaaca agcgctccac 1560

aaggaatggc aacaggtcct cgaccaacgc gccggtctgg ctcgacgcct gggcgaactc 1620

gaccagcgta tggtcgagca ggagcaggca ttgctcgacc tgaaacgaca aggcagccaa 1680

tgcgccgagg aggtgaaggc ggcggagcag gccctgcagg tcacccgcga gttgctccag 1740

cgccaacgtc tggcccgcag cgccagcgtc gagcaactgc gcgccggcct ggtggacggc 1800

gaggcctgcc cggtctgcgg cagccaggag catccctatc accattccga gcaactgctc 1860

gccgccctcg gtgaacacga cgaccaggag caggtccgcg ccgagcagtc cctcgagcgg 1920

ctgcgacaga ccctggtcgg tctgcgcgag ggctattcca gccagcggga aagactcaac 1980

cagagtcgcc aggagcagca ggaactgact ggccaactgg ccgcgctcga tcggcaactg 2040

gaccaatgga cgctgccgga agaactgcga ctcctgcagc cgtccgcgca gttggagtgg 2100

ctggcacaac gcctggacga cctggcaggg cagcgccagc agtgccaacg agacttcgac 2160

cggctgatcg cccgccagcg ccagacccag caattgcagc aggaactgcg ggccgccgag 2220

acgatcctgc aacagcgcca gcaggcgctg acggaacaac ggcagcgcta cgaacatttg 2280

cagcagcagg tcgaggagga cagccagcaa ttgcgtccat tgctctccga cgagcactgg 2340

cagcgctggc aggcagatcc gctgcggact ttccaggcac tcggcgagtc catcgagcaa 2400

cgccggcagc aacaggcgcg gcttcagcag atcgaacagc gtctgcagga gctcaagcag 2460

cgctgcgatg aatcgagctg gcaactgaag caaagcgacg agcaacgcaa cgaagcccgt 2520

caggcagagg aaagggccca ggcggaactc gccgaactga acggacgcct cggcgctcac 2580

ctgggccagc acgcctgcgc ccaggactgg cagctatcgc tggagcacgc cgcgcaagcg 2640

-continued

gcgcagagcg ccgtcgagac gctccaggcg cccctggatt cgctgcgcga ggaacaactg 2700

cgactcgccg aagccctgga acacctgcag cagcaacggc agcgccaaca ggatgagttc 2760

cagcgccttc aggccgactg gcaggcctgg cgcgaacgcc aggacaacct cgacgacagc 2820

cgcctcgacg ccctgctcgg cctttccgag gaacaggcga cgcaatggcg ggagcaattg 2880

cagcgactgc aagaggagat cacccgccag cagacactgg aagcagagcg ccaggcgcaa 2940

ctgctccagc atcgccggca gcggccggaa accgaccgcg aggcgctgga agacaacctg 3000

cggcaacagc gcgaacgcct ggccgccagc gaacaggcct acctggagac ctacagccag 3060

ttgcaggccg acaaccagcg ccgcgagcag agccaggcgc tgcttgccga actggagcga 3120

gcccgcgccg agttccgcag atggggccgc ctgaacgaac tgatcggttc gtccagcggc 3180

gacaagttcc gccgcatcgc ccagggctac aacctcgacc tgctggtgca gcacagcaac 3240

gtgcagttgc gccagttggc gcggcgctac cgcctgcagc gcggcggcag cgaactgggc 3300

ctgctggtgg tggacaccga gatgggcgac gaactgcgct cggtgtattc gctctccggc 3360

ggcgagacct tcctgatttc cctggccctg gcgctcggcc tggcctcgat ggcatcgagc 3420

aagctgcgca tcgagtcgct gttcatcgac gaaggcttcg gcagcctcga cccggaatcc 3480

ctgcaactgg cgatggatgc cctggacaac ctgcaggccc agggacgcaa ggtggcggtg 3540

atttcccacg tccaggaaat gcacgaacgg atcccggtcc aggtgcgggt ccagcgcgag 3600

ggcaacggca tgagcagcct gaaggtggtc ggctga 3636

<210> SEQ ID NO 58
<211> LENGTH: 7407
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 58

atgtcgatcc aggcgaaagt taccccctatc gatcagagta tttcttctgc ggctgccgtc 60

gaggttccgg aaaacgggat actcaaactc tcccagagca gtaatgtcgc gctcgatgtc 120

gcaccggagt cggtggcggg atactcgaag agcggttcgg acctgatcgt ccagctgaag 180

accggggaaa gcgtccggat cgccaacttc tatgcggaag gccagccttc cagccaactg 240

ttcctggccg acaaggacaa gctggtggcg gtagatctgc cgccggtcgc tgccgacggg 300

ccgctgatgg ccggctacat cccgcaggaa agcctggccg gtttcgagtc gctgaccggc 360

gccggtgtgc tcggtggcat gagcgcaggg actgcgctgc tggtcggtgc ggcggccatc 420

ggcgccgggg tggcgatttc caacagcagc ggcggcggtg gcggcggcgg ttcttcggtg 480

cccccggaca ccactccgcc gaaggcggcc agcggcctga agatagcgcc tgacggcagc 540

agcatcagcg gccaggccga ggccggcgcg agcgtcggca tcgataccaa tggcgacggc 600

aagccggacc tcaccgtgat cgccgatgcc aacggcaatt tcaccgctcc gctgaacccg 660

ccgctgacca atggccagac ggtcaccgtg gtggtcaccg acccggctgg caacgccagc 720

ccgccggccc aggtcaccgc tccggacact accgccccgg cgccggctac cgacgtgcag 780

gtggcgccgg acggcagcag cgtcaccggc aaggccgaac ccggctcgac ggtgggcgtc 840

gataccgacg gcgacggcca gccggacacc accgtggtgg tcggccccgg cggcagcttc 900

gaggttccgc tgaacccgcc gctgaccaat ggcgagacgg tgacggtgat cgttaccgac 960

ccggccggca acaacagcac cccggtgacc gtcgaggcgc cggacaccac cgccccggcg 1020

-continued

ccggccaccg acgtgcaggt ggcgccggac ggcagcagcg tcaccggcaa cgcagagccg 1080

ggcgccaccg tcggtgtcga caccgatggc gacggccagc cggacaccac cgtggtggtc 1140

ggtcccggcg gcagcttcga ggttccgctg aacccgccgc tgaccaatgg cgagacggtg 1200

acggtgatcg ttaccgaccc ggccggcaac agcagcaccc cggtcaccgc cgaagccccc 1260

gacttccccg acgcgcccca ggtcaatgcc agcaacggca gcgtcctcag tggtacggcg 1320

gaagcgggcg tgaccatcgt gatcaccgac ggcaacggca atccgatcgg ccagaccagc 1380

gccgatgcca acggcaactg gagcttcacc cccggtagcc aactgccgga tggcaccgtg 1440

gtcaatgtgg tggccaggga cgccgccggc aacagcagcc cggcgacctc catcaccgtc 1500

gacggcgtgg cgccgaacgc gccggtggtc gagccgagca acggcagcga actcagcggg 1560

actgccgaac cgggcagcag cgtgaccctg accgacggca atggcaatcc gatcggccag 1620

accaccgccg atgccaacgg caactggtct ttcacgccgt ccaccccgtt gccggacggt 1680

accgtggtca acgtggtggc cagggatgcc gccggcaaca gcagtccgcc ggccagcgtt 1740

accgtggatg ccgtcgcgcc ggccacgccc accgtcgatc cgagcaacgg tacgaccctc 1800

agcggcaccg ccgagccggg cagtagcgtg accctgaccg acggcaacgg taacccgata 1860

gggcaggtca ccgccgacgg cagcggcaac tggaccttca ccccgagcac gccgttgccc 1920

aacggcacgg tggtcaacgc cacggctacc gacccgtccg gcaacgccag ttcgccggcc 1980

agcgtcaccg tggacgccgt ggcaccggcc acgccagtgg tcaacccgag caacggcacc 2040

acgctcagcg gcaccgccga gccgggcgcc accgtgaccc tgaccgatgg caacggcaat 2100

cccatcgggc aggtcaccgc cgatggcagc ggcaactgga gcttcactcc gaccacgccg 2160

ttgcccaacg gcaccgtggt caacgccacg gccaccgacg cctccggcaa caccagtgcg 2220

ggcagcagtg tcaccgtgga ctcggtagcc ccggccacgc cagtgatcaa ccccagcaac 2280

ggcaccacgc tcagcggcac cgccgagccg ggcagcagcg tgactctgac cgatggcaac 2340

ggcaacccga ttggccaggt caccgccgac ggcagcggca actggagctt caccccgtcc 2400

acgccgctgg cggatggaac cgtggtcaac gccacggcca ccgatccggc gggcaacacc 2460

agcggccagg gcagcaccac cgtcgatggc gtggcgccga ccacgccgac cgtcaacctg 2520

agcaacggca gcagcctcag cggcactgcg gaaccgggca gcacggtgat cctcaccgac 2580

ggcaacggca atccgatcgc cgaggtcacc gccgacggca gcggcaactg gacctacacc 2640

ccgtccacgc cgatcgccaa cggcaccgtg gtcaacgtgg tggcccagga cgccgccggc 2700

aatagcagcc cgggcgccag cgtcaccgtg gactcgcagg ccccggcggc tccggtggtc 2760

aacccgagca acggcactac gctcagcggc accgccgagc cgggcgctac cgtgaccctg 2820

accgacggca acggcaaccc gattggccag gtcaccgccg acggcagcgg caactggagc 2880

ttcacaccgg gcacgccgct ggccaacggc accgtggtca acgccacggc cagcgacccg 2940

accggcaata ccagcgctcc ggccagcacc accgtggact cggtggcgcc ggccgcgccg 3000

gtggtcaatc cgagcaacgg cgcggagatc agcggcaccg ccgaaccggg cgccaccgtg 3060

accctgaccg atggcagcgg caatccgatc gggcaggtca ccgccgacgg cagcggcaac 3120

tggagcttca ccccgtccac gccgctggcg gatggaaccg tggtcaacgc caccgctacc 3180

gacccggccg gcaataccgg cggccagggc agcaccaccg tggacgccat cgcgccggcc 3240

acgccgaccg tcaacctgag caatggcagc agcctcagcg gcaccgccga gccgggcagc 3300

-continued

acggtgattc tcaccgacgg caacggcaat ccgatcgccg aggtcaccgc cgacggcagc 3360

ggcaactgga cctacacccc gtccacgccg atcgccaacg gtactgtggt caacgtggtg 3420

gcccaggacg cctccggtaa cagcagcccg ccggcgacgg tgaccgtcga ttccagcgcg 3480

ccgccggcgc cggtgatcaa cccgagcaac ggcgtcgtca tcagcggcac cgccgaggcc 3540

ggtgccacgg tgaccctcac cgatgccggc ggcaacccga tagggcaggt caccgccgac 3600

ggcagcggca actggagctt cacgccgggc accccgctgg ccaacggcac ggtgatcgtc 3660

gccacggcca ccgacccgac cggcaatacc ggcccgcagg ccgccaccac ggtggacgcg 3720

gtggcgccgc cggcgccggt gatcgatccg agcaacggca cgaccatcag cggcaccgcg 3780

gaggccgggg ccaaggtgat cctcaccgac ggcaacggca acccgatcgg cgaaaccacc 3840

gccgacggca gcggcaactg gagcttcacg cccggcacgc cgctggccaa cggcacggtg 3900

gtcaacgccg tggcccagga ccctgcgggc aataccggcc cgcagggcag cactaccgtg 3960

gacgcggtgg cgccgaacac gcctgtggtc aatccgagca acggcaacct gctcaacggt 4020

accgccgagc cgggcagcac cgtgaccttg accgacggca acggcaaccc gatcggccag 4080

accaccgccg atggcagcgg caactggagc ttcacgcccg gctcgcaact gcccaacggc 4140

accgtggtca acgtgaccgc gagcgacgcc gccggcaata ccagccttcc cgctaccacg 4200

acggtggatt cctcgctgcc gtcgatcccg caggtggatc cgagcaacgg ttcggtgatc 4260

agcggcaccg cggacgccgg caacaccatc atcatcaccg atggcaacgg caacccgatt 4320

ggccaggtca ccgccgacgg cagcggcaac tggtccttca ctccaggcat cccgctgccg 4380

gatggcacgg tggtcaacgt ggtggcgcgc agcccaagca atgtcgacag tgcgccggcg 4440

gtgatcactg tggatggcgt ggccccggcg gcgccggtga tcgatccgag caacggcacc 4500

gagataagcg gtaccgcgga ggccggcgcg acggtgatcc tcaccgatgg cggcggcaac 4560

ccgatcggcc aggccaccgc cgacggcagc ggcaactgga cgttcacccc gagcaccccg 4620

ctggccaacg gcaccgtgat caacgccgtg gcccaggacc cggccggcaa taccagcggt 4680

ccggccagcg tcaccgtcga tgccatcgcc ccgccggcgc cggtgatcaa tccgagcaat 4740

ggagtcgtca tcagcggtac ggcggaagcc ggggccacgg tgatcctcac cgacggcaac 4800

ggcaacccga tcggccaggt caccgccgac ggcagcggca actggagctt cacgcccggc 4860

acgccgctgg ccaacggctc ggtgatcaat gcgctggccc aggacgccgc cggcaacaac 4920

agcagtccca ccagcgccac cgtcgactcg ctggcgccag cagccccggt gatcgatccg 4980

agcaacggta gcgtgatcgc cggtaccgcc gaggctggtg ccacggtgat cctcaccgac 5040

ggcaacggca acccgatcgg ccaggtcacc gccgatggca gcggcaactg gagcttcacg 5100

cccggcacgc cgctgtccaa tggcacggtg gtcaatgcgg tggcccagga cgctgccggc 5160

aacaccagcg gcccggtcag caccacggtg gacgcggtgg ccccggccac cccggtgatc 5220

gacccgagca acggtgtcga actcagcggc accgccgaac ccggcgtccg ggtgatcctc 5280

accgatggca atggcaatcc gatcggccag acccttgccg acggcagcgg caactggagc 5340

ttcacgccgg gcacgccgct ggccaacggc acggtggtca atgccgtggc ccaggacccg 5400

gccggcaata ccagcggccc ggccagcacc acggtggaca cggtggctcc ggccacgccg 5460

gtgatcaatc ccagcaacgg cagcgtgatc accggcaccg ccgaggtcgg cgccaaggtg 5520

atcctcaccg atggcaacgg caacccgatc ggcgagacca ccgccgacgg cagtggtaac 5580

-continued

tggaccttca cccccggcac gccgctggcc aacggtacgg tgatcaacgc cgtcgccgag 5640

gacgccgcgg gcaacgccag cggtccggcc agcaccacgg tggactcggt ggcgccgtcc 5700

gctccgctgc tgagcatcag cgccgacggc gcgctgctga ccggcaccgc cgagccgaac 5760

agccaggtgc gcatcgtggt caacggcgac accgccaacc cgatcacggt caccgtcgac 5820

ggcgccggca acttcagcct gccgttcgcg ccgccgctga tcaccggcga gctgatcgcc 5880

ggggtcgccg tcgacgccgc cggcaacgtc agcgggccgg ccaccatcaa cgccccggac 5940

ctggcgccgc cgaccatcag cgtgccggaa gccgccgata cctggatcaa tgccgcggag 6000

atcggcgacg gtatccaggt cgatgtgacg gtccgtccga ccatgcaggt cggccaggtg 6060

gtcacggtca agttcgccgg gcagaacggc tacgaggccg aggtcagcca taccctcacc 6120

gccggcgaca tcgccgccgg caacctgacc ctgaccctga cgcctcccgg cggcatgggc 6180

ccgttcccgg agggtgcctc gaccgtcacc gccgacatca acggcggcac cgcgtcgacc 6240

ccggtgccgt tcaccatcga caccattccg ccggcgaccc cggtgctgtc cctggtcggc 6300

aacatcctga ccatctcggc ggagccaggg accgagttga cggtgaccgt cgacgtcggc 6360

ggggtgaccg ccaccgccac ggtgaccgcc gacaacagcg ggctggcgtc gctgaacctg 6420

ctcaccgacc tggacatcga cttcagttgg gaccagttgc tcaatgccca ggtgtcggtg 6480

gtcggacgcg acccggccgg caacccgagc aacacggcga gcatcggcgt cggcaccagc 6540

atcgagcaac cggtgaccat cggcaacttc ggcctcgacg tcagcctcaa cccgctgaac 6600

ccgcgtttcg gtttcagcgg aaccaccgag cctgactcca gcgtggtgat ccgggtcatc 6660

accccggcgt tgaacgtcga attgctgccg atccaggcgg attcgtccgg aaacttctcg 6720

ctgaacctgc tgagcccgac catcctcacc cagttggggc tgaacatcac cgacatcctc 6780

aacctcggct cgcagatctc gttcaacctg gtgtccaccg actccaatgg caacgacagc 6840

gccgcctacg ggatcaccct gacccccaac ggactgtcgc tcaatatcgg ccagatcgat 6900

gtcaacggta cttccggcga cgacgtgctg tccggcgcca acggcagttc ggagcacatc 6960

aacggcggcg acggcagcga cctgatcttc aacgtgggca ccggcgatca cgtggtggcc 7020

ggcaacggca acgacaccat ccagatcacc gcgaccgatt tcgtcagcat cgatggcggc 7080

gccgggttcg acaccctggt cctggccaac ggcatcgacc tcgactacaa cgccgtcggc 7140

gtcggcacgc tcagcaacct cgagcgcatc gacctcggca agggcgattc gggtagcgtg 7200

ctgaccctga ccgcggcgga ggtggatgcc atcaccgatg ccaacaacac gttgcagatc 7260

accggcgaga acaacgacac cctgaacgtg gtgggcgcgg tgaataccgg taccacgcaa 7320

ctgatcaacg gcattaccta cgacgtctac accttcggca gtaccaccct gctgatcgag 7380

gacaacacgg tacaggtcgt ggtctga 7407

<210> SEQ ID NO 59
<211> LENGTH: 10608
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 59

atggacatcc gcagcccgct gaaccagtgc atcgccctgt ccctggccgg catcttgttc 60

ctcaacccga tcgtcgccgc ggcggcgggg ctggcgctgg acaaggccgc cggcggcaac 120

accggcctgg gccaggcggg caacggcgtg cccatcgtca atatcgccac gcccaacgac 180

-continued

gccgggctgt cgaacaacca tttccgcgac tacaacgtcg gcgccaacgg gctgatcctc 240

aacaacgcta ccggcaagac ccagggtacc cagctcggcg ggatcatcct cggcaacccc 300

aacctcaagg gccaggcggc gcaggtgatc ctcaaccagg tcaccggcgg caaccgcagc 360

accctggccg gctacaccga ggtggccggg cagtcggcgc gggtgatcgt cgccaacccg 420

cacggcatca cctgccaggg ctgcggcttc atcaacacgc cgcgcgcgac cctcaccacc 480

ggcaagccga tcatggacgg ccagcgcctg gagcgcttcc aggtggacgg cggcgacatc 540

gtcgtcgaag gcgccgaact gaacgtcggc aacctcgaac agttcgacct gatcacccgc 600

agcgccaagc tcaacgccaa gctctacgcg aagaacctca acatcgtcac cggccgcaac 660

gacgtccagg ccgacagcct gcaggccacg ccgcgcgccg ccgatggcag cgagaagccg 720

cagctggcga tcgacagctc ggcgctgggc gggatgtacg ccggggcgat ccgcctggtc 780

ggcaccgagc agggcgtggg ggtgcggctg gccggcgaca tggccgccag cggcggcgac 840

atccgcatcg acgccagcgg caagctgagt ctggcccagg cctccagcca gggcgacctg 900

aagatcgcgg cccaggccgt ggagctgaat ggcaagacct acgccggcgg cagcgccgag 960

atccgcagcg cggaggaact ggtcaaccgg cagagcctgg cggcgcgcga acgcatcgtg 1020

ctggaggcgg cgcatatcga caacgccggg gtgatcgaag ccggcgtcga gccagacgag 1080

cgacgcaacg cgcgcggcga cctcgagctg cgcagcggca ccctgcgcaa cgccggcagc 1140

ctggtggcca gccgcgcgct ggaagcgaag gcgagccagg cgctggacaa ccagggcggc 1200

agcctgaagg gggcgaccgt ccgggtcgac gccgggcacc tggacaaccg tggcggcaag 1260

ctgctcgccg agggcgaact gcgggtcgag gcgagcagcc tggacaaccg ccaggacggc 1320

ctgttgcaga gccgggaccg cgccgtggtc aagacccgtg gcgatctcga caaccgtggc 1380

ggccaggtga tcggcctgaa cgatctggag gtcggcgcgg cgacgctcga caacggccag 1440

caaggcctgc tcggcagcca gcagtccacc cgcgtcagcg cccaggcgct ggtcaaccgg 1500

ggggacggcg aagtctccgg caagcgcgtc gaggctcgcg tcggtagcct cgacaatcgc 1560

ggcggcaagc tgatcggcga cgacctgctg gtggtcgcca gcggtgccat cgacaaccgc 1620

ctcggcttgt tctccgcagc caaccgcctc gacctgcggg cgcgcagcct ggacaacagc 1680

ggcaagggca cgctgagcag ccggggcggc ctggaggtca gcctcggcgg cctgctggac 1740

aaccgcgatg aaggcaacct gctcagccag ggcgcgcagc gcgtgacggt ggggcaactg 1800

gacaaccgcg ccggcggcct gctgtcgagc cgcagcgagt tgaacgtcca cggcgccagc 1860

ctggacaacc gtggcggcgt gctggtggcc gacgccggcc tgagcgccac gggaggcgcc 1920

ttcgacaacc gcgacggcgg cagcgccagc ggcaaggctg gcgtgcgcgt ggaggtcgcc 1980

agcctgcgca acgaccaggg tggcaagctg ctcagcgatg gccgcctgga cctcgcagcg 2040

aacgccgtcg gcaacgccgg agggcgtatc gccgccaagg gcgacctgca ggcgacgctt 2100

ggcagcctgg cccagcaagg tggcgaactg gtcagcgaaa agaccctgaa ggtcgcggcc 2160

gacacgctcg acaacagcca gtccgggctg atcgccgcga atggcggcat cgctatcgag 2220

gcgcggcagg tcgacaaccg cgccggcgag atttccagca cctcgaaggt cgccgtgaac 2280

gcccgcgagc aactggacaa ccgcggcggc aaggtcatcg gcgacagcgg cctgcgcctc 2340

accgtgcagc gcctgctgaa ccaggccaag gggtgctgg ccgggcgcga cggcctgagc 2400

ctggacggcg gcgaactgtt caacggcgac ggcggtcggc tcgacagcca gaacagcctg 2460

-continued

agcgtgagcc tcggcggcgt gctggacaac cagggcggcg cgctggtcag cgaaggcagc 2520

ctgacggcgc gcgccgcgcg cctggacaac cgtggcggga ccttctccag cgccggtgcg 2580

ctggcgctga ccagccaggc cgcgctggac aaccagggcg gcaggctgct cagcgatgcc 2640

ggcgtgacgc tgcagggcgc cagcctcgac aacagccgtt ccggcgtgat cagcgccaag 2700

ggcgcggtgg atatccgcac cggcgtactg gacaacagcc gcaacggcgg catcggcagc 2760

aacgccggca tcaccctggt ggccgcccgg ctggacaacg gccagcaggg ccgggtcagc 2820

gccaagggcc tgctcgacgc caacctgaaa ggcctcgacc agcgcggagg cggcgtcctg 2880

atcagcgaaa ccggcgtcac cctcgacctc aatggcggca cgctggtcaa ccgcgacggc 2940

ggcctgatcg ccacgcccgg cgcgctgctg ctgcgccagc tcggcgcggt ggacaacggc 3000

gccggcgggg aaatctccag cgaccgcgcc ttcaccctcg ccgccgccag cctggacaac 3060

cgcggcgggc gcctgatcgg cgccgccaac ctgaccctgc gcatcgccca ggccctggac 3120

aacagcctgg ccggggtgat ctccggcgcc gccggcctgg acatcgcggc cgctcgcctg 3180

gacaacagcg ccaagggcac cctggccagc cgcgccggca tcgacctgcg cgtcgatggc 3240

gcgctggaca accacgccga aggcaccgtc tccggcgccc gcctgacgct cgccagcgcc 3300

tcgctggaca acagcggcaa gggcctgctc tccggcaacg ccggcctgag cgtcgccact 3360

ggcgcgctgg acaacgccga gggtggccag ttgatcagcc agggcgtcct ggacgtcagc 3420

agcgccgacc tcgacaaccg tggcggcgcc ctcagtggca agcagtcgct gcgcctgagc 3480

gccgccaacc tggacaaccg tggcggcctg ctcaccagcg acggcgaact ggaactgacg 3540

gcagggcgcg tcgattccgc cgacggcggc gaaatctccg cccggggcga cctgcgcctg 3600

acggtcgagc gcctggtgca acgccagggc cggctggtcg gcgagcgcgg cgtcagtctc 3660

gacctgcggg gcggcgacct ggacaaccag ggcggcctga tcagtgcccg cggcccgctg 3720

agcatcgagc ggctgagcgt cctcgacaac cgccagggcg gcgagatttc cagccagcag 3780

ggcttcgagc tgctggccag gcgcatcgac aacggccagc aggggcgcat catcagcgcc 3840

gggaaactgc gcctagacgc cgacgcgctg ggcaacgccg gcgccggcct gctctccgga 3900

tggcagggcc tgacggtgac aggcgggagc ctggacaaca gcgccggcgg caccctttcg 3960

agcaaggacg gcgagctggc catcagcctc ggcggcgcgc tggacaacca cggccagggc 4020

gcgctggtca gcaagggcgc gcaacggatc gacgccgcca gcctggataa cgcccagggc 4080

attgtctccg gcgaaagcga cgtgaccctg agcatcgccg ggaagctgga caacggccag 4140

ggcggcctgg tctcggcgca gcgcgcgctg agcttcgagc gcgacgatac gctgctgaac 4200

aacgccggcg gccggatcaa cggcggcagc ctgctgctca agggcgccag cctggataac 4260

agcgacggcc agttgatcag ccagggccgg ctcgacgcca tcctcggcgg cgccctggtc 4320

aacaccggcg cggcgcgcct ggccagcggc ggcgacctgc tgctgcgcag cgccagcgtc 4380

gacaaccgcg gcggcaagct ggtcagccag gggctgctgg agatcagcgc cggcagcctc 4440

gacaacagcg cctccggcac cctcgccagc caggccggca tgagcctgcg cctgggcggc 4500

ggcgccctgc gcaaccagca ggacggcctg atcttcagcc aggccggcgc cctcgatgtg 4560

caggccggca gcctggacaa ccgccagggc acgctccagg cccagggcga caaccggctg 4620

cgtatcggcg gcgcgctgga caaccagggc ggccgcctgg acagccgggc cggcaacctc 4680

gacctgcaga gcggcagcct cgacaacggc gccggcggcg tgctcaacag cgccaagggt 4740

-continued

tggctgaagc tggtcaccgg gctgttcgac aacagcgccg gcgtcaccca ggcgcagtcg 4800

ctggagattc gcgccgggca aggcgtgcgc aaccagcagg gccacctctc ggcgctgggc 4860

ggcgacaacc gcatcgtcac cgccgacttc gacaaccagg gcggcggcct ctacgccagc 4920

ggcctgctca gcctcgacgg ccagcgcttc ctcaaccagg gcgcggcggc gggccagggc 4980

ggcaaggtcg gcgccgggcg catcgacttc agcctggccg gcgcgctggc caaccgcttc 5040

ggccagttgg aaagcgaaag cgagctgcac ctgcgcgccg ccgcgatcga caacagcggc 5100

ggcagcctgc gcgccctcgg ccgcagcggc agcacgcggt tggtcgctgg cggcctgaac 5160

aacgcctacg gcgtgctgga aagcgccaac caggacctcg acctgcaact gggcagcctg 5220

gccaacgccg gtgggcgcat cctccacacc ggcaatggca ccttcggcct ggattccggg 5280

caggtgatcc gcgccggcgg cgaactgacc accaatggcc tgctggacat ccgcgccagc 5340

gaatggacca acagcagcgt gctgcaagcc ggacgcctga acctggacat cggcaccttc 5400

cgccagacgg ccgagggcaa gctgttggcg gtgcagtcct tcactggccg cggcggcgac 5460

tggagcaacg acggcctgct ggccagcgac ggcagcttcc gcctcgacct gagcggcggc 5520

taccgtggca acggccgcgc caccagcctc ggcgacttcg ccctgaacgc cgccagcctc 5580

gacctcggca acgccgccag cctcgccggc ggtgccaatg tcacgctcgg cgccggcaac 5640

ctgctggtca accgtgggcg gatcaccgcc gccggcgacc tcgtggccag cgccgcgagc 5700

ctgaacaact acggcaccct gggcggcggc ggcaacctgc gattgaacgc gcccgccctg 5760

ctcaacgagc gcgggttgct gttcagtggc gccgacatga ccctgcgcgc cggcgacatc 5820

accaacctct acggggatgt gtacagcctc ggcaggctgg atatcgcccg cgacgatgcg 5880

ggcaaccgtg ccgccagcct gcgcaacctt tccggggtga tcgagagcgg caaggacttc 5940

agcctgcgtg ccagcctgat cgagaaccgt cgcgccgtgc tggaaagcaa gtcgggcctg 6000

tacaccgcga agatggagca gaccgcctgc atcgaaggcg tcaacgcggg cgactgcagc 6060

ggcaagcgca acgccatctg gaccatcacc cagcgcgaca agaccgaggt caccgccagc 6120

agcgccatgg ggcaactgct ggccggaggc gacttcgcca tcgacggcgg caccctgaac 6180

aacctttcca gtctgatcgg cagcggcggc aacctcaccg ccaacctcga agtcctcgac 6240

aaccagggcc tggaaaccgg cgagctggaa accatccgcg tgctgcgtac cgctcgcggc 6300

ggcgatatcg gcggcatcga ccagaagtcg cgcaacttca ccaacctcta ctggtaccag 6360

agcgccaatt tcgacccggc gcgcgcgggc gagatccccg ccgcgctcaa cgcgatcctc 6420

agcgactggt ccttcgagta cgaattcccg agcaaggggc cgaccccgat cagcagtggc 6480

gaccagtcct acgcagcggt gatccaggcc gccggcgacg tcacggtcaa tgccagcacg 6540

cgcatcgaca acggcgtcac ccgccccggc tacaccttcg tcggcagcgg ccgccaggtg 6600

ggcgacagcg cggtgggcgg cagcggggtt tcggtggtcg tgccgctgac ctcgcaactg 6660

ccgcccgacc tggcgcggcg ccaggtcaac ccggttaccc tgcccggctt cagcctgccc 6720

cagggtgaca acggcctgtt ccgtctcagc tcgcgctttg ccgaggacgg caatggcagc 6780

gccgcgctcg gtgccggcgc cgaccgcacc cagggcggta gcggcgtctc ggtcggccag 6840

caaggcgccg gcaacgccgc cggtacctgg cagggccagg gcgtgcgagt cgacggcctg 6900

gctggcgcgg ccaacgtcca gggtcagggc ggcagcacgc tcggcggtag cctgccgggc 6960

gtcgcccggg tccagggcgt gcccggcaac gccacgccga gcgccagcca caagtacctg 7020

-continued

atcgagacca acccggcgct caccgaactg aagcagttcc tcaactcgga ctacctgctc 7080

agcggcctgg gcatgaaccc ggacgatagc aagaagcgtc tcggcgacgg tctctacgag 7140

cagcggctga tccgcgacgc ggtggtggcg cgcaccggcc agcgctacat cgacgggctg 7200

agcagcgacg aggcgctgtt ccgctacctg atggacaacg ccatcgctta caaggaccaa 7260

ctgcacctgc aactgggtgt gggcctgagc gcggagcaga tggcggcgct gacccacgac 7320

atcgtctggc tggaagaggt cgaggtgaac ggcgagaagg tcctcgcgcc ggtggtctac 7380

ctggcccagg cggagggtcg gctggcaccc aacggtgcgc tgatccaggg ccgcgacgtg 7440

aagctggtga gcggcggcga cctgcataac gtcggcaccc tgcgcgcgcg gaacgacctc 7500

tcggcgacgg ccgacaacct cgacaacagc ggcctgatcg aggccggcaa gcgcctcgac 7560

ctgctcgccg gcgactcgat ccgcaaccgc cagggcgggg tcatcgccgg gcgtgacgtg 7620

agcctcaccg cgctgaccgg cgacgtaatc aacgaacgca gcgtgacccg ctacgacagc 7680

gcgctcgacg gccgcacctg ggaacgcagc ttcgccgaca gcgccgcgcg ggtggaggcg 7740

gcgaacagcc tgaacgtcca ggccggacgc gacatcgcca acctcggcgg ggtgctgcag 7800

agccgcggcg acctcagcct cgacgccgga cgcgacgtca ccgtcgccgc cgtcgaggac 7860

cgccagggcc agacccgctg gagcacgtcg cggctccaga gcgtgaccca gctcggcgcc 7920

gaagtcagcg ccgggcggga cctgaacgtc agcgccggcc gcgacttgac ggcggtggcc 7980

agcaccctcg aagcgcgccg cgacatcgcc ctctccgccg ggcgcgacgt gaccctggcg 8040

gcggcggcga acgaggagca tgcctacagc aagaccagga aggtcaccta ccaggaagac 8100

aaggtcgccc agcaaggcac ccgcgtggac gccggcggcg acctggcgat caatgccgga 8160

caggacctgc gcctgatcgc gagccaggcc agcgccggcg acgaggccta cctggtggcc 8220

ggcgacaagc tggaactgct ggccgccaac gacagcaact actacctgta cgacaagaag 8280

aagaaaggcg acttcggccg caaggaaacc cggcgcgacg aagtcaccga cgtcaaggcg 8340

gtgggcagcc agatcagcag cggcggcgac ctcaccctgc tcagcggcgg cgaccagacc 8400

taccagggcg cgaagctgga atcgggcaac gacctggcca tcgtcagcgg cggcgcggtg 8460

accttcgagg cggtgaagga cctgcaccag gaaagccacg agaagagcaa gggcgacctg 8520

gcgtggaaca gcgccaaggg gaaagggcag accgatgaaa cgcttcggca gacccagatc 8580

gtggcccagg ggaatctggc gatcaaggcc gtggaagggc tgaagatcga cctcaagcat 8640

atcgaccaga agaccgtaag ccagaccatc gacgcgatgg tgcaggcgga tccgcaactg 8700

gcgtggctga aggaggccga gcagcgcggg gatgtggact ggcgcatggt gcaggaggtg 8760

cacgatagct ggaagtacag caactcgggc atggggccgg cgacgcagat cgctgtcgcc 8820

atcgcggcgg cagccatcgg tggcatggcg gcagcgggag cgctcagtgg tgcaggagtg 8880

ggtgccagta gcttcgccat gggcgcagga gttggtgcgg caggaagcct gtcgggcacg 8940

gcagcggtca gcctgatcaa caacaagggc gatctcggga aggtgctgaa agacagcttc 9000

agtagtgaca gtctgaagca gattgctatt gcgagcctga ccggggggct gacggctgag 9060

tacttcgacg ggattcttca gaccaagact gatccgctta ctggaaaggt cacggtagac 9120

ctcagcagcc tatctggtgt tggtcgcttc gctgccaatc aggcgatgca gaacgctaca 9180

tccactgtac tgagccaggc cttgggccag ggcgggagcc tgaacgaggc gctgaagagc 9240

gcgctctaca acagtttcgc ggcggcaggt ttcaacttcg tcggcgatat cggccaggaa 9300

-continued

tacagcctga agccaggcga tccttcgatg gtgaccatgc acgccctgat gggtggcctg 9360

gcggcgcagg tcagcggtgg cgatttcgcc acgggcgccg cggcggctgg cgccaatgaa 9420

gcgctggtgg ccaagctaga ccaggccttc aagagcttga gccctgagaa ccgtgaagcc 9480

atggtcacta tggggtcgca attggttggt gttctggctg cggcggtacg cgatcctgat 9540

gtgacaggca aagctctgga aagcgctgct tgggtagcga agaactcgac gcaatacaac 9600

ttcctcaacc atcaggatgt ggccgatctg gataatgcct tgcagaaatg caagtcccag 9660

ggaaattgcc gtcaggtaga ggaagagttc aaggcgcgta gcgacgagaa ccggcggagg 9720

ttgaatggct gcgtggctgt gggtaattgc gcggagattc gtgcggagat cgatgcgggg 9780

tctacggctc tcaacgagct ggtggcccgg caggaaacag ctaatccggg aggaagtgac 9840

agcgatatag cctacggttt cctgatgggc cgaaatgttg tcgactggac gacggctggt 9900

cagttgcacc tggagcagac cgccaacctc tggtggaacg gtaatccaca gtggcagaag 9960

gaagtcggtg catacctaga ccagacgggg ttcaatccgt tcggaatcgg cgttccggca 10020

atgggcggtg ccgctggcaa ggtaacggcc aaggcgctca tgaatgcgct gaaggcggga 10080

gagttgccca aggagaggt ggccccagga aaggctaatc tgcctaccat tggggcgttg 10140

gcggatgctg aggcgggaat gccttatacc catccagtta agctcgccgc aaaagcgact 10200

gggacagcag ggaagattaa gattgaagcc ggcgcaatac ctgacgcaaa tgaagtacgt 10260

gcaggacaag ggttatctgg tcttgggtac gatgttacgc accaaaccac tgcgtcagct 10320

aaaggtattc aagggcagcg aactgcggac ttgcatgttg atggactcgg ttccattgat 10380

gtgtatacgc cgaagaatct tgatccgaca aagatagttc gagcgataga gaagaagtcg 10440

aatcaagccg gcggagtctt ggtgcaggcg gacttgccaa gcactgacat gtcgtccatt 10500

gctgctcgta tgtgggggaa gactaacgcg cagagtataa aaactatatt tttccagaaa 10560

ccagacggat cattggtccg atttgatcga cctgctggag gaggctga 10608

<210> SEQ ID NO 60
<211> LENGTH: 16884
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 60

atggacatcc gcagcccgct gaaccagtgc atcgccctgt ccctggccgg catcctgttc 60

ctcaacccga tcgtcgccgc ggcggcgggg ctggcgctgg acaaggccgc cggcggcaac 120

accggcctgg gccaggcggg caacggcgtg cccatcgtca atatcgccac gcccaacggc 180

gccgggctgt cgaacaacca tttccgcgac tacaacgtcg gcgccaacgg gctgatcctc 240

aacaacgcca ccggcaagac ccagggtacc cagctcggcg ggatcatcct cggcaacccc 300

aacctcaagg gccaggcggc gcaggtgatc ctcaaccagg tcaccggcgg caaccgcagc 360

accctggccg gctacaccga ggtggccggg cagtcggcgc gggtgatcgt cgccaacccg 420

cacggcatca cctgccaggg ctgcggcttc atcaacacgc cgcgcgcgac cctcaccacc 480

ggcaagccga tcatggacgg ccagcgcctg gagcgcttcc aggtggacgg cggcgacatc 540

gtcgtcgaag gcgccgaact gaacgtcggc aacctcgaac agttcgacct gatcacccgc 600

agcgccaagc tcaacgccaa gctctacgcg aagaacctca acatcgtcac cggccgcaac 660

gacgtccagg ccgacagcct gcaggccacg ccgcgcgccg ccgatggcag cgagaagcca 720

-continued

caactggcga tcgacagctc ggcgctgggc gggatgtacg ccggggcgat ccgcctggtc 780

ggcaccgagc agggcgtggg ggtgaagctg gccggcgaca tggccgccag cggcggcgac 840

atccgcatcg acgccagcgg caagctgagc ctggcccagg cctccagcca gggcgacctg 900

aagatcgcgg cccaggccgt ggagctgaac ggcaagacct acgccggcgg cagcgccgag 960

attcgcagcg cggaggaact ggtcaaccgg cagagcctgg cggcgcgcga acgcatcgcg 1020

ctggaggcgg cgcatatcga caacgccggg gtgatcgaag ccggcgtcga gccagacgag 1080

cgacgcaacg cgcgtggcga cctcgagctg cgcagcggca ccctgcgcaa cgccggcagc 1140

ctggtggcca gccgcgcgct ggaagcgaag gcgagccagg cgctggacaa ccagggcggc 1200

agcctgaagg gggcgaccgt ccgggtcgac ggcggacacc tggacaaccg tggcggcaag 1260

ctgctcgccg agggcgaact gcgggtcgag gcgagcagcc tggacaaccg ccaggacggc 1320

ctgttgcaga gccgggaccg cgccgtggtc aagacccgtg gcgatctcga caaccgtggc 1380

ggccaggtcg tcggtctgaa cgaactgcag gtccaggctg ccgcactgga caatcgcagt 1440

gccggtctcc tttccagcaa gggagacatg gacatcgagt tcgctcgtct ggacaacagt 1500

gcgggcggca agctggtcag cgagcgccgt acgctcctga aggcggatcg gctcgataat 1560

cgcagcggtc gcattgtcgc cggccaggat ctcgacttga gctctcggtt gatcgacaac 1620

cgagcgggcg atatctccag cacgtcgagg gtggtggcga gcgctcgcga acagttggac 1680

aaccgcggtg gcaagatcgt cggtgacagt ggcctggaca tcacaacgcc acgcatgctc 1740

aaccaggaca aggggtact cgccagccgc gatgggctgc gcctgagtgc tacggagttg 1800

ttcaacggcg cggggggcct gctgtccagc cagaagggta tcgacgtctc cctggccggt 1860

gcgttcgata accaggccgg cagcctggac agccggggct tcctgacggt gaagtcagcc 1920

tggctcgaca accagggcgg tacgctatcc agcgcagggg cattggcagt gaccagccag 1980

ggcgccctga acaatcaggg cggcagactg gcgagcgacg ccggacttag cttgagcagc 2040

gccagcctcg acaacagcca ggccggtgcg atcagtggca agggggccgt ggagattcgt 2100

accggcaacc tgaacaacag ccggaaagcc agtatcggca gcgatgcggg actcaccctg 2160

gtcgccgctc gggtagacaa cagccaggcg ggccggatcg ccgccaaggg tgtgatcgat 2220

gcggatctcc aagggctgga ccagcatgac aggggcaacc tggtcagcga taccggcatc 2280

acgctcgatc tgaacaaggg aagcctggtc aatcgcgctc aaggcctgat cgccacgcct 2340

ggcaccttgc tcctgcgcca actcggcgtg gtggacaaca gcggtgggga aatctccagc 2400

gaccgcgcgt tcactcttgc cacctccgcg ttgaacaacc agggggacg cctgctcagc 2460

ggcggagccc tgaccttgcg tatcgcgcag gccctggaca acagcctcga ggggattgtc 2520

tccggtgctg gaggtctgga tatccaggca ttcgtcctgg acaaccgtag tggctccatc 2580

ggcagcaagg gcgccatcga tatcggtgtg acccgcctgg aaaacgacgc tggcacactg 2640

atcgctgaac gcggcctgaa gctggtagcc gatgaggcga acagttccaa ggggcgtatc 2700

gccgccaatg gtagcctgca tgccaaggtt ggcacgctga gccagaaggg aggagaactg 2760

accagtcagg actcgctgac tctcgacctg ggcatcctaa acaataacgc tggccgtatc 2820

gctggcaacc agggcgtgga catcacggcc cggcaggtgg acaacagcgt cggcgagatt 2880

gccagccagg gcgtggtggc gctgaacctc actgagcagc tggacaaccg tggcggcaag 2940

atcgtcggtg acagtggtct gggcatcacc gcgccgcacg tgctcaacca ggacaagggg 3000

-continued

gtactcgcca gccgcgatgg gctgcgcctg agtgctacgg agttgttcaa cggcgcgggg 3060

ggcctgctgt ccagccagaa gggtatcgac gtctccctgg ccggtgcgtt cgataaccag 3120

gccggcagcc tggacagccg gggcttcctg acggtgaagt cagcctggct cgacaaccag 3180

ggcggtacgc tatccagcgc aggggcattg gcagtgacca gccagggcgc cctgaacaat 3240

cagggcggca gactggcgag cgacgccgga cttagcttga gcagcgccag cctcgacaac 3300

agccaggccg gtgcgatcag tggcaagggg gccgtggaga ttcgtaccgg caacctgaac 3360

aacagccgga aagccagtat cggcagcgat gcgggactca ccctggtcgc cgctcgggta 3420

gacaacagcc aggcgggccg gatcgctgcc aagggtgcga tcgatgcggc tctccaaggg 3480

ttggaccagc atgacagggg cagcctggtc agcgataccg gcatcacgct cgatctgaac 3540

aagggaagcc tggtcaatcg cgctcaaggc ctgatcgcca cgcctggcac cttgcttctg 3600

cgccaactcg gcgtggtgga caacagcggt ggggaaatct ccagcgaccg cgcgttcact 3660

cttgccacct ccgcgttgaa caaccagggt ggacgcctgc tcagcggtgg agccctgacc 3720

ttgcgtatcg cgcaggccct ggacaacagc ctcgagggga ttgtctccgg cgccggaggt 3780

ctggatatcc aggcattcgt cctggacaac cgtagtggct ccatcggcag caagggcgcc 3840

atcgatatcg gtgtgacccg cctggaaaac gacgctggca cgctgatcgc cgaacgcggc 3900

ctgaagctgg cggccgatga ggcgaacaac tccaaggggc gtatcgtcgc caaggatgaa 3960

ctgcgtgcca aactcggtgc gctggtgcag aacgggggag agctgacgac tcagggcgcg 4020

ctggccctcg acgccgacaa agtcgacaac ggcgctggtc gcatcgccgg caaccgaggt 4080

gtggtcatcg atgcccggca ggtggacaac cgtgccggcg agattgccag ccagggcgtg 4140

gcgacgctga atctcactga gcaactggac aaccgtggcg gcaaagtcgt tgctgacagt 4200

ggtctgggca tcaccgcgcc acgcgtgctc aaccaggaca agggagtaat cgccagccgc 4260

gatgggctgc gcctgagtgg taccgaattg ttcaatggca atgccggact gctcagcagt 4320

cagagacata tagaggtcac tctggacggc gtgctggaca atcagggcaa gggcgcgctg 4380

ctcagcgacg gtaccctgac ggtgagcgcc gggcgcatac acaaccagga cgccactctg 4440

tccagcgccg gtgcgctgag actgagcagc caggaggcgg tggacaaccg tggcggcaag 4500

ttggtgacgg actccagcct gcgcctgacc agcgccagcc tggacaacag ccgatcaggg 4560

atcatcagtg ccaacgctgc ggcggagatc cataccgggg ttctgaacaa cagccagaaa 4620

ggcaatcttg gcagtaatga cgggctcggc ctgattgcta ctgaggtgga taacagccag 4680

gaaggtcgga tcactgccaa aggcatgatc gacgcaaata tcaagggact cgatcagcag 4740

ggcaaagggc ggctggtcag taatgccggc atcatactcg acctgaacga gggaaccctg 4800

gccaatggcg ctcagggcct gatcgccacg cctggaacct tgctcctgcg ccaactcggc 4860

atggtggaca acagcggcgg ggaaatttcc agcgaccgag ccttcacact caccacctcc 4920

gcgctgacca accagggtgg ccgcctgcgc agcggcggtg tactgacgtt gcgcatcgcc 4980

caggctctgg acaacagcct cgaaggtgtt ctctccggca ccggaggcct ggatatccgg 5040

gcgcttgccc tggacaaccg cagtggctcc atcggcagca agggcgccgt cgatatcgac 5100

gtgtcccgtt tggaaaacga tgacggcgac ctgcttagcg aaggtcgtct gaaactgact 5160

gccgagcgag cgaacagtgt caggggacgg atcgcggcca ggggtgacct gcacgccagc 5220

gtgacagcct ttaaccaggc gggtggcgaa ttgagcagcg agggtgcgct gatgctcgag 5280

-continued

gccgatagcc tcgacaaccg cagcggcggt ctggtcagtg ctgatggcaa cctgaccgtt 5340

tccgcccgga ggatcgacaa ccgtgcgggc gaaatcgcca gcccgggcca ggtgacactg 5400

gacgtcgccg agcagttgga caaccgaggc ggcaaggcca tcggcgatag cggacttcgc 5460

ctcgccgcgc cacgggtact caaccaggac ggcggggtac tcgccagtcg tgatgggctg 5520

cgcctgaatg gcgccgaact gttcaatggc aacggcggcc tgctcagcag ccagcaaagc 5580

atcgacgtca ttctggacgg cgtattgggc aatcaggcag gcagcttgag cagccaggga 5640

cgcctgagcg tgaagagcgg tcggctggac aaccagggcg gtgcagtctc cagcgccggg 5700

accttgtcgc tttccagcca gggtgcgttg aacaaccagg ggggcagggt ggtcaccgac 5760

gccggtgccg tcctgcgcag cgccagcctc gacaatagcc agggcggcat cgtcagcgcc 5820

aagggggccg cggagatccg tactggcagc ctcaacaata gccagaaggg cggcataggc 5880

agcggtgccg ggctcgcgct ggtcgcggac ctggtggaca acagccagaa cggccggatc 5940

actgccaagg gtgcgatcga tgccaacctg aaggggctgg atcagcaggg cagcggcagg 6000

ctggtcagcg atacggccat cgcgctcgat ctgcgcgggg gagaactggt caaccgtgct 6060

cagggcctga tcgccacgcc tggagccttg ctgctgcggc aactgggtgt cgtggacaac 6120

agtggcggtg gcgagatctc cagcgatcga agctttaccc tcgccgcgac cgcgctgagc 6180

aaccggggtg gccgcgtgat cagcggcgac tccctgaccc tgcgcatcgc ccaggcactg 6240

gacaacagcc tccaaggcgt tctttccgca agcggagggc tggatgtcgc tgcactcgtc 6300

ttcgacaacc atagcggcat cgttgctagc aagggcgata cacacatcgg ggtgaaccgc 6360

ctggagaacg aggcaggccg cgtggtcagc gaaggcgccc tggatctgac cgccaagcag 6420

gtgagcagcg ccaaggggcg cattgccgcg aagggcgatc tgcaggtcac ggttggcacc 6480

ctggagcagc agggtggaga actggccagt caggggacgc tgactctcga cgccgatagc 6540

ctggataacc gcaatggcgg cctggtgagc gccgatggcg gggtcaccgc cgaggcacgc 6600

cagatcgata accgcggtgg ggaaatatcc agcgtggcca aggtggctct ggctgtccgg 6660

gaacaactgg acaaccgggg gggcaaggtg atcggcgaca gtgagctgag cctaaccgtg 6720

cagcgcctgc tgaaccaggc caagggtgtg ctcgccagtc gcgatggatt gcacctggac 6780

ggcgcggaac tgctcaatgg cgatggcggc ctgctcagca gccaacgcct ggtggatgta 6840

acgctcagtg gtgcattgga caaccagggg agcggtgcac tggtcagcga agagtcgctg 6900

acagtgaagg ccgaccaggt caataaccag gcggggactt tctccagtgc gggtagcctg 6960

ctcgttacca gccggggcga gttgaacaac cagggtggca ggttggtgac cgatgctgga 7020

gccaccctga acagcactgg cttcgacaac agccgtgcgg gcctggtcag tgcgaaaggg 7080

gctgtggcca ttcgtaccgg agccctgaac aacagtcaga agggatccat tggcggcaat 7140

acgggcgtca ccctggtcgc cgggttggtc gacaacggcc gggaaggacg gatcagcacc 7200

aagggtacgc tcgacgccaa cctgaaaggg ttgcttcagc agggggagg ctcgctggtc 7260

ggcgagcgcg gtgtcaccct cgacctcaac ggtggcaccc tggacaacca cgacctcggt 7320

ctggtttcaa cgcctggcgc gctcctgctg cgccaactcg gcatggtgga caacagcgtc 7380

ggcggagaga tatccagcga ccgtgctttt accctcgccg ccaacacact gaacaatcag 7440

ggcgggcggc tgatcagcag cgaagctttg accctgcgca tcgccaagac actggacaac 7500

agtctcaagg ggcaggtcct ggcgaccgac ggactggcca tcgagtctca ggtcttggac 7560

-continued

```
aaccgtgcgg gaaccatcgg cagcaagggt gatgcccgta tcagcgtgac cagcctggac   7620

aacgccgaac aaggcagcct ggtgagtgaa ggccgcctgg agcttgtagc cgaccaggtg   7680

agcaacggca accaaggccg tatcgccgcc agaggcgtgc tggaggcggc ggtcggtacg   7740

ctgctccagc aaggcggcga actggtcagc caggggagcc tggaccttcg cgccgacacg   7800

ctcgacaaca gccagtccgg gctgatcgcc gcgaatggcg gcatcgctat cgaggcgcgg   7860

caggtcgaca accgcgccgg cgagatttcc agcacctcga aggtcgccgt gaacgcccgc   7920

gagcaactgg acaaccgcgg cggcaaggtc atcggcgaca gcggcctgcg cctcaccgtg   7980

cagcgcctgc tgaaccaggc caagggggtg ctggccgggc gcgacggcct gagcctggac   8040

ggcggcgaac tgttcaacgg cgacggcggt cggctcgaca gccagaacag cctgagcgtg   8100

agcctcggcg gcgtgctgga caaccagggc ggcgcgctgg tcagcgaagg cagcctgacg   8160

gcgcgcgccg cgcgcctgga caaccgtggc gggaccttct ccagcgccgg tgcgctggcg   8220

ctgaccagcc aggccgtgct ggacaaccag ggcggcaggc tgctcagcga tgccggtgtg   8280

acgctgaagg gcgccagcct cgacaacagc cgttccggcg tgatcagcgc caagggagcg   8340

gtggatatcc gcaccggcgt actggacaac agccgcaacg gcggcatcgg cagcaacgcc   8400

ggcatcaccc tggtggccgc ccggctggac aacggccagc agggccgggt cagcgccaag   8460

ggcctgctcg acgccaacct gaaaggcctc gaccagcgcg gaggcggcgt tctggtcagc   8520

gaaaccggcg tcaccctcga cctcaatggc ggcacgctgg tcaaccgcga cggcggcttg   8580

atcgccacgc ccggcgcgct gctgctgcgc cagctcggcg cggtggacaa cggcgccggc   8640

ggggaaatct ccagcgaccg cgccttcacc ctcgccgccg ccagcctgga caaccgcggc   8700

gggcgcctga tcggcgccga cagcctgacc ctgcgcatcg cccaggccct ggacaacagc   8760

ctggccgggg tgatctccgg cgccgccggc ctggacatcg cggccgctcg cctggacaac   8820

agcgccaagg gcaccctggc cagtcgcgcc ggcatcgacc tgcgcgtcga cggcgcgctg   8880

gacaaccacg ccgaaggcac cgtctccggc gcccgcctga cgctcgccag cgcctcgctg   8940

gacaacagcg gcaagggcct gctctccggc aacgccggcc tgagcgtcgc cactggcgcg   9000

ctggacaacg ccgagggtgg ccagttgatc agccagggcg tcctggacgt cagcagcgcc   9060

gacctcgaca accgtggcgg cgccctcagt ggcaagcagt cgctgcgcct gagcgccgcc   9120

aacctggaca accgtggcgg cctgctcacc agcgacggcg aactggaact gacggcaggg   9180

cgcgtcgatt ccgccgacgg cggcgaaatc tccgcccggg gcgacctgcg cctgacggtc   9240

gagcgcctgg tgcaacgcca gggccggctg attggcgagc gcggcgtcag tctcgacctg   9300

cggggcggcg acctggacaa ccagggcggc ctgatcagtg cccgcggccc gctgagcatc   9360

gagcggctga acgtcctcga caaccgccag ggcggcgaga tttacagcca gcagggcttc   9420

gagctgctgg ccaggcgcat cgacaacggc cagcaggggc gcatcatcag cgccgggaaa   9480

ctgcgcctgg acgccgacgc gctgggcaac gccggcgccg gcctgctctc cggatggcag   9540

ggcctgacgg tgacaggcgg gagcctggac aacagcgccg gcggcaccct ttcgagcaag   9600

gacggcgagc tggccatcag cctcggcggc gcgctggaca accacggcca gggcgcgctg   9660

gtcagcaagg gcgcgcaacg gatcgacgcc gccagcctgg ataacgccca gggcatcgtc   9720

tccggcgaaa gcgacgtgac cctgagcatc gccgggaagc tggacaacgg ccagggcggc   9780

ctggtctcgg cgcagcgcgc gctgagcttc gagcgcgacg atacgctgct gaacaacgcc   9840
```

-continued

ggcggccgga tcaacggcgg cagcctgctg ctcaagggcg ccagcctgga taacagcgac 9900

ggccagttga tcagccaggg ccggctcgac gccatcctcg gcggcgccct ggtcaacgcc 9960

ggcgcggcgc gcctggccag cggcggcgac ctgctgctgc gcagcgccag cgtcgacaac 10020

cgcggcggca agctggtcag ccaggggctg ctggagatca gcgccggcag cctcgacaac 10080

agcgcctccg gcaccctcgc cagccaggcc gacatgagcc tgcgcctggg cggcggcgcc 10140

ctgcgcaacc agcaggacgg cctgatcttc agccaggccg gcgccctcga ggtgcaggcc 10200

ggcagcctgg acaaccgcca gggcacgctc caggcccagg gcgacaaccg gctgcgtatc 10260

ggtggcgcgc tggacaacca ggccggccgc ctggacagcc gggccggcaa cctcgacctg 10320

cagagcggca gcctcgacaa cggcgccggc ggcgtgctca acagcgccaa gggttggctg 10380

aagctggtca ccgggctgtt cgacaacagc gccggcgtca cccaggcgca gtcgctggag 10440

attcgcgccg ggcaaggcgt gcgcaaccag cagggccatc tctcggcgct gggcggcgac 10500

aaccgcatcg tcaccgccga cttcgacaac cagggcggcg gcctctacgc cagcggcctg 10560

ctcagcctcg acggccagcg cttcctcaac cagggcgcgg cggcgggcca gggcggcaag 10620

gtcggcgccg ggcgcatcga cttcagcctg gccggcgcgc tggccaaccg cttcggccag 10680

ttggaaagcg agagcgagct gcacctgcgc gccgccgcga tcgacaacag cggcggcagc 10740

ctgcgcgccc tcggccgcag cggcagcacg cggctggtcg ctggcgacct gaacaacgcc 10800

tacggcgtgc tggaaagcgc caaccaggac ctcgacctgc aactgggcag cctggccaac 10860

gccggcgggc gcatcctcca cactggcaac ggcaccttcg gcctggattc cgggcaggtg 10920

atccgcgccg gcggcgaact gaccaccaat ggcctgctgg acatccgtgc cagcgaatgg 10980

accaacagca gcgtgctgca agccggacgc ctgaacctgg acatcggcac cttccgccag 11040

acggccgagg gcaagctgct ggcggtgcag tccttcactg gccgcggcgg cgactggagc 11100

aacgacggcc tgctggccag caacggcagc ttgcgactcg agctgagcgg cggctaccgt 11160

ggcaacggcc gcgccaccag cctcggcgac ttcgccctga acgccgccag cctcgacctc 11220

ggcaatgccg ccagcctcgc cggcggcgcc aatgtcacgc ttggcgccgg caacctgctg 11280

gtcaaccgtg ggcggatcac cgctgccggc gacctcgtgg ccagcgccgc gagcctgaac 11340

aactacggca ccctgggcgg cggcggcaac ctgcgattga acgcgcccgc cctgctcaac 11400

gagcgcgggt tgctgttcag tggcgccgac atgaccctgc gcgccggcga catcaccaac 11460

ctctacgggg atgtgtacag cctcggcagg ctggatatcg cccgcgacga tgcgggggc 11520

tgggcaaatc gcttggagaa catttccggg aatttagaga gcacaggtga tatgcgtttc 11580

tccgtgagtt cacttctcaa tagaagggaa actctagaga ttgaaggtga cttgcagaat 11640

agcgctattg gcgtccgctg tacggggtgt cagctttctg agaggtgggg aaaaactagg 11700

tcttcgagcg agcttgtctg gatcagggaa tataagtcta cattgggaga ttcttctgcc 11760

gctgcttcaa ttacggctgg tcgagatctg cttgttgtag gtgcaagcct gcagaatatt 11820

gcttctaata taagtgctgt aagagacgcc acgctatctc tgagtaattt cgaaaacaaa 11880

ggttatgcgt taggggaata tgcggtcagg ggcgtttatt cgccgccgag taaatttggc 11940

gaagaattgc ttatgcgcat attggcgtat aacgctgtca acgatcccag ttatggggag 12000

ggatatgcga gcacaggggg gagacttccg aatattcatt atttcgacaa gaattttaat 12060

gaaaaagtct ctccgctgga ggtcattcat ggaaacggga aaaatggtgg gccgggttgg 12120

-continued

cacctgtact tcggtacctt agatgttgag tatccggaca cagatcgctg gaataaggct 12180

attggacgaa taccggcgcc gaattattca tcgaaaaaaa cggatgctat tccagatcta 12240

cttaagggat tggctcctct cgatgagttg acgattaaca aaggggcgaa ctcaacggtt 12300

ggtgctgtcg tgcaagctgg cggtcgtgta acggtgaatg ctgcggagag tttcaataat 12360

tctgtcctac agggatttca ggccgttcag gaaacccagt tacctcatca ggacatagct 12420

gtttcaagca cgacgagcgc cgtagtgact ctgaagagtc aactgccagc ggatttggca 12480

aggcaacaga tcaatcctct caccctgccg ggcttcagcc tgcctcaagg ccagaatggg 12540

ctcttccgcc tggcgtccca aggagcccag gtgaaccagg caagtggtgc tctgaaatcc 12600

gccagcgatc tcacccagag cggccatggc gtatctgtat ccgcacagac aggcagtggc 12660

gcaagtggct ggagtaccca ggcgcgtcgt gtcggcgatg atcgggtcac ctcgcttgcc 12720

ggttccgcct atcaaggccg ggtagctgag gctatcgatg cgctacgggc ttccgcgcca 12780

atctcgggcg acgggggaaa cactggccgt ttccaggccg gtgagcacca ggcgaccacg 12840

ggactgggtg gactcgtcga gggcaatgca tcgggtcaca gcggcaatgg cgtcatcctc 12900

gccgatctgc gcggtggtct accctcgttc tcaagccttc ccgcgtctga tcatgttcaa 12960

ggcacagtgc ccggtcacga tgggaatgga actattctcg ccaattggca gggtgcgcag 13020

gcgacggtcc aggcctcgcc ttcgacagtg cgtgtagagg gggtagtctc cagtccaggt 13080

ggcaatggca gcatccttgc cgatctgccg gctgaacagt cgtcggtgca ggcactgcct 13140

tcggccgtta gggctcaggg cagcctgcct cgcctcgaag agcggagcgc ccttcttgcc 13200

gagcctccgg ttgggcagcc ggcgttgcaa accctgccgt cggttgcgcg cgttgagggc 13260

gtgcccagca atgccacacc gagcaacagc cacaagtatc tgatcgagac caacccggcg 13320

ctcaccgagc tgaagcagtt cctcaactcg gactacctgc tcggtggtct gggtatcaat 13380

ccggacgata gcaagaagcg cctgggtgac ggtctatacg agcagcgcct ggtacgcgaa 13440

gcgatcgtcc agcgtacggg gcagcgcttc atcgccggat tgaacagcga cgaagcgatg 13500

ttccgctatc tgatggacaa cgccatcgcc agcaaggacg tattgggact gacccctggc 13560

gtcaccctca gcgccgccca ggtggcggcg ctgacccacg atatcgtttg gctggaagaa 13620

gtcgaggtga atggcgaaaa ggtcctcgcc cccgtggtct acctggccca ggccgagggg 13680

cggttgggcc cgaacggcgc gctgatccag ggcgcgacgg tgaacctgat caccggcggg 13740

gacctgagga acgccggtac cctgcgcgcg cagaacgacc tcagcgcgac agccggcaac 13800

atcgacaaca gcggcctgat cgaggccggc aaccgcctcg acctgctggc cagcggctcc 13860

atccgcaatg accagggcgg catcattgcc gggcgcgagg taagcctctc tgcccttacc 13920

ggagacgtca tcaatgaacg gacggtgacc cagcaccagt cctcctacag gggaaccggt 13980

accactgagg catttgccga tagcgccgcg cgtatcgagg ctgcgcagaa gctgaccgtt 14040

tcggcaggac gcgatgtagc caatattggc ggtgtcatcg acagcaaggg cgacctcgcc 14100

ttgcaaggcg gcagggatgt cctggtttcg gctgcggtag cggagcgggg ctggacggca 14160

ggaagccagg cataccagac ccagacgacc cagatgggcg ccgaggtcgt ggcggggcgc 14220

gatatcagcg tcagcgccgg acgcgatatc agcgtcgtgg gcagccgcat cgacgctcgt 14280

cgcgacgtga cattcgaggc gggtcgcgat gtgggcctgg tcgcggctgc caacgaagag 14340

catgcctatg gcaagaccaa gaaggtcact ttccaggacg acaagatcac ccagcaggcc 14400

-continued

actcgcgtgg acgctggcgg cgacctggcg atcaatgccg gacaggacct gcggctggtc 14460

gcgagccagg ccagcgccgg cgacgaagcc tacctggtgg ccggcgacaa gctggagctg 14520

ctggccgcga acgacagcag ttactacctc tacgacaaga agagcaaagg cagcttcggt 14580

agcaagaaga cccggcgcga cgaaatcacc gatgtgacgg cagtgggcag ccaaatatcc 14640

agcggcggcg acctcaccct gctcagtggc ggcgaccaga cttaccaggg cgcgaagctg 14700

gaatcgggca acgacctggc catcgtcagc ggcggcgcgg tgaccttcga ggcggtaaag 14760

gacctgcacc aggaaagcca cgagaagagc aagggcgacc tggcgtggca gtcgtcgaag 14820

ggcaagggcc agaccgacga aaccgtgcgc cagagccaga tcgtggccca ggggaatctg 14880

gcgatcaagg ccgtggaagg gctgaagatc gacctcaagc acatcgacca gaagaccgtg 14940

agccagacca tcgacgcgat ggtgcaggcg gatccgcaac tggcctggct gaagcagatg 15000

gagcagcgcg gcgatgtgga ttggcggcgc gtgcaggaac tgcatgacag ctggaagtac 15060

agcaactccg ggctgggcgt cggcgcgcag ttggcgatag cgatcgttgt ggcctacttc 15120

acggcgggtg cggcgagtgc ggcattggga tcgatggcgg gagtgggggc gggctcagga 15180

agcatgatgg ctgctgccgg tagcactgca atggtccagg ccggtacagc agtaggaaca 15240

gctgccgccg gctgggcgaa tgcagctgga actgccgtgg ctatgggcat ggccagcaat 15300

ggagcgatca gcaccatcaa caaccgggga aacctggggg atgtcgtcaa ggacgtgacc 15360

tccagcgatg cgctgagggg ctatgtagtc gctggcacga ctgcggggct gactgccggc 15420

gtctacgaca aatggacctc gacccagacc ggcacctcga ccgctctacc gaacaccggg 15480

gccgtggcgc ccgccgcagg gttgggcacc tggcaaggcg tgggccagtt cacctcgaac 15540

cagttgctgc agaatggtac ttcggtgctg ttggaccggg cgctgggcgg caagggcagc 15600

ctgggcgatg cgttgcaaaa cagcctggca aatgcctttg cggcctacgg cttcaagctg 15660

attggcgaca ccacccatgg cgtgctggac gacggcagcc tcggcaagat cggcttgcac 15720

gccctgatgg gaggtctggc cgccgaagcg gtcggtggcg atttccgtac cggagccctg 15780

gctgcgggag tcaacgaggc gctggtggat agcctcgcca agcaatacgc cagcctgccc 15840

atcgatgaca agaagggcct gctgatcatg agttcgcagt tgatcggcgt gctggcggct 15900

tcgacgcagg gcgatgcgga cgccaagagc ttgcagacgg gggcctgggt ggcggggaat 15960

gccacccaac acaactacct cagtcattgg caggaggaga agaagcggca ggaggtcgat 16020

ggctgcaaag acaaacagct ctgcaaaacc ggaatagaag ccaaatgggc aattatttcg 16080

gcccagcagg atgtcggtat cgtcgtaggt gttggaggag gcatcggtct ttcgacagct 16140

gaaaccgcag tgggtgttta tgagctggtc aagaactgga gggaaaccta tgcagctctg 16200

gagcagttgg ccacttcgcc agagttccgg cagcaatttg gcgataacta cctgaagggg 16260

ctggaggagc gcgccgcatt cttgacccag gcatacgagg atgccggctg gcaaggttcg 16320

gtcacagctg gtgtcgaggg cggtaggttc gctgcggaac ttgttggcgt tctgacggca 16380

gtgaaaggtg gcgcgcagat aaccgccaag ctgccaacag cagccaagaa cctggtcaac 16440

gcgattgcgg agtcacctgt ttccggtagt atgagttcgc agcttggggc agtgggggat 16500

ttgggtcggc tgggtggggg aggtaaaggt tatgtcgata ttctttccca cgaagctaaa 16560

cagcatattt tgtatggcga caaacctggg agtggtggcc atttgtggcc ggggcaggca 16620

gggaagacag ttttccctca aaactggtcg gcagataaga tagttcacga ggttggtgat 16680

-continued

attgcgacgt cccctagtac caaatggtat gcccaaacag gaactggtgg ggtttataca 16740

agcaagggtg atcccgctaa atgggttgct tatgaggttc gtgatggagt tcgtatgcgc 16800

gttgtttatc agcccgctac aggaaaggtg atcacagcct tccccgacaa cgcacctatc 16860

ccaccttata agcccattaa atag 16884

<210> SEQ ID NO 61
<211> LENGTH: 201
<212> TYPE: RNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 61

augagucagg aaccccacgu acacggcccg aacugcaacc acgaccacga ucaucaucac 60

gaucauggcc auggucaugu ccaugguccg cacugcaacc acagccacga gccggugcgc 120

aauccgcuca aggccguagg ccgcaacgau cccugccccu gcggcagcga gaagaaauuc 180

aagaagugcc acggcgccug a 201

<210> SEQ ID NO 62
<211> LENGTH: 237
<212> TYPE: RNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 62

augaaaaaga ccguaacucu ugcccugcug cucgcugcca gccuuggccu ggccgcuugc 60

gacaagaaag aggaagacaa ggcagcggcc ccggcagcuc cggcuaccga gacccagccg 120

agcgcuccgg cuacuccccc ugccgagccc agcgccccgg cgccgucgag cgacacuccg 180

gcaaccccgc agacuccggc accgacuccg gagcaaccgc aacagaacca gcaauaa 237

<210> SEQ ID NO 63
<211> LENGTH: 315
<212> TYPE: RNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 63

augaaaaaga uuucccucgc uucuuccguc gucggcgcug cucugcucgg cguagccagu 60

gucggcgcgc augccgcgca gaaucccuuc gccgugcagg agcugagcag cggcuacagc 120

guggcugccg ccgagaaagc caaggaaggu uccugcggcg aggccaagug cggugccgac 180

aagggcaagc gcgaagccuc caaggccggu caugaaggca gcugcggugc ggaucgcaag 240

gccaaggaag guuccugcgg uggcgagaag aaggccggcg aaggcaacug cggcgccgac 300

aagaagaagu cguaa 315

<210> SEQ ID NO 64
<211> LENGTH: 468
<212> TYPE: RNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 64

auguccguuu ucgauucgcg ucaaaagacu uccgccagcc ugcucggugc cguacuggug 60

gggggaaugc ugcucggcgg uucggcguuc gccgucgagc cgcugggcca ggggcugcaa 120

guggcggcgg cgagcgccgg cgaaggcaag ugcggagaag gcaagugugg uagcggcggc 180

uccgcgaaga ccccggccaa ggccggcgcc gagggcaagu gcggggaggg caagugcggc 240

-continued

gacgccuccu uugcccgaac cgacaccgau cacgauggca aggucucgcg cgccgaguuc 300

cucgcggugg ccaaggaccg ugccggugag uucgacagca ucgauagcga ccaugacggc 360

uucauuuccg aagccgaggc cuacgaacac cugcgcaaga ccuacgaggc caacggcaag 420

ccgaugcccg ccgggcuguu cagcaagcug gagcaaggcc agcacuga 468

<210> SEQ ID NO 65
<211> LENGTH: 540
<212> TYPE: RNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 65

augcguuccc ugucccuccu ucuccuccuc ucgcuggcgu ccaccugcga ggccgcugcg 60

guauuccgcu gcgaagacgc cagcggccau gucagcuuca cccaacucgg uugccccgcc 120

gggcaggccg gcgagaccgu cguggcggac aacccgccgc cgggaggcag gagcgucacg 180

ccgauggccg agacgaagac gaaaaaggcg uccaucggcc ggaaaagcgu gccgcucgcg 240

gugaucggag aaagagaaga ucgcugcggc agacgccugg acgagaagga acgccgcaag 300

gcgaucgugg agcagcggau aauggcggga augacccgcu ccgaugugga gcgggcgcug 360

ggcaagccgg accgggucag cgggaacaau gcggaggugc guuaucagua caaggccgac 420

aagcgacggg gagcgagaag cgugagcuuc gaucaggagg gaugugugaa gggaagagaa 480

gguaccgggu ggagcgaguc gaucccggga gcuaaggccg ggccguccuc auaccgauga 540

<210> SEQ ID NO 66
<211> LENGTH: 915
<212> TYPE: RNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 66

augagccaac ccagcgaaaa ccguuugauc accucggcgc gcuacgcgcu cugccuguug 60

accgccagcg gcgugcugcu cagcggcugc gccagcagcg gcgucggcuc ggucgcccag 120

accacccgcg cggaauacua cccguccugc uacgagccgg ugucgcaccu gcgcagcacc 180

gauaacgcag ugcgcaauuc ggccaucacc ggcgccauua ccggcggccu ccugggcggc 240

cuggccggcg gccuggccag cgacgagaac cgcggccgca augccgcccu cgcugccgca 300

ggcggcgccc uggccggcgg cgcggcgggc uacuacaugg agaagcagaa gcagaucagc 360

gaugaccgcg cgcgcaucgg cuccuacggu accgacgucg accgcagcac cgucgagauc 420

aaccguagcg uggccuacgc caagucggcg caaagcugcu accagagcca guucaaggcu 480

cugcucgacg gucgcaagaa caagucgauc aacgaagccg aagggcgcaa gcgccuggcc 540

gagaucguca gcggccugca ggagaccaac gccuugcugg ucgccgccaa cggccgugcc 600

ggcgagaaca ucagcaacua cacccaggcc uacgagaaag accugcagca ggucggcgua 660

ccgcgcgccg aggugaccaa ggucgccgag gccgagaacc gcgccagcac uacgaaaggc 720

ggcagcaagc ccaagaccgg cagcaauccc aaggugccga aggaagcggu cgccaccgag 780

cagaccaucc gcaaggccca ggacgcgcaa agcgaaggca acaaggugge cucccagggc 840

cagggcauga uccgggaagu cugcaacagc ccggacaugg gcgacugggc gccgccgagc 900

ugcgccaagg ccuga 915

<210> SEQ ID NO 67

-continued

<211> LENGTH: 930
<212> TYPE: RNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 67

auggcuggca agaagaagag cgaaaaagag uccaguugga ucggcgagau cgagaaauac 60

ucgcggcaga ucuggcuggc uggucugggg gccuacucga aggucagcaa ggacggcagc 120

aagcuguucg agaccuuggu gaaagacggc gagaaggcug aaaaagaagc gaaguccgau 180

guggacgcgc aggucggugc ggcgaaggcu uccgcccgcu cugcgaagag caaggucgac 240

gagguucggg accgugcgcu cggcaagugg agcgagcucg aggaagcuuu cgacaagcgc 300

cugaacagcg ccaucucgcg ucucggcgug ccgagccgca acgaggugaa ggagcugcac 360

agcaaggucg auacgcugac caagcagauc gagaaacuca ccggcgucag cgucaagccg 420

gcggcgaagg cagcggccaa gccugcggcg aaaccggcug ccaagcccgc ggcgaaaacc 480

gcagcggcca agccggcagc uaaaccggca gccaaggccg ccgccaagcc ugcggcgaaa 540

cccgcggcga aaaaaaccgc ggcgaaaacc gcggccgcca agccggcagc caagcccgcc 600

gccaaaccga cugcgaaggc cgcagcgaaa ccggcgacca agccggcagc caaggccgcg 660

gcgaagccug cugcgaaacc ugccgcagcc aagccugccg cgaagccggc agccaagccg 720

gccgcugcga ccgccgccaa gcccgcggcg aaaccugccg ccaagccggc ugcgaaaaag 780

ccugcggcga agaagccggc agccaagccc gccgcggcga aaccggccgc ucccgccgcg 840

ucuucgagcg cgcccgcugc ccccgccgcc acaccggcug ccagcgcucc ggcagcgaac 900

gcuccggcga cgccgagcag ccagggcuga 930

<210> SEQ ID NO 68
<211> LENGTH: 1023
<212> TYPE: RNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 68

augaaagcga cuaugguccu gaccccgcug gcccuggcaa uggcugcagu gcugucggua 60

ucggccuacg ccggaaacga agguggcugg cacccgccga aacccaaccc gcagucgaac 120

aacaagggcg gagccacggc ccugguggug gauacgcagc agaacuacaa caacaagguc 180

agcaacuucg gcacgcugaa caaugccucg gugagcggcu cgaucaagga ugccucgggc 240

aacgucgggg ucaacgucgc cgccggcgac aacaaccagc aggccaacgc cgccgcgcug 300

gccagcgccg acgccagcuu cguguucggc accgcgaccg ccagcaccag cgugcugcag 360

agcggcuacg gcaauacgcu gaacaacuac uccaacccca acaccgcauc gcugagcaac 420

ucggccaaca acgucucggg caaccugggc gugaacgucg ccgccggcaa cuucaaccag 480

cagaagaacg accuggccgc cgccgucucc aacggccagu acagcacugc cgguagcgcc 540

gcgucgcaga ccuccaccgg caacaccacc gucaacagcg ccaacuacgc cuauggcggc 600

accuacgugu cgcugaagcu gaacgccgac ggcagcuaca agggcaccuc cgaccagauc 660

ggcgacgucu accucgacac cugggaaggc cagacccauc cgggcggcag caauaccggc 720

cacaucgacg uggacagcca ggcccagggc gccaaggacc ugaaccacga cggcggcgcg 780

uucgccuuca aggaaaaggg cgacgucgac cugaaaggca cggugaccgg cuucaucccg 840

gcgaucgucg gcuucaagac cccggucacc aacaacgcca gccugagcaa cucguugcag 900

-continued

aacgucucgg gcaacgucgg ggugaacauc gccgccggug gcggcaacca gcagagcaac 960

ucccugucca ucgccgccgg uugcagcagc ugcccggccg guggcgagag ccuuggcuuc 1020

uga 1023

<210> SEQ ID NO 69
<211> LENGTH: 1044
<212> TYPE: RNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 69

augaagcaac aguucgaacg cucgccuucc gagaguuauu ucuggcccgu cguccuggcg 60

gugguccugc acguucugau cuucgccaug cuguucguca gcugggcguu ugcuccggag 120

cuuccucccu ccaagccgau cgugcaggcc acgcucuacc agcucaaguc gaagagccag 180

gcgacgacac agaccaacca gaagaucgcu ggcgaggcga agaagaccgc cuccaagcaa 240

uacgaagucg agcagcucga acagaagaag cucgagcagc agaaacucga gcaacaaaag 300

cuggaacagc agcaggucgc ugcugcgaaa gcggcggaac aaaagaaggc ugacgaggcu 360

cgaaaggccg aggcccagaa agccgccgag gcgaaaaagg ccgaugaagc caagaaagcu 420

gccgaggcca aggccgccga acagaagaag caggcugaca uagccaagaa gcgcgccgag 480

gacgaggcca agaaaaaggc cgcugaggac gccaagaaaa aggcagccga ggacgcgaag 540

aagaaagcgg ccgaggaggc caagaagaag gcugcugcgg aagcggcgaa gaagaaagcc 600

gccgucgagg ccgccaagaa aaaggccgcc gccgcugccg cggcagcccg caaggcugcc 660

gaggacaaga aggcgcgggc auuggccgag uugcuuucgg auacgaccga gcgccagcag 720

gcccuggccg acgagguggg cagcgagguc accggcaguc ucgacgaccu gaucgucaac 780

cuggugagcc agcaguggcg gcguccucca ucggcgcgua auggaaugag cguagaagua 840

cugaucgaaa ugcugccgga cgguaccauc accaaugcca gcgucagccg uucgaguggc 900

gacaagccuu ucgacaguuc ggcgguggcg gcggugcgca acgucggccg uauucccgag 960

augcagcaau ugccgcgggc uaccuucgac agccuguauc gucagcgccg caucaucuuu 1020

aaaccggagg auuugagucu guga 1044

<210> SEQ ID NO 70
<211> LENGTH: 1059
<212> TYPE: RNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 70

augucggcca acaagaagcc cgucaccacc cccuugcacc uguugcagca acuuucccac 60

agccuugucg agcaccugga aggugcgugc aaacaagcgc uggucgauuc ggaaaagcuc 120

cuggccaaac uugaaaagca acguggcaaa gcccaggaaa agcugcacaa ggcucgcacc 180

aagcugcagg augcugccaa ggccggcaag accaaggcac aggccaaggc gcgcgagacc 240

aucagcgacc uggaagaggc guuggauacc cugaaggccc ggcaggcgga cacccguacc 300

uacaucgucg gccucaagcg ugacguacag gaaagccuca agcuggcgca gggugucggc 360

aaggugaagg aagcugcugg caaggcucug gagagccgca aggcgaaacc cgcgaccaaa 420

ccugcugcga aggcggcagc caagccugcg gugaaaaccg uagcggcgaa gccugcggcc 480

aagccggcug cgaagccugc ugcgaaaccg gcggccaagc cugcggcgaa aaccgcggca 540

-continued

gcgaagcccg cagccaagcc gacggcgaag ccugcugcga aaccggcggc caagcccgcg 600

gcgaaaaccg cagccgcgaa gcccgcagcc aagccggcgg cgaagccugu ggcgaaaccg 660

gcggccaagc cugcggcgaa aaccgcagcc gcgaagcccg ccgccaagcc ggcagcgaag 720

ccugucgcga aaccgacggc caagcccgcg gcgaaaaccg cagccgcgaa gcccgcagcc 780

aagccagcug cgaagccugc ggcgaaaccg gcggccaagc cuguggcgaa auccgcggcc 840

gcgaagccug cagccaagcc ggcugcgaag ccugcggcga aaccggcggc caagccugcg 900

gcgaaacccg uagccgcgaa accugccgca accaagcccg ccaccgcucc ugcugcgaag 960

ccugcggcga cucccagcgc cccggcagcc gccuccagcg cugcuucggc aacgccugcc 1020

gcgggcagca acggcgccgc cccgaccagc gccuccuaa 1059

<210> SEQ ID NO 71
<211> LENGTH: 1263
<212> TYPE: RNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 71

augugggguc uuacgaugaa guuugcgagc cugauucuga ugcuucucuu ugccacggug 60

gcgagggcug aggauuacua cuggaaaauu cagucacugc cugaacgcuu uucuucgccc 120

ucggcagcuu gcgcggcgug ggccaaagcc acgggacgcc cuggggaguu caccuucacc 180

gggucuauga aagcccguga ccagaccucg uuuuggugcg aguucacgaa caacgaaacc 240

ggcaagacug cugccgggua ugguccugcc ggacgcuaug gcgauagcug ucccgagggg 300

acggaauacg auaaggcgac cgggguuugu aagucgccuc cgcaagaaug caaggaaggc 360

gaacuguucc cggccaaagg cccggacucu cccgugguua ccucgggagg ccguaacuau 420

gucggugacg gcggcgcccc gaccgccugc uaucaaagcu gugaguaugg cggcaauccc 480

agcccggcca guugcuaucu ggucaaaggc uccaccacga ccggcuucug caauuacauc 540

cucaagggca ccggacagaa uugcggugcc gauuccuaca ccuucuccca gaccggcgau 600

ucgcugaacc cgcccgacac uccgaacacc gauccuuccg acccgaacga ccccggcugc 660

ccgcccggcu ggucgugguc gggaacuacc ugcgucaagg ccccgaccga ucccacggau 720

ccaaccgacc cgaccacgcc gggcagugac ggcggcggcg auggcaaugg cgguggaaac 780

aauaacggcg gcggcaauga cggcggcacc ggcaauggcg gcgacggcag cgggggaggg 840

gacggcaacg gcgggggcga ugguagcggc gacggugacg gcagcggcac gggcggcgau 900

ggcaacggca ccugcgaccc ggcgaaagag aacugcucca ccggccccga aggccccggc 960

ggcgaacuca aggagcccac gcccggcacc ugggaugacg ccaucgccac cugggaaaag 1020

aaggucgagg acgccaagca agaacucaag accaagguga aggccaacgu cgaucagaug 1080

aagggcgccu ucgaccucaa ccuggcggaa ggcggcgggc aacugcccug cgaguccaug 1140

accauuuggg gcaaguccua cucccucugu aucuccgacu acgccggcca acucuccagc 1200

cugcgcgugg cgcugcugcu gauggccgcg cugaucgccg cccucauucu gcugaaggac 1260

uga 1263

<210> SEQ ID NO 72
<211> LENGTH: 1284
<212> TYPE: RNA
<213> ORGANISM: Pseudomonas aeruginosa

-continued

<400> SEQUENCE: 72

auggccgucg ccccuggugu guuguugccg ccgacgccug auguaaagcc caaggccgcu 60

gcgccgaaga gccagcagaa aacgccugag cccaguaacg acaagacuuc cagcuucucc 120

gacauguaug ccaaggagac cgcgaagaag cccgccgagc gcgccgacgg ucccgcgaag 180

gguucgcggg acaagccacg ggacgccggc aaggacgccg ccgaagcgca gccgacggau 240

gccgucaggc agccggccgu ugccgaagac ggcaagccuu ugccggccga cggccaggcc 300

aaggccgacg gcgaagauaa agucgaaacg ccggucgauc cgcugcaauu gcucggccuc 360

ggcggugccg uaccguugcu cgacgagaau acccaggcga cuuugcugcc accggccgug 420

ccgacggcca gcagugcucc ggccagccuu accgaagcca gcagcgaccc gacccugguc 480

aagcucaacg gcgugccggc ggugaacaug gcccuggagc agggcgccca ggacgccgcg 540

cagacggcga aaggcgggcc ggcgaagagc gccgaucccc gccaggcgaa ccucggcgau 600

gcccuugccg gccugaccuc ggauuccuug accaaggccg ucgacggcaa ggcgcucgag 660

gcccaguugc agcagaccgc cgagccggcc gucgccagcg ccgccuccga gagccugcug 720

gagagcaagg cggaaccccg cggugaaccu uucgcggcca agcucaacgg gcugacccag 780

gccauggcgc aacaggcccu gaccaaccgu ccggugaacg gcacggugcc cggccagccg 840

guggcgaugc agcagaacgg cuggagcgag gcgguggugg accgggugau guggaugucc 900

agccagaacc ugaagucggc ggagauccag cucgaccccg ccgagcuggg acgccuggac 960

gugcgcaucc acaugaccgc cgaccagacc caggugaccu ucgccagucc caacgccggc 1020

guucgcgacg cccuggaaag ccagaugcac cggcugcgcg acauguucag ccagcagggc 1080

augaaccagc ucgacgugaa cgucuccgac cagucgcugg cgcggggcug gcagggccag 1140

cagcagggcg agggcggauc ggcgcgcgga cgcggcuugg ccggcgaggc cucgggcgau 1200

gaggaaaccc ucgccggagu cagcgagauc cgcagccggc cgggugcguc ggcggcgcgc 1260

ggucuggucg acuacuacgc cuga 1284

<210> SEQ ID NO 73
<211> LENGTH: 1287
<212> TYPE: RNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 73

augcuccgcc uccuuccucu ccugcuaucc cucgccuguc ucgcuccggc cuucgccgac 60

gagcgcgccg acacccaacg ccagcuggaa cagacgcaga aggacaucgg cgagcugaag 120

aagcugcugg acggcaucca gcaggaaaag agcggcgugc agaagcagcu gaaguccacc 180

gagaccgaga ugggcgaccu ggaaaaacag aucaaggccc ugcaggacga gcuggacaag 240

agcgaagccg agcugaaacg gcuggauggg gagaaaaaaa aacuccagga cgcgcgcauu 300

gagcagcagc gccuccucgc cauccaggcc cgcgcggccu accagagugg acgcgaggaa 360

uaccugaagc ugcugcugaa ccaggaacac ccggaaaaau ucagccgcac ccucaccuac 420

uacgacuaca ucaacaaagc ccgucucgaa cagcucgcca gcuucaacga aacccuccgc 480

cagcuggcca acgucgagca ggacaucucu gcgcagaaag ccgaacaacu gagcaagcaa 540

ggcgagcugg acagccgccg cgaggcgcug gcagcgaccc gcaaggagcg ccagcaagcc 600

cuggccaagc ugaacagcga cuaccgcgaa cgcgaccaga agcucaaguc ccgccaacag 660

-continued

gaccaggccg agcuggccaa gguacugcgg accaucgagg aaacccuggc ccgccaggcc 720

cgcgaagccg ccgccgcggc ggagcgcgag cgccagcgcg cgcuggccgc cgaacgcgag 780

cgugcgcgcc agcagcaggc cgcccccgga cgagucacca gcccgccgcg cgaaccugcg 840

ccgggcccgc uggucucaag cacuggcgcg gucuacggcg gcgcguucgg cucggcccgc 900

ggcaagcugc cguggccggu gaauggccgc gucguggcgc gcuucggcag ccagcgcggc 960

gacgauccgc gggcgaaaug ggacggcgua cugauuucgg cgagcgccgg cagcaccguc 1020

cgcgcggugc acggcggacg cgugguauuc gccgacuggu ugcgcggagc cggccuguug 1080

gucauccucg accacggugg cggcuaccuc agccuuuaug gccauaauca aagccugcug 1140

aaagacgccg gcgacaccgu gaaggccgga gacccgaucg ccaccguugg aaccagcggc 1200

ggccagagua gcccggccgu guacuucgcc auucgccauc agggccgccc ggcggacccu 1260

acuaccuggu gccgcgcaca gggauag 1287

<210> SEQ ID NO 74
<211> LENGTH: 1707
<212> TYPE: RNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 74

augcaaagac ugucgcguau cggccgcaac acccucgccg ucuccguuuc caccuugcuc 60

cucagcgccu gcaaccaggg cgacgaugcg ccgaagccug cggcagucgc gccgcaaccg 120

gccgcaccga gcauggcugc acugagcauc ccgcuaugcc ucaacggcca gugcgcggug 180

aucgaccagg acgccaagcu gcucgugccg uucgacaacg acuacgacaa uaucgucgcc 240

agcgccuacc agggcacccu gauggcggcg cgcgaggagc gcuggaaccu gauccaggcg 300

aaggacggca agguguugcg cgacgauauc ggcgaagccc ugucgcugcu cacccccaac 360

cucuauggcu ucguccgcga uggcaaguac ggcguggucg acggccaggg caaggaaguc 420

caggcgccgc guuucgacga caucuacccc aacagugcca acgaauucau caucuacgag 480

aucgauggca agcgcggcau ccucgaugcc aagggcaagc agcucaccga ggcgcucuac 540

gacaccaccc uggucaacgg cagcgucgcc gaacacggug gcuugaucag cgccgagcgu 600

ggcgaggaga aguggaucau caaccucgcu accggcgaac agaaggccgu ggccuacgag 660

agccugggcg accuccacga cggcgugaug agcgccagcg ucaucggcaa gggcucccaa 720

cugguggaug ccaagggcga cgguggucggu gacggcaaga gcuacgauua ccugggcacc 780

ccggccaacg gccuggucgc guuccgcgag aaguacgaca gccccugugg cuaccucgac 840

uaccagggca agguggcgau cgccgcccag uucgccgguu gcggcgccuu cggcaagcag 900

ggcgggcugg cccagcagcg cauggaagau ggcucgucgg gcaaguacgg ccugaucgau 960

cgcagcggcg ccuggaaggu gcagccgcag uacgauucgg ccgacagcgc cggccucacc 1020

gcgcuuggcu acaccgucga cgugcccggc cuggcugccg ucggcgugag caccggccug 1080

uucagcgccg acuucggcau cuucaaccuc gacgaaggca gcgagugggu gaagccgggu 1140

uaugcgcaga ucggcgcgcu gggcaacgac cuguucgucg uggcgaagaa gggcgggccg 1200

cagaagaccg ucagcuucau ggguucggaa agccaggugc cgguggugggg ccugauggac 1260

cgcagcggca agaugcugcu ggagccggac gaacugauca gcauccaguc ugcuuaugac 1320

ggucguuucc uggaaggucu cgacgguaug gacaacgcug cccacaccgu guugcucgau 1380

-continued

cgccagggac gcacgcuggu uccagcgcuc uggcagaagc uggaggugaa uccgcagcag 1440

gguuacaucc ugggcuacga agucagcggc acuggcgacg aggcgacgga aaccuugcgc 1500

gcacuguacg accugaacgg caagccgcgc uucaccgugg ccaccaccga uugcggcgcc 1560

gaacaguugc ucgacggcaa uggcaaggcg aucuggccgc aggacccgac cccguauugc 1620

cagucggacg acgagcagga cgacgaaggc gagccggagc aggagccggc gcccgucgaa 1680

gagagcgagg aaaccagcga gagcuga 1707

<210> SEQ ID NO 75
<211> LENGTH: 1740
<212> TYPE: RNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 75

augcuucgcc ccgccagguc ucucucgcuc ugcuccgccc uggucauccu gcucgccgcc 60

uguggcgagg gcgaaccgcu gcucccggcc gaugcgcgcc ugccugacgg cgcgcgcuau 120

cgcggcgagc ugguggacgg gcgccuggaa ggccagggcc ggcuggacua cgacaacggc 180

gccugguacg ccggccgcuu cgagcauggc cugcugcacg gccauggcac cuggcagggc 240

gccgacggca gccgcuacag cgguggcuuc gcggccggcc uguucgacgg ucagggacgc 300

cuggcgaugg ccgauggcag cgucuaccag ggcgguuucc gccagggccu guucgauggc 360

gaaggcagcc uggaacaaca gggcacucgc uaccgcggcg guuuccgcaa gggccuguac 420

agcggccagg gcacgcugga cggcagcgau ggcagccgcu accagggcag cuuccgccag 480

ggccgccugg aaggcgaagg cagcuucagc gacagccagg gcaaccagua cgccgguacc 540

uuccgcgacg ggcaacugaa cggcaagggg cgcuggagcg ggcccgaugg cgaccgcuac 600

gucggccagu ucaaggacaa ccaguuccau ggccaggggc gcuacgaaag cgccagcggc 660

gaugucugga ucggccgcuu cagcgaaggc gcgcugaacg gccccggcga gcuucucggc 720

gccgacggca gccgcuaccg cggcgguuuc caguucuggc gcuuccaugg ccagggccug 780

cucgaacaac uggacggcac ccgcuacgaa ggcggcuucg ccgccggcgc cuaugccggc 840

caaggcaccc uggaccgcgc cgacggcagc cgugagcagg gacucugggc cgacggcaag 900

cgcauccgcg acgccgccgg caaggcccug cccgacacuc uggaagucgg ccuguuggcc 960

cagggucgcc ugcucgacga agaacugcgc aagaucccgg ccucgacgcc ggccagcgaa 1020

cucuaugccc ugagccuggg cggcgauggc cgccagggcg uguuccugcg cgaggccgau 1080

uacgccggcg accugcucgg ccagcguuuc gccgcucgug gcgugauucg ccuggucaac 1140

caccgcgacc acuucggcga ccgcccgcug gcuacccggg aaagccuguc ccgcgccgug 1200

cgcacccugg ccgaacgcag cgggccggaa gaccuggucu ucaucuaccu gaccagccac 1260

ggcuccagcg accaccaguu ggcccuggac augcccggcc ugaaccucgg cgaccugccg 1320

gccgcggaac uggccgaacu gcucgcgccg cugcgccagc gcgacaaggu gcugguggua 1380

ucggccugcu acagcggggg cuucaucccg ccgcugaaag acgaacguac ccugauccug 1440

accgccgcgc gugccgaccg ggucucguuc ggcuguuccg acgacgccga cuucaccuau 1500

uucggccgcg ccuugcuggc caaugcgcug aaccgcaccg acgaucuguc caaagcguuc 1560

gaacuggcga aagaggaagu gcgucaaagg gagaaggagg aagguuucga agcuucggaa 1620

ccgcaagccu gguuaccgga acgcgugcuc gcgcacuggc ggacgcugcg ggggcagcaa 1680

-continued

```
gccgagcgcg cgcucgcguc ccgggaagga aaaaccggcg agggcgcggc gggcaaauag   1740


<210> SEQ ID NO 76
<211> LENGTH: 1866
<212> TYPE: RNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 76

augcugcaga acaucaggga uaauucccag ggcuggaucg ccaagaccau cauuggcgug     60

aucaucguuc uccugucgcu gaccggcuuc gacgcgauca uccgggccac cgaccacucc    120

aacguggccg ccaaggucaa cggcgacgau aucagucuca augaagucca acaggccgug    180

gacaugcagc gucgccagcu gcugcaacgc cugggcaagg auuucgaucc auccaugcug    240

gaugacaagc ugcucaagga agcggcccug aaggggcuga ucgagcguac ccugcugcuc    300

caggccgcca aggacgacaa guucgccuuc uccgaccagg cgcuggacca guugauccug    360

caaacucccg aguuccaggu cgacggcaag uucaacgcgg aucgcuucga ccaggucauc    420

cgccagauga acuacagccg caugcaguuc cgccagaugc ucggccagga aaugcucauc    480

ggccagcuuc gcgccggccu ggcgggcacc gguuucguca ccgacaacga auugcagucc    540

uucgcucgcc ucgagaagca gacccgcgac uucgccaccc uggcgaucaa ggccgacgcc    600

uccaagagca gcgugagcga cgacgaggug aaggccuucu acgaaggcca caagagcgag    660

uucaugacuc ccgagcaggu ggucgucgaa uacguggagc ugaagaaguc cuccuucuuc    720

gaccagguca aggugaagca ggaagaccuc gaggcgcugu accagaagga aaucgccaac    780

cuuuccgagc agcgcgaugc cgcccacauc cugaucgagg ugaacgacaa ggucggcgac    840

gagcaggcca aggcgaagau cgacgagauc aaggcucgcc uggccaaggg cgaggauuuc    900

gccgcgcugg ccaaggaguu cucccaggau aucggcucgg ccgccaccgg cggcgaccug    960

ggcuacgccg gucgcggcgu guacgacccc gcguucgagg aggcgcugua ugcgcugaag   1020

caaggugagg uauccgcccc ggugaagacu ccguacggcu accaccugau caagcugcug   1080

ggcgugcagg cgccggaagu accgagccug gaaagccuca agccgaagcu cgaggacgaa   1140

cugaagaaac agauggucga gcagcgcuuc gucgaggcua ccaaggaccu ggaaagcucc   1200

gccuacgaag ccgccgaccu gagccagccg gcgcaggaaa ugggccugaa gguccagacc   1260

agccagccgu ucggacguuc gggggcgac ggcaucgcug ccaaccgcca gaucgugcag   1320

accgcguuca gcgccgaggu gcuggaagaa gccgccaaca guggcgccau cgagcuggau   1380

ccggacaccg ugguggugcu gcgggucaag gaacacaaca agccgaagga gcaaccgcug   1440

gagcaggucg cggcgaacau ccgcgagcgc cuggccgccg aaaaggccgc cgaggaggcg   1500

cagaagcgug gcgaggcccu gaucgcagag cugcgugaag gccguaccuc uuccgcagcg   1560

ggugagucgu ggaaagugg u cgaggcggcc ucccgcggcc acgaaggcgu cgauccgaaa   1620

cugcuccagg cgguguuccg caugcagcgu ccggaggcca aggacaagcc uucguucucu   1680

ggcgugaccc uggccaaugg cgauuacgug gugauccgcc ugaauggcgu cagcgagccg   1740

gaggaggcua ucuccgacga cgagaaggcc auguaccgcc gcuuccuggc uucgcgcagc   1800

ggacaggcag acuucgccgc cuuccgccgu caguugcagg acaaggcgga agucgagaaa   1860

uacuga                                                              1866


<210> SEQ ID NO 77
```

-continued

```
<211> LENGTH: 2067
<212> TYPE: RNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 77

auggauauga cgucgcugau gccccuccug cugggagugg gccuggucgu ucugcugguc      60

gugggccugc uggcccuguu caaggccuuc uacaucaagg ucccgcaagg caccgcgcug     120

aucgucaacg acaugucguc gacgcccaag gugcauuuca ccggugcgcu ggucuauccg     180

gugauccacc ugaaggaguu caugcgcauc ucgcugauca cccuggaggu cgaccggcgc     240

ggcaaggacg gccugaucug ccgcgacaac augcgcgcgg acaucaccgu ugccuucuac     300

cugcggguca acgagaccca ggacgacgug cucaaggugg ccaaggccau cggcgucgac     360

cgugcuuccg accguucggc ggugaacgag cuguucaaug ccaaguucuc cgaggcgcug     420

aagaccgucg gcaagcaguu cgacuucguc cagcuguucg agaaucgcca ggacuuccgu     480

gaccgcauca ucgaggugau cggcaacgac cugaacggcu acguccugga agacgucgcc     540

aucgacuacc uggagcagac cgcgaagaac ucgcuggacc cgagcaacau ccuugaugcc     600

gagggcaucc gcaagaucac cgagcugacc gccacccaga acgucaucac caacgaacug     660

gagcgcaacg aagagcuggc gaucaagaag aagaacgucg agacccgcga ggcggcccug     720

gcccuggagc gccagcaggc ugacgccgag gcccggcaga agcgcgagau cgagaccauc     780

cgugcccgcg aggaagcgga aaccgcgcgg gucaaggaag aggagcggcu gaaggccgag     840

caggcgcgga uccaggcgca gcaggaaauc gacgugcgca ccgagaacca ccagcgcgag     900

gucgaggugg cgcagcagaa ccgccagcgc gcggugguca ucgaggugga gaaggucacc     960

cgcgccaagg accuggagau cgucgcccgc gagcgugagg uggagcugca gaagaucgag    1020

aaggaaaagg cgcuggaaga gcagcgcaag aacauugcca augugauucg cgagcgcguc    1080

gcgguggaaa agaccguggc ccaagaggag gagcggauca aggaggugcg cgagguuucc    1140

gaggccgagc gggucaagca ggugauacug cugcaggccc aggcggaagc cgagcaggag    1200

cugguacgcc aggucaagca ggcggaagcc gacgaggccc gcuccaagca caaggcggug    1260

gaaaucaaca ccauggcgca ggccgagcug gaggcggcgu cgaagcaggc cgaggcgaag    1320

aagcgucugg ccgagggcau cgaggccgag cgcgcagcgc cgggccuggc cgaugcgcgg    1380

gugcuggaag ucaccgccgc ggcgaaggaa aaggauggcu uggcagcggc gcggguacgu    1440

gccgaacaac ugaucgccga agccaggggc gacgaagagc gcggccuggc cgacgcccgg    1500

gugcucgagg cgcaggccgc ggccaaggag aaggacggcc uggccgaagc caaggugcug    1560

gccgagaagc ucggcgccca ggcgcgcggc gaggagcagc ucggcgcggc caaggccaag    1620

gccaccaagg accagggcag cgcggaagcg gaaguacugc ugcagcgccu gaaugccgag    1680

gccgaggggc uuggcaagaa guucggcgcc cuggaugccc ucagcgacag cgcucgccag    1740

cacgaagagu uccgcaugca gcuggagaag agcuucgagg aggccauggc ggccaucgcc    1800

gcgaacaagg acaucgccaa ggaccaggcc gaggugcucg ccaccgcgcu gggcaaggcg    1860

aacaucgaga ucgucggcgg cgagggcgac uucuucaacu ccuucgccaa gucgcugucg    1920

gugggcaagg ccaucgaagg uguggucggc aagagcccgg uggugcagga cguccucgcc    1980

cgccugcuca acggccgugg cgcagccgcu gcggugaugc cggaacgcaa gagcggccac    2040

gagaacgagc cggcggcgga agucuga                                        2067
```

-continued

<210> SEQ ID NO 78
<211> LENGTH: 2229
<212> TYPE: RNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 78

auguaccccc aauuccgucg cggccaucuc gccgcugccg uccuuuucgc uucaucgagc 60

cugcugggcg ggcaggcccu ggccgaggac gagcgccugg aagaacugga cgaacgcgcc 120

gaaucggugg uccagcuggg ugacgaggug gugcugggca ccgccgaaca ggagcucaag 180

caggcaccgg ggguauccau caucaccgcc gaggacauca ggaagcgccc gccggugaac 240

gaucucuccg agaucauccg caccaugccc ggggucaacc ucaccggcaa caguuccagc 300

ggccagcgcg gcaacaaccg gcagaucgac auccgcggca uggggccgga gaacacccug 360

auccuggucg acggcaaacc ggucagcucg cgcaacucgg ugcgcuacgg cuggcgcggc 420

gaacgcgaca cccgcggcga cagcaacugg gugccgccgg aggaggucga gcgcaucgag 480

guccuccgug ggcccgcggc ggcacgcuac gguuccggcg cggcgggcgg gguagucaac 540

aucaucacca agcgcccgac cgaucguuug cgugguucca ugacggyguu caccaacauu 600

ccggaaagcu ccaaggaugg cgccacgcgc cgcgccaacu ucagccuuag cgggccgcug 660

accgaagccu ugagcuuccg cgcguacggc agcgcgaaca agaccgauuc ggacgauacc 720

gacaucaacc ucggacauac cgucaacccg agccguaccg uggccggacg cgaaggggua 780

cgcaaucgcg aucucagcgg gaugcugucg uggcagguga cccccgacca ggucgucgau 840

uucgaagcgg gcuucagccg acagggcaau aucuaugccg gcgauaccca gaacaacaac 900

ggcaccgcca auacccaggg acucgccgac gacggugcgg agaccaaccg cauguaucgc 960

gagaacuacg ccaucaccca caacgggacc uggucguucg guacuuccag guucgucgcc 1020

caguacgacu ccacccgcaa caaccgucug gaggaggggc uggccgguuc cgucgagggg 1080

cagaucggcg ccgaccguuc guucagcgcc agcaagcugg agaacuaucg ccucagcggc 1140

gaacucaacc uuccguugca ugcguuguuc gagcaggugc ugacgguggg cgcggagugg 1200

aacaaggaaa cccucaacga cccguccucg cucaagcagg gcuucguggg aagcgauagc 1260

uugccgggga cccccgcggc cggcucgcga agcccgaaaa gcaaggcgga gauccgcgcg 1320

cuguacgugg aagacaauau cgaacugcgc cccggcacca ugcucacccc cgggcugcgc 1380

cuggacgauc acagcgacuu cggccugaac uggagcccga gccugaacgc uucccaaacg 1440

cucggcgaau acuucacggu caaggccggu aucgcacggg ccuucaaggc gcccaaccug 1500

uaccagagca acccgaacua ccugcucuau acccguggca acgguugccc gauccagacu 1560

agcagcggcg gcugcuaccu ggucggcaac gagaaccugg acgccgagac cagcguaaac 1620

aaggaacugg gcaucgaguu ccggcgcgau ggcugggucg ccgggcucac cuacuuccgc 1680

aacgacuaca agaacaagau cgucgcgccg cuggauguca ugggacagac cgggaccggc 1740

aacaacaucc ugcaauggag caacgcgaag aaagcagugg ucgagggccu ggaaggcaac 1800

cugcuggucc cccugcacga ggaccugagc uggagcacca accugaccua uaugcugcaa 1860

uccaaggaca aggacaccgg caacccgcuu ucggugaucc ccgaguacac ccugaacucg 1920

acccuggacu ggcaggccag cgagcgucuu uccacccaac ugaccagcac caucuacggc 1980

cgccaggagc cgccgaagca uggcaccagc cgcaacacgc cgguggucuc gcgaaaagag 2040

-continued

gugggguaccu auggcaucug gggcgucagc gccggcuaca ccuucagcga gaaccugagc 2100

guacggggcg ggguaagcaa ccucuucgac aagcgccugu accgccaggg caacuccuuc 2160

gacgccggcg cggcaaccua caacgagccg ggucgcgccu acuacguuuc gaugaccacc 2220

ucguucuga 2229

<210> SEQ ID NO 79
<211> LENGTH: 2241
<212> TYPE: RNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 79

auguccucac gcgcccuucc cgccguuccc uuccugcugc uguccaguug ccugcucgcc 60

aacgccguac acgccgccgg ccagggcgac ggcuccguca ucgagcuggg cgagcagacc 120

guggucgcca ccgcccagga ggaaaccaag caggcgccgg ggguuuccau caucaccgcc 180

gaggacaucg ccaagcgacc gccgagcaac gaccugucgc agaucauccg gaccaugccg 240

ggggucaacc ugaccggcaa cagcuccagc ggccagcgug gaaacaaccg gcagaucgac 300

auccgcggca ugggcccgga gaacacccug auccuggucg acggcaagcc ggucagcucg 360

cgcaacucgg ugcgcuacgg cuggcgcggc gagcgcgaca gccgcggcga caccaacugg 420

gugccggccg accaggucga gcgcaucgaa gugauccgcg gcccggcggc ggcgcgcuac 480

ggcaacggcg cggcgggcgg cguggugaac aucaucacca agcaggccgg cgcggaaacc 540

cacgguaauc ucagcgucua cagcaauuuc ccgcaacaca aggccgaagg cgccagcgaa 600

cggaugagcu ucggucucaa cgggccgcuc acggaaaacc ucagcuaccg cgucuacggc 660

aacaucgcca agaccgacuc ggacgacugg gacaucaacg ccggccacga auccaaccgu 720

accggcaagc aggccggcac ccucccccgcc ggucgcgaag gcgugcgcaa caaggacauc 780

gacgggcugc ucagcuggcg ccugacgccc gagcagaccc ucgaguucga ggccggcuuc 840

agccgccagg gcaacaucua caccggcgac acgcagaaca ccaacagcaa caacuacgug 900

aagcagaugc ucggccacga gaccaaccgc auguaccgcg agaccuacuc ggucacccau 960

cgcggcgaau gggacuucgg cagcucgcug gccuaccugc aguacgagaa gacccgcaac 1020

agccggauca acgaaggccu ggccggcggc accgaaggua ucuucgaccc caacaacgcc 1080

ggcuucuaca ccgccacccu gcgcgaccug accgcccacg gcgaggucaa ccugccgcug 1140

caccugggcu acgagcagac ccugacccuc ggcagcgagu ggaccgagca gaagcucgac 1200

gaccccagcu ccaacaccca gaacaccgag gaaggcggcu cgaucccccgg ucucgccgga 1260

aagaaccgca gcagcaguuc cucggcgcgg aucuucucgc uguucgccga ggacaacauc 1320

gagcugaugc ccggcaccau gcucacccca ggccugcgcu gggaccacca cgacaucguc 1380

ggcgacaacu ggagcccauc gcugaaccug ucccacgcgc ucaccgagcg ggucacccug 1440

aaggccggua ucgcccgcgc cuacaaggcc cccaaccugu accagcugaa ccccgacuac 1500

cugcucuaca gccguggcca ggguugcuac gggcaaagca ccaguugcua ccugcgcggc 1560

aacgacggcc ucaaggccga gaccagcgug aacaaggaac ugggcaucga guacagccac 1620

gacggccugg uagcggggcu gaccuacuuc cgcaacgacu acaagaacaa gaucgaaucc 1680

ggccugucac cggucgacca cgccagcggc ggcaagggcg acuacgccaa cgcggcgauc 1740

uaccaguggg agaacgugcc caaggcggug gucgagggcc ucgaaggcac ccugacccug 1800

-continued

ccccuggccg acggccugaa guggagcaac aaccucaccu acaugcugca aucgaagaac 1860

aaggaaaccg gcgacgugcu cucggugacg ccgcgcuaca cccucaacuc gaugcucgac 1920

uggcaggcca ccgacgaccu cucgcugcaa gccacggcua ccugguacgg caagcagaag 1980

ccgaagaaau acgacuauca cggcgaccgu gucaccggca gcgccaacga ccagcucucg 2040

cccuacgcca ucgccggccu cggcggcacc uaucgguuga gcaagaaccu gagccucggc 2100

gccggcgucg acaaccuguu cgacaagcgc cuguuccgcg ccggcaaugc ccagggcgug 2160

gucggcaucg acggggccgg cgcggcgacc uacaacgagc ccggacggac cuucuauacc 2220

agccugaccg cgucguucug a 2241

<210> SEQ ID NO 80
<211> LENGTH: 2355
<212> TYPE: RNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 80

augucccogu cacgcgcccu gucgccgcuc agccgcgccc ugcuccucgc cugccucggc 60

ggucccgucc ugguuuccgc cggcagcgcc ugcgccgccg agauccgcac cgaugcccgc 120

caguacuacc gccugccugc cgagccgcug gagcaggcgc ugaaccaccu aggccgccag 180

gccggcgugc ugaucgccuu cagcccggaa cagaccgccg cgcgacgcag ccaggcgcug 240

gacggcgagu acacccugga ggaagcccug gccgcccugc ucgucggcuc cggccuggag 300

gcgcgcgccc gcggcgacgg cgccuacacc cuggaagcgc ugccggugga agacccggcc 360

aaccugcagg cgcucaccgu ggucggcgac uggcuggccg acgccagcgc cgccgacguc 420

uucgagcauc ccggugcgcg cgacgugguc cgccgcgagc aguuccaggc ccaaggcgcg 480

gccagcaccc gcgaagugcu ggagcgcauu cccgggguca gcgcgccgcu caacaacggc 540

accggcagcc acgaccuggc auugaacuuc ggcauucgcg gccucaaccc gcgccuggcg 600

ucgcgcucga cggugcugau ggacggcauc ccggugcccu ucgcccccua cggccagcca 660

caguugucgc uggcgccggu guccaucggc aacauggacg cgguggacgu gguccgcggc 720

ggcggcgcgg ugcgcuacgg gccgcagaac gucggcggca ucgucaacuu cgugacccgg 780

gcgauccccg aggacuucgc caccaagcuc gacgugcaca gcgaacucag ccccagcucc 840

agccaggacg gccugaagac cacccacaac gugcugaucg gcggcaccgg cgccaacggc 900

cucggcggcg cccugcucua cuccggcacc cgcggcggcg auuggcgcga gcacagcgau 960

acgcggaucg acgaccugau ccucaagggc cgcuuccagc ccagcgacga acacacguuu 1020

ucggcgauga cccaguacua cgacggcgag gccgacaugc ccggcggccu cggcaccgcg 1080

gccuaccacg acgacccgua ccagucgacc cgucccuacg acaaguucug ggccgccgu 1140

acccuggcca gcgccagcua cgaauacacc cccaacgcca gccagaagcu caacgucacc 1200

ggcuucuuca ccaagacccu gcgcagcggc uaccucgacc agggccgcaa ccucacccug 1260

ucgccgcgcg aauacugggu gcgaggccug gaaacccgcu ucagccaggg cuucgagcug 1320

ggcgaaaguc gccacgaagu gggcaucggc caccgcuacg ucaacgaagc cagccacgag 1380

cugcgcuacu ggacccgcgc cgacagcggc cagcuaccca gcaccggcag ccgcaacgac 1440

cgcgacaccc gcggcagcac cgaagccaac gcguucuaca ucgacgaucg caucgacauc 1500

ggcaacugga ccaucacccc cggcauccgc uacgagaaga ucgauuccga acagaagaac 1560

-continued

cugcugaaga acagcaagga cagcggccgc uacaacgccu cgcugccggc gcucaacgug 1620

aucuaccacc ucacgccgag cuggaaccuc uacgccaaca ccgagggcuc guucggcacc 1680

gugcaguaca gccagauggg caaggcggug cgcagcggcg acaucgagcc ggagaaggcc 1740

cgcaccuggg aacucggcag ccgcuacgac gacggcaucc ugcgcgccga acugggcgcc 1800

uuccugauca acuucgacaa ccaguacgag agcaaccagc agaccgacag cgugaccgcc 1860

cgcggcaaga cccggcacaa gggcaucgag gcggcgaucg ccuacgaccu ggccgaucuc 1920

gacccgcugc ucuccggcuu cgacgucuau gccagcuacg ccuacgucga cgcgagcauu 1980

cgcgaagacg ggccgaacaa gggcaaccag gugccguucu ccucgaagca caagggcacc 2040

cuuggcgcca acuaccgcac cggcgccugg agcuacaacc ucgacggcag cuuccagacc 2100

agccaguacg ccgacaacgc caacaccgag agcgaaagcg ccgacggcag caccgggcgg 2160

aucgccggcu ggauggucug gagcgcgcgc ggcaccuacg acuucggccc gcaacugaac 2220

gaccucaagc ucggccuggg ggugaagaac cuguucgauc gccgcuacua cacccgcucg 2280

uucgacgaca acaacaaggg ccucuacguc ggccagccgc gcacccugua cguacaggcc 2340

ucggucgguu ucuga 2355

<210> SEQ ID NO 81
<211> LENGTH: 2556
<212> TYPE: RNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 81

augaccuugc cuuucacccg cgccgccugg cgcccgcugu guuccgccgc cgugcucggc 60

gccgcguugu gggccgccgg cgccagcgcu gccgaacgac gcuucgaccu gccggcgcag 120

ccgcuggccg ccucgcuguc gcgccuggcg cagcaggcgc agguccaggu gcuguucgac 180

gagucgcucc ugcggggccu gcgcgcuccg gcgcugagcg gcagcuacgg ggugcgcgag 240

gcgcuggagc gguugcuggu cgguuccgag cuggagcugg uggaggcggg cggcggcuac 300

guggugcgcc ggcgccaggu cgacgccuac agcgacaacg cgcugcaacu ggacgcgcag 360

accaucgucg gcaacggucg cgaaguggac gccagcaacg ucggccguuc gacccugacc 420

cggcgggaua ucgaacgcca gcaggcggac aacaucccca gccugcugca gacccugccc 480

ggagugacca ugggcggcuc gcccaagccg ggcggacaga ccaccaacau cuggggccug 540

ggcgacgccg aggacgugcc cuauacccug gacggcgcgc agaagagcgg cuucgagcgc 600

uaccagcagg gcaccguguu caucgaaccg gaaaugauca agcgcaucga gguggagaag 660

ggaccgcacu cgguguucac cggcaauggc ggcuucggcg gcaccgugca cauggagacc 720

aaggacgcgc cggaccugcu gcgcgaaggc cgcgacgucg gcgccaugcu caaguacggc 780

uaucacucca acgaccagca gaagaucuac uccggcgccg uguucggucg cagcgaagac 840

cgccgcgucg augcccugcu cuaucucaac ggucgcgacg gccgcgacau gaagcuggcc 900

gacaaccugc cgcugucgcc caccgacuac ccgaucaacc ccaagcgccu gcccaacagc 960

gcccaggacg agaagaccgg ccuguucaag cucaaccugc accccaccga ggagcacgac 1020

cuggguuuca ccuaccugcg cucgaaaagc ucgcgcugga cgccguucuc cgccagcagc 1080

uacccgaccc cgccgagcca guggaccauc gaccgcuacg gcuacgagcu gggccugacc 1140

cgccugcugg cccaccgcga uaccaccgac accaccugga ccggcaagua caacuaccau 1200

-continued

ccgcuggaca accccuggau cgaccugcaa cugagcuauu ccgacgcccg caccgagcaa 1260

cucgaccguc gcgaggacac cgccuucuac cagcucgcca ccgguggcaa gcggaugcgu 1320

accgaguacc aggacaaggu ccuggaacug cgcaacacca gccguuucga uaccggagcg 1380

cuacagcacg agcugacccu gggcgcggcg cugcacaagc acaagcgcga cauccucaug 1440

cacaugccgg gcaagaccua cgagaccccg cgcuacaauu acggcuggcu gcaaccggca 1500

uucaugccgg ccggcaagca ggacacgcag agcuucuaca uccaggacgc gaucaccuac 1560

ggcagccuga ccgucacccc aucgaugcgc uucgacagcg ugcgcaacga cggccaggcc 1620

aaccuggcgc cgaucuacga caaucccaag cucggccaug acuaucgcgc ccagaccuac 1680

uccggcuggu caccgcggcu gucgguguuc uggaccgcga cgccgaaccu ggcguucuuc 1740

gccgacuaca ccgagaccug gcgagcgccg gugaucgacg agcaguacga agugcagaac 1800

aguucgacca ucgguggcag cagccgcgac cuggacgccg agcgcaucca ugcgauccgu 1860

ggcggcagcg ugaucaaccu gccggaccug cuggucgccg gcgacagccu gcagauccgc 1920

accacguugu uccagaaccg caucaaggac gagauauucc gcacccgcag cgucggcugc 1980

cgccagcagu cgaucgacaa cggcaguauc ggugguagcu gcggcgacau gcugccgcug 2040

agcaacuacc gcaacuugcc gggccugacc aucaagggcu ucgagaucga gagcuucuac 2100

gacagccagc ggcuguucgg cagccugucc uacucgugga ugaccggcaa gcacgauggg 2160

gccuacagca aucccugggg accgaacgug ugggcgcgcg acaucccgcc gccgaagugg 2220

guggccaugc ucggccugaa gguuccggaa ugggaugcca agcucggcug gcagggcgag 2280

uucgugcgca agaccgaccg ccugcccagc gaucgcuaca gcggcgggau ggguaccggu 2340

uccggcgaua ucuacuggga ucacgcggcc aacgacagcu acgacacuca ucggcuguuc 2400

gccgaguggg ucccggccaa gcugggccug aaggacaccc gcaucgacuu caccguggac 2460

aaccuguuca accgcuccua ucgccagccg cugggcggcg accuggucua cagccaggga 2520

cgcaacgcca agaucagcgu cacccaguuc uucuga 2556

<210> SEQ ID NO 82
<211> LENGTH: 2643
<212> TYPE: RNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 82

augcaccgau cgcuccacac cgacgcgccg cugggcgccg cccugcugcu ggcccugcag 60

cucgcucccg gcagcgccgc cgcggcggag gaacaggcgc cugucgaccc gcccacgguc 120

caguugcaac gaaucgaggu gaccggcagc gcgauccgcc gggucgaugc ggaaaccgcg 180

gugccgauca gcguccugcg cgccgaggag cugcgccaac agggcgugac cagcaccgag 240

gaacugaucg gccggcuuuc cggcaaccag ggcguauaca acuccagucg cucggucggc 300

agcgccaccg gcggcgccuc guucgccgac cugcgcggaa ucggcgcgaa caagacccug 360

gugcugcuca acggccggcg ccuggcgaac aaugccaucg acggcuccgc gguggaucuc 420

aacaccauuc ccuucgccgc caucgaccgg gucgaggugc ugcgcgacgg cgccuccgcg 480

cuguacggca ccgaugccau cggcggggug aucaacuuca ucacccgcaa gagccugaac 540

gaaggccgcu ucgacagcgg cuacgccucc cccacccacg acggcggcgg caaccagcgc 600

aacgucagcg cuagcugggg cuucggcgag cuggaggagg aucgcuucaa ugucuucgcg 660

-continued

guggccaacu acgacaagca ggagcgccuc ggcgccaagg accgcggcua caccuacaac 720

uaccagccgg gacgcggccu cgacuacagc uccggcaccg ccuuccccgg caacuggagc 780

cagggcgcca acgccagcaa uccgcuggcc gccggcgguu gcaagggcgc cgaccugauu 840

ccgcgcaacg gcaucugccg gcagagccug uggcgcuacc ucgaccuggu gccggaaacc 900

gagaagaccu cgguguucag ccgcgccacc ggcaagcugg ccgacgagca caacgucagc 960

cuggaguacu ucuggucgcg cagcgacaac gcuacccagg ucggcccagg gacccucacc 1020

ggccugcaga ucgaucccgg caccgccuuc uaucccggca acggcaucac ucccggaccc 1080

ggcggcuucg uccucgaccc gagccggccg guggagguca acuggcgaca gagcgugcuc 1140

gggccgcgcc ugcaauccuc gcagaacacc ggccagcgcc ugcugcucgg cuucgacggc 1200

caguucgccg gcugggacua cgauaucggc gccucguaca accagaacaa gguggucgac 1260

cauauccaca gcggcuacgu cgaugaucgc gccgccgccc ucggcaucgc caacgggacg 1320

cugaacccgu ucgggccgca gaccgacgcc ggccucgccu accucggcag ccaugcccug 1380

agcggcgacu uccguaccuc ggucggccgc gucaagggcc uggacgcccg cgccagccgg 1440

gagaucggcg acugguucgg cgccgggccg gcggcccugg cgcugggcgg cgaguuccgc 1500

aaggaagcgu uccaccagga cauccaggac uucgccggca acgugcagag ccucggcguc 1560

gaucccgccg ccacggucag cggcgagcgc aaccugaagg cgcaguacgc cgaacucaac 1620

gugccggugc uggacagccu ggaacucagc gcggcgaucc gccacgacaa guacagcgac 1680

uucggcagca ccagcaaccc gaaauauucg uuccgcuucc agccguuccg ccaguugguc 1740

cugcgcggcg ccuacagcga agguuuccgu gcgccgucgc uguacgaacu guacaacccg 1800

accuucacca ccuauaccag cgccaacuac gacgacccgc gccugugcgc cggcggccag 1860

ccgagccagg gcggcaucgc caaccgcgac ugcgcccagc aguucuacaa cgccaccggc 1920

ggcaauaccg accugcgacc ggaaaccgcg cgcaacguua cccugggccu ggucuaccag 1980

ccgcugcgcg accuuuccgu cggccuggac uucuggugga ucaggaucgc caaccagauc 2040

gccgaguuuc ccgaagcggc gaucuucgcc gacccgcagg ccuacgccgg acgcaucgug 2100

cgcaaggccg acggcucgau cgaucacguc gucaccggac uggccaaccu cggcaaagug 2160

aagaccagcg gcgucgaccu gagccucgau uaucguuucc cggccagccg cuacgggcag 2220

uucgggcucg accugcaagg caccuacgug ucccgcuacg acuuccagca gcagaucggc 2280

ggccaguacc uggacaacgu cggcgacuuc cagggcgucg gcgugaucgc ccgcuggaag 2340

cacgucgcca acgccaccug gagccgcgac gccuggcagg ccacccugag caaccgcuac 2400

accagcggcu acaacgacua cgaccgcgcc agccacggca aggucggcuc guggaaccuc 2460

ugggaccugg ccggcagcua ccgccucagc cacgcgcugg ggcugacccu cggggugaag 2520

aaccuguucg accgcgaacc gccguucagc aaccagaccu acaccuucca gagcggcuac 2580

gacccgcgcu acaccgaucc cuacgggcgc auccuguucg gccgccucag cuacagcuuc 2640

uga 2643

<210> SEQ ID NO 83
<211> LENGTH: 2760
<212> TYPE: RNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 83

-continued

```
augguucggc uucguacacu gguucgggca aucgcggcgg ccucgguccu gacuuccggc     60
auggcgcaug gauugggacu gggggaaauc acccugaagu cggcguugaa ccaaccguug    120
gaugccgaga ucgagcugcu cgaaguucgu gaccuggguu cgggcgaggu gaucccgagc    180
cuggcgucgc cggaagaguu cagcaaggcg ggcgucgauc gccuguacua ccucaccgac    240
cugaaguuca cgccgguggu gaagcccaac ggcaagagcg ucauucgcgu gaccucgucg    300
aagccggugc aggagcccua ccugaacuuc cugguccagg ugcucuggcc gaacggccgc    360
cugcugcgcg aguacaccgu ccugcuggau ccgccgcugu acuccccgca ggccgcggca    420
agcgcuccgc aagcgccggu cagcgcgccg cgcgcgaccg gcgccccgcg agccccgcag    480
gcuccggcuc cggugcguac caccgcgccg gcaggcagcg acaccuaucg caccguuucc    540
aacgacacgc ucugggagau cgcccagcgc aaccguaccg aucgcguuuc cguaccccag    600
gcgaugcucg cguuccagga gcugaauccg ggcgccuucg ucgauggcaa caucaaccgg    660
cugaagagcg gccagguccu gcgcauuccc accgaacagc agaugcugga gcgcucgccg    720
cgcgaggcgc ugucccaggu gcaggcgcag aaccagagcu ggcgcggcag ccgcaauccg    780
gccgcgggca gcgcuggcgc caggcaguug gaugcgaccc agcgcaaugc cgccgggucg    840
gcgccaucca aggucgacgc cacggacaau cugcgccugg ugucuggcga gggcaaggcc    900
agcaagggug ccgacaaggg cggaaagggc gacagcaagg cgaucgccga uacccuggcg    960
gugaccaagg aaagccucga cagcacucgc cgcgagaacg aagaacugca gagucgcaug   1020
caggaucugc agagccaguu ggacaagcug cagaaguuga uccagcugaa ggacgcccag   1080
uuggccaagc ugcaagggca guugggcgcc gaaggccagg gcgcagccca gccgaacgca   1140
gcccugccgg augcguccca gcccaaugcg gccgcgcagg cgccggcuca gcccgggacu   1200
ccugcugcgg cagcgccgac uccugcucca gccggagaag cacccgccgc uccggcgcag   1260
ccuccggugg cgccgccgcc cgcgccagcu gccgagaagc cuccggcacc ugccguuccg   1320
gcgcccgcuc cgguacaggc ggcagagcag ccggcaccga gcuuccucga cgaacugcug   1380
gccaacccgc ugugguuggc ggugaucggc gguagcgcac ugcuggcguu gcuggugcug   1440
cugaugaucc ugucgcggcg caaugcgcag aaagagaagg aagaagccca ggcuuucgcc   1500
gcggauaccg gcgaggaaca ggaggaugcg cuggaccugg gaaaggacgg cuucgacgac   1560
cugacccucg acgagccuga gccgcagguc gcagccgucg cuccgcaggu cgagaagacc   1620
accgcgcaga cuuccgaugc gcugggcgag gccgacaucu auaucgccua cgggcguuuc   1680
aaccaggccg ccgaacuguu gcagaacgcc aucuacgacg agccgcagcg caccgaccug   1740
cgccucaagc ugauggaagu cuaugccgag augggcgauc gcgaagguuu cgcucgccag   1800
gaaaacgagc ugcgcgaaau cggcggcgca cagccgcagg ucgagcagcu caagucgcgc   1860
uauccggcaa uggucgcggu cgccgcgguu gccggccugg ccggcgccaa gcuggcgcag   1920
gacgagcugg auagcuucag ccuugacgac cugucgcucg acgacagcgg ucacgcggcc   1980
aagccggaug cggcaggaca ggaucucgac gacgccuucg accugagccu ggacgaccug   2040
ggcggcgacg acgugcaggc cgaccucaag uccgacagcg ggcgcugga cgaccugacc    2100
cuggacagcg aucuggaccu ggcggccucg accccggcgg acaagccugu cgacgaucuc   2160
gacuucggcc uggauuucgc ggaguuggca gagacuccga gccaacccaa gcaugacgac   2220
cugggcgauu ucucccugga ucucgacgcg ccggaagaca agcuuucgga cgacgacuuc   2280
```

-continued

```
cugcuuucgc ugaacgacga agugcccgcc gcggcgccug ccgacaacga auucacccuc   2340

gauaccgagg cugccgaaga gccggcguug ucccugccgg acgacuucga ccugucgcug   2400

gccgacgagc cgacggagcc ggccgcuccg gagaagggcg aggacaguuu cgccgcccag   2460

uuggacgagg ugagugcgca guuggacgag uuggccagca accuugacga gccgaagagc   2520

gcgacgccga guuucuccgc cgaagaugca gcggucgccu ccgcccugga cggagacgcc   2580

gacgaugacu ucgacuuccu cuccggugcc gacgaagcgg cgaccaagcu ggaucuggcu   2640

cgcgccuaca ucgacauggg cgauagcgaa ggcgcgcgcg auauccucga cgaaguccug   2700

gccgaaggua augacagcca gcaggcggaa gcccgcgagu ugcuggagcg ccuggccuga   2760


<210> SEQ ID NO 84
<211> LENGTH: 2988
<212> TYPE: RNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 84

augaccgacg accacuccuu ccgcccucgc cccaccucgu ugucagccgc ccugcugcug     60

ggcgccugga ucgcacagcc ggccacggcc gccuaugucg aagccggucg gcccggcgau    120

ccggccaguu ggcgcuccgc cgaauaccag caggacuggg gccuggaacg gaugcgggcc    180

gaccaggccu augccgccgg caucgacggc cagggcguga agaucggcga gauggacucc    240

gguuucgacc cgagccaucc ggauacuccc gccucgcgcu accagccggu gacggccagc    300

ggcaccuaug ucgacggcac gccguucagc gucagcggcg cgaugaacgg caacaacgac    360

ucccacggua cccacgucgg cggcacccuc ggcgccucgc gcgacggcgu cggcaugcac    420

gggguggccu acgcggcaca gguguauguc gccaacacca accagaacga cagcuuccug    480

uucggcccga cgcccgaccc gaacuauuuc aaggccgccu accaggcgcu ggccgacgcc    540

ggggugcggg cgaucaacaa caguuggggc agccagccca aggacgucag cuacgagacc    600

cucgacggcc ugcacgccgc cuaugcccag cacuacgggc gcuccaccug gcuggacgcc    660

gccgccggcg ucucccgcca gggcgugauc aacgucuuca gcgccggcaa cagcggcuac    720

gccaacgcca gcgugcgcuc cgcccugccc uacuuccagc cggaccugga aggccacugg    780

cuggccgugu ccggccucga ccagcagaac ggccagcgcu acaaccgcug cggcaucgcc    840

aaguacuggu gcaucaccac gcccggccgc cugaucaaca gcaccaugcc cggcggcggc    900

uacgccaaca aguccgguac cucgauggcc gcgccccacg ccaccggcgc gcuggcccug    960

gucaugcagc gcuauccgua ccugaacaac gagcaggcgc ugcagguucu gcugaccacc   1020

gccacccagc ucgacggcac gccgaccggc gcccccaccg acaccgucgg cuggggcgug   1080

ccggaucucg gucgggcgau gcaugggccu ggacaauugc ucggccgcuu cgaggccaac   1140

cucccggccg gccugcgcga cgaauggagc aacccgauuu ccgauagcgc ccugcuccag   1200

cgccaggccg aggacgccgc cgagcacgcg gccuggcagc ggacgcugaa ggacaagggc   1260

ugggaaaacg gcuugccggc cggugccagc cagcaggaac gcaccgacua ugccaucggc   1320

auggcccgcg accaggccgc cgcccagcgc caguaccagg gcagccuggu caaggccggu   1380

gccggcagcc ugguccugag cggcgacagc accuaucgcg ggccgacccu ggucgauggc   1440

gggcugcuca gcgucgacgg uucgcugcug uccgccgucg aagucaaugc cggcggcacc   1500

cucggcggca gcggcaggau cggcggccug cuggcgcgcu ccggcggcac gguggccgcg   1560
```

-continued

ggcaacucca ucggcacccu ggaggucgcc ggggaccugc gcuucgaauc cggcucgacc 1620

uacgcggugg agcuuucgga aagcgccagc gaccggaucg ucgccagcgg caaggcgagc 1680

aucgcgggcg gcaacgucac ccuggccaug gaaaacagcc ccgaccugcu cagccagucc 1740

caggucgaga gccuggucgg ccgccgcuac gacauccucg acgccgccgg cggcaucgac 1800

gggcgcuucg acgcgguauu gccgaacuac cuguuccucg gcggcacccu ggacuacgcg 1860

gccaacgcca uccgccugga uaucggacgc aacggcacga cccucgccag cgucgcgcag 1920

acgcccaacc aggcggcggu cgcuggggcc guggaaacgc ucggcgccgg caacccgguc 1980

uacgaaagcc ugcuccuguc ggaaaacgcc gcaaccgccc aacgggccuu ccagcaauug 2040

uccggggaaa ucuacccggc gcucgccggc cuguugcuca acgacagccg cuaucugcgc 2100

gacagcgucg gcgaacgccu gcgccagacc agcgacggcg aggccggcgg ggaggcuccc 2160

gaaggcuggu ucaaggcgcu cggcuccugg ggcaagagcg ccgauggcag ccacgguagc 2220

gaaggcuacc ggcauucggu cggcggcuuc cugcucggcg ucgacagcca ggucgccagc 2280

gacacgcgcc ucggccuggu ggccggcuac agcaacagcu cgcugaacau ggacagcagc 2340

cugcaauccu ccgccagcau cgacagcuac caccucggcg ccuaccucgg ccggcaauug 2400

cagcaauggc gccugagccu cggcgcagcg cacgccuggc accgcgccga ggucaagcgc 2460

gaccugcaau acggcgccgu ggccggcaag cagaaggcca agcucgacgc acagagcagc 2520

caguuguucg ccgaggccgc cuacgcgcug gguuggcgca gccuggagcu ggaacccuuc 2580

gccgggcugg ccuacgugca cgucgccagc gaugacuucc gcgaacgcgg uagcgccgcg 2640

gcccuggagg guggcgacga caaccuggac gccgccuuca ccacccuggg ccugcgcgcg 2700

aaacggcauu ucgagcugga ugccggacgc cgccuggcgc ucuccggcac ccucggcugg 2760

cgccacaacc ugagcgacac caccccgcaa cgccaccugg cguucgccag cggcagccag 2820

ccauucagcg uggaaagcgu ggcccugucc cgcgacgccg cgcugcucgg cgucgacgcc 2880

agccucgcgg ugaaucgcga agugagcgug cggcugggcu acaacggccu gcugggcagc 2940

cgcgagaagg accauggcgu cggacuggcc gucgacuggc guuucuga 2988

<210> SEQ ID NO 85
<211> LENGTH: 3174
<212> TYPE: RNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 85

augaaaagaa ugcugaucaa cgcgacucaa cccgaggagu ugcguguugc acuggucgac 60

ggccaacgcc uguucgaccu cgacaucgag ucgggcgccc gcgagcagaa gaaggccaac 120

aucuacaaag gccgcaucac ucgcgucgaa cccagccucg aagccgccuu cgucgacuuc 180

ggcgccgaac gccacggcuu ccuccccuc aaagaaaucu cccgcgaaua cuucaagaaa 240

ucccccgaag gccggaucaa caucaaggaa guccugagcg aaggccagga agucaucguc 300

caggucgaga aggaagagcg cggcaacaag ggcgccgccc ugaccaccuu caucagccug 360

gccggccguu accuggugcu gaugccgaac aacccgcgcg ccggcggcau cucccgccgu 420

aucgaaggcg aagagcgcaa cgagcugcgc gaggcccuga acggccucaa cgcaccggcc 480

gacaugggcc ugaucgugcg caccgccggc cucggccgca gcaccgagga acugcagugg 540

gaccucgacu accugcugca acuguggagc gcgaucaagg aagcguccgg cgaacguggc 600

-continued

```
gcgcccuucc ugaucuacca ggaaagcaac gucaucaucc gcgccauccg cgacuaccug    660

cgccaggaca ucggcgaagu gcugaucgac agcaucgacg cccaggaaga agcccugaac    720

uucauccgcc aggugaugcc gcaguacgcc agcaaggaga agcuguacca ggacagcguu    780

ccgcuguuca aucgcuucca gaucgagagc cagaucgaga ccgcuuucca gcgcgaagug    840

aagcugccgu ccggcggcuc caucgucauc gacccgaccg aggcccuggu uuccaucgac    900

aucaacucgg cgcgcgccac caagggcggc gacaucgagg aaaccgcccu gcagaccaac    960

cuggaagcgg ccgaggaaau cgcccgccag cugcgccugc gugacaucgg cggccugauc   1020

gucaucgacu ucaucgacau gaccccggcg aagaaccagc gcgccgugga agagcguguc   1080

cgcgaagccc ucgaggccga ccgcgcgcgc guccaggucg gucgcaucuc gcgcuucggc   1140

cugcuggaaa ugucccgcca gcgccugcgu ccgucccucg gcgagaccag cggcaucguc   1200

ugcccgcgcu gcaacggcca gggcaucauc cgcgacgucg agucgcuguc gcuggccauc   1260

cugcgccuga ucgaggaaga agcccugaag gaccgcaccg cggaaguccg cgcccgcgug   1320

cccuuccagg ucgccgccuu ccugcucaac gagaagcgca acgccaucac caagaucgaa   1380

cugcguaccc gcgcgcgcau cuucauccug ccggacgauc aucuggaaac cccgcauuuc   1440

gaaguccagc gucugcgcga ugacagcccc gaacugguug ccggccagac cagcuacgaa   1500

auggccaccg ucgagcacga agaagcccag ccggucagcu cgacccgcac ccugguccgc   1560

caggaagcag cagucaagac cgucgcuccc cagcagcccg caccgcaaca caccgaagca   1620

ccggucgagc cggccaagcc gaugcccgag ccgagccugu uccagggccu ggugaagucc   1680

cuggucggcc uguucgcagg caaggaucaa ccugccgcca agccugcuga aaccagcaag   1740

ccggcugccg agcgccaaac ccgccaggac gagcgucgca acggccgcca gcagaaccgc   1800

cgccgcgaug gccgcgaugg caaucgccgc gacgaagagc gcaaaccgcg cgaggagcgu   1860

gcagagcguc aaccgcgcga agagcgcgcc gaacgcccga accgcgaaga gcgcagcgaa   1920

cgucgccgcg aagagcgcgc cgagcgcccg gcucgcgagg agcgccagcc gcgcgaaggc   1980

cgugaagagc gcgccgagcg gacaccccgc gaagagcgcc agccgcgcga aggccgcgaa   2040

ggucgcgagg aacgcagcga acgccgccgc gaagagcgcg ccgaacgccc ggcccgcgaa   2100

gagcgccaac cccgcgaagg ccgugaagaa cgcgccgagc gcccggcccg cgaagagcgc   2160

cagccgcgcg aggaucgcca ggcucgcgac gccgcggccc uggaagccga ggcauugccg   2220

aacgacgaga gccuggagca ggacgagcag gacgauaccg auggcgagcg cccgcgccgc   2280

cgcucccgcg gccagcgucg ucgcagcaac cgccgcgaac gccagcgcga ggucagcggc   2340

gagcuggaag gcagcgaggc gaccgauaac gccgccgcgc cgcugaacac cgucgcagcc   2400

gccgccgcug ccgguaucgc ugucgccagc gaagccguag aagcaaacgu ggagcaagcc   2460

ccggccacua ccagcgaggc ugccagcgaa accacggcaa gcgaugagac cgacgcgucg   2520

accagcgaag ccgucgaaac ccagggcgcg gacagcgagg ccaauaccgg cgaaaccgcc   2580

gacaucgaag cgccggugac cgucagcgug guccgggacg aagccgacca gagcacccug   2640

cuggucgcgc aagccacuga agaagcuccc uucgccagcg aaagcgugga aagccgcgaa   2700

gacgccgaga gcgccgugca accggcaacg gaagcggccg aagaaguugc cgcuccggug   2760

cccgucgaag uagcagcccc uagcgagccc gcagccaccg aggagccgac cccggccauc   2820

gcggcggugc cggccaacgc gacuggccgu gcccucaacg acccacggga aaaacgucgc   2880
```

-continued

cugcaacgcg aagccgagcg ucuggcacgc gaagccgcag cagcagccga agcggcagcu 2940

caggccgcuc ccgccgucga ggagaucccg gcuguagcga gcgaggaagc gucggcccag 3000

gaggaaccug cugcacccca ggcugaagaa aucacccagg ccgacguucc gucccaggcg 3060

gacgaagccc aggaagcggu acaggccgag ccugaagcuu ccggcgaagg cgccgccgac 3120

acggagcacg cgaaaaagac cgaggaaagc gaaaccucgc gcccgcaugc cuga 3174

<210> SEQ ID NO 86
<211> LENGTH: 3486
<212> TYPE: RNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 86

augaaaucgg uacuccacca gaucggcaag accucgcugg cagccgcgcu cagcggcgcc 60

guccugcucu ccgcccagac cacccacgcc gccgcccugu cggucagcca gcagccgcug 120

augcugaucc agggcgucgc cccgaacaug cuggugacuc ucgacgacuc gggcaguaug 180

gcguucgccu augcgccaga cagcauuucc ggcuauggaa acuauacguu cuucgcgucg 240

aacagcuuca acccgaugua cuucgauccg aacacgcaau acaagcuucc gaagaaacuc 300

acacugguga acggacaggu acagauccag gauuauccgg cccccaacuu cuccucugcc 360

uggcgcaaug gcuucacucg cagcgggagu aucaaucugu cgaacagcua caaggucacc 420

aucgaguacg gcaggggaua ugauaaggag ucgacgauaa aagccgacgc ugccuacuac 480

uaugacuuca cgggcucauc caguugcaac cgcaccaauc aggcaugcua cacccgccgu 540

uaugugagca cagagcaaag gcagaacuuc gccaacuggu auucguucua ccgcacccgc 600

gcccuugcca cucagaccgc cgccaaccug gcguucuaca gccugccuga aaacgcucgg 660

gugagcuggc aauugcugaa cgacucgaac ugcaaccaga ugggcagcgg cuccagcucc 720

ggcaacuguu ucagcaacua ucuacgggac uucaccgguc aacaccgggu gaacuucuuc 780

aauuggcugg aaaaacuuuc ggucaauggu gguacgccac ugcgccaggc gaugacccgg 840

gcaggcgagu uucucaagaa gaccggcguc aacgguccca augccuaucg cccagggacc 900

cagaccgcgc ccgaguacag uugccggggc agcuaucaua uccugaugac cgacggucuc 960

uggaacaacg acucggccaa cguaggcaau gccgacagca ccgcucguaa ccuccccgac 1020

gggaagagcu auagcagcca gacacccuac agggacggua cguucgauac ccuggccgac 1080

caggccuucc auuacugggc caccgaugcc cggccggaua ucgacgacaa uaucaaaccg 1140

uacauucccu acccggacca ggccaauccc ucggcggaau acuggaaucc ccgcaacgau 1200

ccggcaaccu ggcaacacau ggugaccuac acccugggcc ugggccugac caccagccuc 1260

accaguccga gaugggaagg cuccaccuuu uccgguggcu acaacgauau cguggcuggc 1320

aaccugagcu ggccccgcgc gucgaacaac gacuccaaca acgucuacga ucuguggcac 1380

gccgcaguga acucccgggg cgaguucuuc agcgccgacu cgccggacca acuggucgcg 1440

gccuuccagg acauccucaa ccgaauuucg ggcaaggacc ugccggcauc ccgccccgcc 1500

aucagcucgu cccugcagga agacgacacu ggcgacaagc ugacccgcuu cgccuaccag 1560

accagcuucg ccagcgacaa gaacugggcu ggcgaccuga cccgcuacag ccugaccacc 1620

caggacaagg ccaccgugca gaccaagcug uggagcgcgc agagcauccu cgacgcgaug 1680

cccaacggug gagcuggccg caagaucaug auggccggau ccgguaccuc gggccucaag 1740

-continued

gaguucaccu ggggcagccu cagcgccgac cagcagcggc aguugaaccg cgauccggac 1800

cgcaacgaug ucgccgacac caagggccag gaccgcgugg ccuuccugcg cggcgaucgc 1860

cgcaaggaga acagcgacaa cuuccgcacc cgcaacucga uccucggcga uaucaucaac 1920

uccucgccgg cgacggucgg caaggcccag uaccugaccu accuggccca gccgaucgag 1980

cccagcggua acuacuccac guucgcagaa gcacagaaaa cccgugcccc gcggguauac 2040

gucggcgcca acgacggcau gcugcacggu uucgauaccg acgguaacga gaccuucgcc 2100

uucaucccaa gcgcggucuu cgagaagcuc cacaaguuga ccgcccgcgg cuaccagggc 2160

ggcgcccacc aguucuacgu cgacgguucg ccgguggucg ccgacgccuu cuucggcggc 2220

gccuggcaua ccgugcugau cggcagccug cgcgccggcg gcaagggccu guucgcccuc 2280

gacgugaccg aucccgccaa caucaagcug cucugggaaa ucggcgugga ccaggagccc 2340

gaccuuggcu acagcuuccc caaacccacg gucgcccggc ugcacaacgg caagugggcc 2400

guggucaccg gaaacgguua uuccagccug aacgacaagg ccgcgcugcu gaucaucgac 2460

cuggagaccg gggccaucac ccgcaaacug gaagucaccg gcaggaccgg cguacccaac 2520

ggccuaucca gcccucgccu ggcagacaac aacagcgacg gcguagccga cuacgccuac 2580

gccggcgacc ugcaaggcaa ccucuggcgc uucgaccuga ucgccggcaa ggucaaccag 2640

gacgauccgu ucagccgagc caacgacggc ccggcggugg ccucgagcuu cagggugucu 2700

uucgguggcc agccgcucua uucggcaguc gacuccgccg gcgcggcgca agcgaucacc 2760

gccgcgcccu cgcugguucg ccauccgaca cgcaagggcu acaucgugau cuucgguacc 2820

ggcaaguauu ucgagaacgc cgacgcccgg gccgauacca gccgcgccca gacgcucuac 2880

ggcaucuggg accagcaaac caagggcgaa gccgcgggca gcacaccccg acugacgcgc 2940

ggcaaccugc agcagcagac ccuggaccuc caggccgacu cgaccuucgc cucgaccgcu 3000

cgcaccauuc gcaucgccag ucagaacccg gucaacuggc ugaacaauga cggcagcacc 3060

aagcaguccg gcugguaucu ggacuucaug gucaacggca cccugaaggg cgagaugcug 3120

aucgaggaca ugaucgccau cggccaggug gugcugcugc aaaccaucac cccgaacgau 3180

gaccccugug ccgacggcgc cagcaacugg accuauggcc ucgaucccua uaccggcggu 3240

cgcaccagcu ucaccguguu cgaccuggca cgccagggcg ucguggacuc gaaauccgac 3300

uacagcuaca acaagcagaa cgucgcggua uccgguaccg agcagaaagg ccugggaggc 3360

uugacgcuga gcaccaacga acagggcaau ccggaagucu gcuccucggg cgaaugccug 3420

accgugaacc ccgguccgaa cacccguggc cgccagaacu ggcgccccau cgaaggaaag 3480

aacuga 3486

<210> SEQ ID NO 87
<211> LENGTH: 3636
<212> TYPE: RNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 87

augaagauuc ucgccauccg ccugaagaac cucgccuccc ucgcuggcga gcaggaaauc 60

gacuucaccc gcgaaccgcu guccagcgcc ggccuguucg ccaucaccgg uccgaccggc 120

gccggcaaga gcaccgugcu ggacgcccug ugccuggccc uguucggcag cacgccgcgg 180

cuggaaagca cuucggccag cagcaagguu cccgauggcc ggaacgagcu guccagcaac 240

-continued

```
gacgaacgca accugcugcg ccgcgguugc gccagcggcu acgccgaagu ggauuucguc    300

ggcaucgacg gccaccgcua ucgcgcccgc ugggaaaccc ggcgcucccg ggacaaggcg    360

gacggcgccu ugcaaaagag ccagcagagc cuccaggacc uggagaccca gcaaaugcug    420

gcagcgaaca agaaaagcga guuccgcgaa cagcuggagc agaagcucgg ccucaauuuc    480

gcccaguuca cucgcgccgu gcugcuggcc cagagcgaau ucagcgccuu ccucaaggcc    540

agcgacaacg accgcggcgc auugcuggag aaacucaccg acaccggccu guacagccaa    600

uugagcaaag ccgccuauca gcgcgccagc caggccgacg agcagcgcaa gcaacucgag    660

caacgccugg aaggcagccu gccccuggcc gagcaggccc gggccgggcu cgaggcggcg    720

cuggaauccc acgcccaggc gcgucuccag gagcaacagg cacugcaacg ucuggaaggc    780

cagcaacaau gguucaccga ggagcagcgg cugcugcaau ccugcgagca cgcacaaggc    840

caacuggccg aggccaggca ggccugggac gcccuggcga cggagcggga aacccugcaa    900

uggcuggagc gccuggcucc gguucgcgga cugaucgaac gccugaagca acucgagcag    960

gaacuccggc acuccgagca gcagcagcgg cagcgcaccg agcagcaagc cgcgggcacc   1020

gagcgcuugc aaggauugca ggcccgcuug caggaggcgc gcgagcgcca ggcccaggcc   1080

gacaaccauc ugcgucaggc ccaggcgccg uugcgcgagg cuuuccagcu ggagagcgag   1140

gccaggcgcc uggagcgaac gcuggccgag cgacaggaac uccaucggca aucgaaccag   1200

cgccacgccc agcaaagcga cgccgcucgg caacuggaua uggagcagca gcgccauguc   1260

gcggaacagg cgcaacugca ggcggcauug cgcgacagcc aggcucucgc cgcgcucggc   1320

gacgccuggg ugacccacca gggccagcuc gccaccuucg ugcaacgucg ccagcgcgcg   1380

cucgaaagcc aggcgcagcu ccccgagcug gaaaaauccc uggcccacgc cggggaaccg   1440

cucgaacgcu ugcaggcgca auggaccgcc cuccauggca gcgagccgga cgaccuggcg   1500

gcacgccugg ucgaauugcg ccggcagacc gauagccugg aacgacaaca agcgcuccac   1560

aaggaauggc aacagguccu cgaccaacgc gccggucugg cucgacgccu gggcgaacuc   1620

gaccagcgua uggucgagca ggagcaggca uugcucgacc ugaaacgaca aggcagccaa   1680

ugcgccgagg aggugaaggc ggcggagcag gcccugcagg ucacccgcga guugcuccag   1740

cgccaacguc uggcccgcag cgccagcguc gagcaacugc gcgccggccu gguggacggc   1800

gaggccugcc cggucugcgg cagccaggag caucccuauc accauuccga gcaacugcuc   1860

gccgcccucg gugaacacga cgaccaggag cagguccgcg ccgagcaguc ccucgagcgg   1920

cugcgacaga cccuggucgg ucugcgcgag ggcuauucca gccagcggga aagacucaac   1980

cagagucgcc aggagcagca ggaacugacu ggccaacugg ccgcgcucga ucggcaacug   2040

gaccaaugga cgcugccgga agaacugcga cuccugcagc cguccgcgca guuggagugg   2100

cuggcacaac gccuggacga ccuggcaggg cagcgccagc agugccaacg agacuucgac   2160

cggcugaucg cccgccagcg ccagacccag caauugcagc aggaacugcg ggccgccgag   2220

acgauccugc aacagcgcca gcaggcgcug acggaacaac ggcagcgcua cgaacauuug   2280

cagcagcagg ucgaggagga cagccagcaa uugcguccau ugcucuccga cgagcacugg   2340

cagcgcuggc aggcagaucc gcugcggacu uuccaggcac ucggcgaguc caucgagcaa   2400

cgccggcagc aacaggcgcg gcuucagcag aucgaacagc gucugcagga gcucaagcag   2460

cgcugcgaug aaucgagcug gcaacugaag caaagcgacg agcaacgcaa cgaagcccgu   2520
```

-continued

caggcagagg aaagggccca ggcggaacuc gccgaacuga acggacgccu cggcgcucac 2580

cugggccagc acgccugcgc ccaggacugg cagcuaucgc uggagcacgc cgcgcaagcg 2640

gcgcagagcg ccgucgagac gcuccaggcg ccccuggauu cgcugcgcga ggaacaacug 2700

cgacucgccg aagcccugga acaccugcag cagcaacggc agcgccaaca ggaugaguuc 2760

cagcgccuuc aggccgacug gcaggccugg cgcgaacgcc aggacaaccu cgacgacagc 2820

cgccucgacg cccugcucgg ccuuuccgag gaacaggcga cgcaauggcg ggagcaauug 2880

cagcgacugc aagaggagau cacccgccag cagacacugg aagcagagcg ccaggcgcaa 2940

cugcuccagc aucgccggca gcggccggaa accgaccgcg aggcgcugga agacaaccug 3000

cggcaacagc gcgaacgccu ggccgccagc gaacaggccu accuggagac cuacagccag 3060

uugcaggccg acaaccagcg ccgcgagcag agccaggcgc ugcuugccga acuggagcga 3120

gcccgcgccg aguuccgcag auggggccgc cugaacgaac ugaucgguuc guccagcggc 3180

gacaaguucc gccgcaucgc ccagggcuac aaccucgacc ugcuggugca gcacagcaac 3240

gugcaguugc gccaguuggc gcggcgcuac cgccugcagc gcggcggcag cgaacugggc 3300

cugcuggugg uggacaccga gaugggcgac gaacugcgcu cgguguauuc gcucuccggc 3360

ggcgagaccu uccugauuuc ccuggcccug gcgcucggcc uggccucgau ggcaucgagc 3420

aagcugcgca ucgagucgcu guucaucgac gaaggcuucg gcagccucga cccggaaucc 3480

cugcaacugg cgauggaugc ccuggacaac cugcaggccc agggacgcaa gguggcggug 3540

auuucccacg uccaggaaau gcacgaacgg aucccggucc aggugcgggu ccagcgcgag 3600

ggcaacggca ugagcagccu gaaggugguc ggcuga 3636

<210> SEQ ID NO 88
<211> LENGTH: 7407
<212> TYPE: RNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 88

augucgaucc aggcgaaagu uaccccuauc gaucagagua uuucuucugc ggcugccguc 60

gagguuccgg aaaacgggau acucaaacuc ucccagagca guaaugucgc gcucgauguc 120

gcaccggagu cgguggcggg auacucgaag agcgguucgg accugaucgu ccagcugaag 180

accggggaaa gcguccggau cgccaacuuc uaugcggaag gccagccuuc cagccaacug 240

uuccuggccg acaaggacaa gcugguggcg guagaucugc cgccggucgc ugccgacggg 300

ccgcugaugg ccggcuacau cccgcaggaa agccuggccg guuucgaguc gcugaccggc 360

gccggugugc ucgguggcau gagcgcaggg acugcgcugc uggucggugc ggcggccauc 420

ggcgccgggg uggcgauuuc caacagcagc ggcggcggug gcggcggcgg uucuucggug 480

cccccggaca ccacuccgcc gaaggcggcc agcggccuga agauagcgcc ugacggcagc 540

agcaucagcg gccaggccga ggccggcgcg agcgucggca ucgauaccaa uggcgacggc 600

aagccggacc ucaccgugau cgccgaugcc aacggcaauu ucaccgcucc gcugaacccg 660

ccgcugacca auggccagac ggucaccgug guggucaccg acccggcugg caacgccagc 720

ccgccggccc aggucaccgc uccggacacu accgccccgg cgccggcuac cgacgugcag 780

guggcgccgg acggcagcag cgucaccggc aaggccgaac ccggcucgac ggugggcguc 840

gauaccgacg gcgacggcca gccggacacc accguggugg ucggccccgg cggcagcuuc 900

-continued

```
gagguuccgc ugaacccgcc gcugaccaau ggcgagacgg ugacggugau cguuaccgac    960

ccggccggca acaacagcac cccggugacc gucgaggcgc cggacaccac cgccccggcg   1020

ccggccaccg acgugcaggu ggcgccggac ggcagcagcg ucaccggcaa cgcagagccg   1080

ggcgccaccg ucggugucga caccgauggc gacggccagc cggacaccac cguggugguc   1140

gguccggcg  gcagcuucga gguuccgcug aacccgccgc ugaccaaugg cgagacggug   1200

acggugaucg uuaccgaccc ggccggcaac agcagcaccc cggucaccgc cgaagccccc   1260

gacuuccccg acgcgcccca ggucaaugcc agcaacggca gcguccucag ugguacggcg   1320

gaagcgggcg ugaccaucgu gaucaccgac ggcaacggca auccgaucgg ccagaccagc   1380

gccgaugcca acggcaacug gagcuucacc cccgguagcc aacugccgga uggcaccgug   1440

gucaaugugg uggccaggga cgccgccggc aacagcagcc cggcgaccuc caucaccguc   1500

gacggcgugg cgccgaacgc gccggugguc gagccgagca acggcagcga acucagcggg   1560

acugccgaac cgggcagcag cgugacccug accgacggca auggcaaucc gaucggccag   1620

accaccgccg augccaacgg caacuggucu uucacgccgu ccaccccguu gccggacggu   1680

accgugguca acgugguggc cagggaugcc gccggcaaca gcaguccgcc ggccagcguu   1740

accguggaug ccgucgcgcc ggccacgccc accgucgauc cgagcaacgg uacgacccuc   1800

agcggcaccg ccgagccggg caguagcgug acccugaccg acggcaacgg uaacccgaua   1860

gggcagguca ccgccgacgg cagcggcaac uggaccuuca ccccgagcac gccguugccc   1920

aacggcacgg uggucaacgc cacggcuacc gacccguccg gcaacgccag uucgccggcc   1980

agcgucaccg uggacgccgu ggcaccggcc acgccagugg ucaacccgag caacggcacc   2040

acgcucagcg gcaccgccga gccgggcgcc accgugaccc ugaccgaugg caacggcaau   2100

cccaucgggc aggucaccgc cgauggcagc ggcaacugga gcuucacucc gaccacgccg   2160

uugcccaacg gcaccguggu caacgccacg gccaccgacg ccuccggcaa caccagugcg   2220

ggcagcagug ucaccgugga cucgguagcc ccggccacgc cagugaucaa ccccagcaac   2280

ggcaccacgc ucagcggcac cgccgagccg ggcagcagcg ugacucugac cgauggcaac   2340

ggcaacccga uuggccaggu caccgccgac ggcagcggca acuggagcuu caccccgucc   2400

acgccgcugg cggauggaac cguggucaac gccacggcca ccgauccggc gggcaacacc   2460

agcggccagg gcagcaccac cgucgauggc guggcgccga ccacgccgac cgucaaccug   2520

agcaacggca gcagccucag cggcacugcg gaaccgggca gcacggugau ccucaccgac   2580

ggcaacggca auccgaucgc cgaggucacc gccgacggca gcggcaacug gaccuacacc   2640

ccguccacgc cgaucgccaa cggcaccgug gucaacgugg uggcccagga cgccgccggc   2700

aauagcagcc cgggcgccag cgucaccgug gacucgcagg ccccggcggc uccggugguc   2760

aacccgagca acggcacuac gcucagcggc accgccgagc cgggcgcuac cgugacccug   2820

accgacggca acggcaaccc gauuggccag gucaccgccg acggcagcgg caacuggagc   2880

uucacaccgg gcacgccgcu ggccaacggc accgugguca acgccacggc cagcgacccg   2940

accggcaaua ccagcgcucc ggccagcacc accguggacu cgguggcgcc ggccgcgccg   3000

guggucaauc cgagcaacgg cgcggagauc agcggcaccg ccgaaccggg cgccaccgug   3060

acccugaccg auggcagcgg caauccgauc gggcagguca ccgccgacgg cagcggcaac   3120

uggagcuuca ccccguccac gccgcuggcg gauggaaccg uggucaacgc caccgcuacc   3180
```

-continued

gacccggccg gcaauaccgg cggccagggc agcaccaccg uggacgccau cgcgccggcc 3240

acgccgaccg ucaaccugag caauggcagc agccucagcg gcaccgccga gccgggcagc 3300

acggugauuc ucaccgacgg caacggcaau ccgaucgccg aggucaccgc cgacggcagc 3360

ggcaacugga ccuacacccc guccacgccg aucgccaacg guacuguggu caacguggug 3420

gcccaggacg ccuccgguaa cagcagcccg ccggcgacgg ugaccgucga uuccagcgcg 3480

ccgccggcgc cggugaucaa cccgagcaac ggcgucguca ucagcggcac cgccgaggcc 3540

ggugccacgg ugacccucac cgaugccggc ggcaacccga uagggcaggu caccgccgac 3600

ggcagcggca acuggagcuu cacgccgggc accccgcugg ccaacggcac ggugaucguc 3660

gccacggcca ccgacccgac cggcaauacc ggcccgcagg ccgccaccac gguggacgcg 3720

guggcgccgc cggcgccggu gaucgauccg agcaacggca cgaccaucag cggcaccgcg 3780

gaggccgggg ccaaggugau ccucaccgac ggcaacggca acccgaucgg cgaaaccacc 3840

gccgacggca gcggcaacug gagcuucacg cccggcacgc cgcuggccaa cggcacggug 3900

gucaacgccg uggcccagga cccugcgggc aauaccggcc cgcagggcag cacuaccgug 3960

gacgcggugg cgccgaacac gccugugguc aauccgagca acggcaaccu gcucaacggu 4020

accgccgagc cgggcagcac cgugaccuug accgacggca acggcaaccc gaucggccag 4080

accaccgccg auggcagcgg caacuggagc uucacgcccg gcucgcaacu gcccaacggc 4140

accgugguca acgugaccgc gagcgacgcc gccggcaaua ccagccuucc cgcuaccacg 4200

acgguggauu ccucgcugcc gucgaucccg cagguggauc cgagcaacgg uucggugauc 4260

agcggcaccg cggacgccgg caacaccauc aucaucaccg auggcaacgg caacccgauu 4320

ggccagguca ccgccgacgg cagcggcaac ugguccuuca cuccaggcau cccgcugccg 4380

gauggcacgg uggucaacgu gguggcgcgc agcccaagca augucgacag ugcgccggcg 4440

gugaucacug uggauggcgu ggccccggcg gcgccgguga ucgauccgag caacggcacc 4500

gagauaagcg guaccgcgga ggccggcgcg acggugaucc ucaccgaugg cggcggcaac 4560

ccgaucggcc aggccaccgc cgacggcagc ggcaacugga cguucacccc gagcaccccg 4620

cuggccaacg gcaccgugau caacgccgug gcccaggacc cggccggcaa uaccagcggu 4680

ccggccagcg ucaccgucga ugccaucgcc ccgccggcgc cggugaucaa uccgagcaau 4740

ggagucguca ucagcgguac ggcggaagcc ggggccacgg ugauccucac cgacggcaac 4800

ggcaacccga ucggccaggu caccgccgac ggcagcggca acuggagcuu cacgcccggc 4860

acgccgcugg ccaacggcuc ggugaucaau gcgcuggccc aggacgccgc cggcaacaac 4920

agcaguccca ccagcgccac cgucgacucg cuggcgccag cagccccggu gaucgauccg 4980

agcaacggua gcgugaucgc cgguaccgcc gaggcuggug ccacggugau ccucaccgac 5040

ggcaacggca acccgaucgg ccaggucacc gccgauggca gcggcaacug gagcuucacg 5100

cccggcacgc cgcuguccaa uggcacggug gucaaugcgg uggcccagga cgcugccggc 5160

aacaccagcg gcccggucag caccacggug gacgcggugg ccccggccac cccggugauc 5220

gacccgagca acggugucga acucagcggc accgccgaac ccggcguccg ggugauccuc 5280

accgauggca auggcaaucc gaucggccag acccuugccg acggcagcgg caacuggagc 5340

uucacgccgg gcacgccgcu ggccaacggc acgguggucа augccguggc ccaggacccg 5400

gccggcaaua ccagcggccc ggccagcacc acgguggaca cgguggcucc ggccacgccg 5460

-continued

gugaucaauc ccagcaacgg cagcgugauc accggcaccg ccgaggucgg cgccaaggug 5520

auccucaccg auggcaacgg caacccgauc ggcgagacca ccgccgacgg caguggguaac 5580

uggaccuuca cccccggcac gccgcuggcc aacgguacgg ugaucaacgc cgucgccgag 5640

gacgccgcgg gcaacgccag cgguccggcc agcaccacgg uggacucggu ggcgccgucc 5700

gcuccgcugc ugagcaucag cgccgacggc gcgcugcuga ccggcaccgc cgagccgaac 5760

agccaggugc gcaucguggu caacggcgac accgccaacc cgaucacggu caccgucgac 5820

ggcgccggca acuucagccu gccguucgcg ccgccgcuga ucaccggcga gcugaucgcc 5880

ggggucgccg ucgacgccgc cggcaacguc agcgggccgg ccaccaucaa cgccccggac 5940

cuggcgccgc cgaccaucag cgugccggaa gccgccgaua ccuggaucaa ugccgcggag 6000

aucggcgacg guauccaggu cgaugugacg guccguccga ccaugcaggu cggccaggug 6060

gucacgguca aguucgccgg gcagaacggc uacgaggccg aggucagcca uacccucacc 6120

gccggcgaca ucgccgccgg caaccugacc cugacccuga cgccucccgg cggcaugggc 6180

ccguucccgg agggugccuc gaccgucacc gccgacauca acggcggcac cgcgucgacc 6240

ccggugccgu ucaccaucga caccauuccg ccggcgaccc cggugcuguc ccuggucggc 6300

aacauccuga ccaucucggc ggagccaggg accgaguuga cggugaccgu cgacgucggc 6360

ggggugaccg ccaccgccac ggugaccgcc gacaacagcg ggcuggcguc gcugaaccug 6420

cucaccgacc uggacaucga cuucaguugg gaccaguugc ucaaugccca ggugucggug 6480

gucggacgcg acccggccgg caacccgagc aacacggcga gcaucggcgu cggcaccagc 6540

aucgagcaac cggugaccau cggcaacuuc ggccucgacg ucagccucaa cccgcugaac 6600

ccgcguuucg guuucagcgg aaccaccgag ccugacucca gcgugguggau ccgggucauc 6660

accccggcgu ugaacgucga auugcugccg auccaggcgg auucguccgg aaacuucucg 6720

cugaaccugc ugagcccgac cauccucacc caguuggggc ugaacaucac cgacauccuc 6780

aaccucggcu cgcagaucuc guucaaccug guguccaccg acuccaaugg caacgacagc 6840

gccgccuacg ggaucacccu gacccccaac ggacugucgc ucaauaucgg ccagaucgau 6900

gucaacggua cuuccggcga cgacgugcug uccggcgcca acggcaguuc ggagcacauc 6960

aacggcggcg acggcagcga ccugaucuuc aacgugggca ccggcgauca cguggugggcc 7020

ggcaacggca acgacaccau ccagaucacc gcgaccgauu ucgucagcau cgauggcggc 7080

gccggguucg acacccuggu ccuggccaac ggcaucgacc ucgacuacaa cgccgucggc 7140

gucggcacgc ucagcaaccu cgagcgcauc gaccucggca agggcgauuc ggguagcgug 7200

cugacccuga ccgcggcgga gguggaugcc aucaccgaug ccaacaacac guugcagauc 7260

accggcgaga acaacgacac ccugaacgug gugggcgcgg ugaauaccgg uaccacgcaa 7320

cugaucaacg gcauuaccua cgacgucuac accuucggca guaccacccu gcugaucgag 7380

gacaacacgg uacaggucgu ggucuga 7407

<210> SEQ ID NO 89
<211> LENGTH: 10608
<212> TYPE: RNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 89

auggacaucc gcagcccgcu gaaccagugc aucgcccugu cccuggccgg caucuuguuc 60

-continued

```
cucaacccga ucgucgccgc ggcggcgggg cuggcgcugg acaaggccgc cggcggcaac    120

accggccugg gccaggcggg caacggcgug cccaucguca auaucgccac gcccaacgac    180

gccgggcugu cgaacaacca uuuccgcgac uacaacgucg gcgccaacgg gcugauccuc    240

aacaacgcua ccggcaagac ccaggguacc cagcucggcg ggaucauccu cggcaacccc    300

aaccucaagg gccaggcggc gcaggugauc cucaaccagg ucaccggcgg caaccgcagc    360

acccuggccg gcuacaccga gguggccggg cagucggcgc gggugaucgu cgccaacccg    420

cacggcauca ccugccaggg cugcggcuuc aucaacacgc cgcgcgcgac ccucaccacc    480

ggcaagccga ucauggacgg ccagcgccug gagcgcuucc agguggacgg cggcgacauc    540

gucgucgaag gcgccgaacu gaacgucggc aaccucgaac aguucgaccu gaucacccgc    600

agcgccaagc ucaacgccaa gcucuacgcg aagaaccuca acaucgucac cggccgcaac    660

gacguccagg ccgacagccu gcaggccacg ccgcgcgccg ccgauggcag cgagaagccg    720

cagcuggcga ucgacagcuc ggcgcugggc gggauguacg ccggggcgau ccgccugguc    780

ggcaccgagc agggcguggg ggugcggcug gccggcgaca uggccgccag cggcggcgac    840

auccgcaucg acgccagcgg caagcugagu cuggcccagg ccuccagcca gggcgaccug    900

aagaucgcgg cccaggccgu ggagcugaau ggcaagaccu acgccggcgg cagcgccgag    960

auccgcagcg cggaggaacu ggucaaccgg cagagccugg cggcgcgcga acgcaucgug   1020

cuggaggcgg cgcauaucga caacgccggg gugaucgaag ccggcgucga gccagacgag   1080

cgacgcaacg cgcgcggcga ccucgagcug cgcagcggca cccugcgcaa cgccggcagc   1140

cugguggcca gccgcgcgcu ggaagcgaag gcgagccagg cgcuggacaa ccagggcggc   1200

agccugaagg gggcgaccgu ccgggucgac gccgggcacc uggacaaccg uggcggcaag   1260

cugcucgccg agggcgaacu gcgggucgag gcgagcagcc uggacaaccg ccaggacggc   1320

cuguugcaga gccgggaccg cgccgugguc aagacccgug gcgaucucga caaccguggc   1380

ggccagguga ucggccugaa cgaucuggag gucggcgcgg cgacgcucga caacggccag   1440

caaggccugc ucggcagcca gcaguccacc cgcgucagcg cccaggcgcu ggucaaccgg   1500

ggggacggcg aagucuccgg caagcgcguc gaggcucgcg ucgguagccu cgacaaucgc   1560

ggcggcaagc ugaucggcga cgaccugcug gugguccgcca gcggugccau cgacaaccgc   1620

cucggcuugu ucuccgcagc caaccgccuc gaccugcggg cgcgcagccu ggacaacagc   1680

ggcaagggca cgcugagcag ccggggcggc cuggagguca gccucggcgg ccugcuggac   1740

aaccgcgaug aaggcaaccu gcucagccag ggcgcgcagc gcgugacggu ggggcaacug   1800

gacaaccgcg ccggcggccu gcugucgagc cgcagcgagu ugaacgucca cggcgccagc   1860

cuggacaacc guggcggcgu gcugguggcc gacgccggcc ugagcgccac gggaggcgcc   1920

uucgacaacc gcgacggcgg cagcgccagc ggcaaggcug gcgugcgcgu ggaggucgcc   1980

agccugcgca acgaccaggg uggcaagcug cucagcgaug gccgccugga ccucgcagcg   2040

aacgccgucg gcaacgccgg agggcguauc gccgccaagg gcgaccugca ggcgacgcuu   2100

ggcagccugg cccagcaagg uggcgaacug gucagcgaaa agacccugaa ggucgcggcc   2160

gacacgcucg acaacagcca guccgggcug aucgccgcga auggcggcau cgcuaucgag   2220

gcgcggcagg ucgacaaccg cgccggcgag auuuccagca ccucgaaggu cgccgugaac   2280

gcccgcgagc aacuggacaa ccgcggcggc aaggucaucg gcgacagcgg ccugcgccuc   2340
```

-continued

accgugcagc gccugcugaa ccaggccaag ggggugcugg ccgggcgcga cggccugagc 2400

cuggacggcg gcgaacuguu caacggcgac ggcggucggc ucgacagcca gaacagccug 2460

agcgugagcc ucggcggcgu gcuggacaac cagggcggcg cgcuggucag cgaaggcagc 2520

cugacggcgc gcgccgcgcg ccuggacaac cguggcggga ccuucuccag cgccggugcg 2580

cuggcgcuga ccagccaggc cgcgcuggac aaccagggcg gcaggcugcu cagcgaugcc 2640

ggcgugacgc ugcagggcgc cagccucgac aacagccguu ccggcgugau cagcgccaag 2700

ggcgcggugg auauccgcac cggcguacug gacaacagcc gcaacggcgg caucggcagc 2760

aacgccggca ucacccuggu ggccgcccgg cuggacaacg gccagcaggg ccgggucagc 2820

gccaagggcc ugcucgacgc caaccugaaa ggccucgacc agcgcggagg cggcguccug 2880

aucagcgaaa ccggcgucac ccucgaccuc aauggcggca cgcuggucaa ccgcgacggc 2940

ggccugaucg ccacgcccgg cgcgcugcug cugcgccagc ucggcgcggu ggacaacggc 3000

gccggcgggg aaaucuccag cgaccgcgcc uucacccucg ccgccgccag ccuggacaac 3060

cgcggcgggc gccugaucgg cgccgccaac cugacccugc gcaucgccca ggcccuggac 3120

aacagccugg ccgggguggau cuccggcgcc gccggccugg acaucgcggc cgcucgccug 3180

gacaacagcg ccaagggcac ccuggccagc cgcgccggca ucgaccugcg cgucgauggc 3240

gcgcuggaca accacgccga aggcaccguc uccggcgccc gccugacgcu cgccagcgcc 3300

ucgcuggaca acagcggcaa gggccugcuc uccggcaacg ccggccugag cgucgccacu 3360

ggcgcgcugg acaacgccga ggguggccag uugaucagcc agggcguccu ggacgucagc 3420

agcgccgacc ucgacaaccg uggcggcgcc cucaguggca agcagucgcu gcgccugagc 3480

gccgccaacc uggacaaccg uggcggccug cucaccagcg acggcgaacu ggaacugacg 3540

gcagggcgcg ucgauuccgc cgacggcggc gaaaucuccg cccggggcga ccugcgccug 3600

acggucgagc gccuggugca acgccagggc cggcuggucg gcgagcgcgg cgucagucuc 3660

gaccugcggg gcggcgaccu ggacaaccag ggcggccuga ucagugcccg cggcccgcug 3720

agcaucgagc ggcugagcgu ccucgacaac cgccagggcg gcgagauuuc cagccagcag 3780

ggcuucgagc ugcuggccag gcgcaucgac aacggccagc aggggcgcau caucagcgcc 3840

gggaaacugc gccuagacgc cgacgcgcug ggcaacgccg gcgccggccu gcucuccgga 3900

uggcagggcc ugacggugac aggcgggagc cuggacaaca gcgccggcgg cacccuuucg 3960

agcaaggacg gcgagcuggc caucagccuc ggcggcgcgc uggacaacca cggccagggc 4020

gcgcugguca gcaagggcgc gcaacggauc gacgccgcca gccuggauaa cgcccagggc 4080

auugucuccg gcgaaagcga cgugacccug agcaucgccg ggaagcugga caacggccag 4140

ggcggccugg ucucggcgca gcgcgcgcug agcuucgagc gcgacgauac gcugcugaac 4200

aacgccggcg gccggaucaa cggcggcagc cugcugcuca agggcgccag ccuggauaac 4260

agcgacggcc aguugaucag ccagggccgg cucgacgcca uccucggcgg cgcccugguc 4320

aacaccggcg cggcgcgccu ggccagcggc ggcgaccugc ugcugcgcag cgccagcguc 4380

gacaaccgcg gcggcaagcu ggucagccag gggcugcugg agaucagcgc cggcagccuc 4440

gacaacagcg ccuccggcac ccucgccagc caggccggca ugagccugcg ccugggcggc 4500

ggcgcccugc gcaaccagca ggacggccug aucuucagcc aggccggcgc ccucgaugug 4560

caggccggca gccuggacaa ccgccagggc acgcuccagg cccagggcga caaccggcug 4620

-continued

cguaucggcg gcgcgcugga caaccagggc ggccgccugg acagccgggc cggcaaccuc 4680

gaccugcaga gcggcagccu cgacaacggc gccggcggcg ugcucaacag cgccaagggu 4740

uggcugaagc uggucaccgg gcuguucgac aacagcgccg gcgucaccca ggcgcagucg 4800

cuggagauuc gcgccgggca aggcgugcgc aaccagcagg gccaccucuc ggcgcugggc 4860

ggcgacaacc gcaucgucac cgccgacuuc gacaaccagg gcggcggccu cuacgccagc 4920

ggccugcuca gccucgacgg ccagcgcuuc cucaaccagg gcgcggcggc gggccagggc 4980

ggcaaggucg gcgccgggcg caucgacuuc agccuggccg gcgcgcuggc caaccgcuuc 5040

ggccaguugg aaagcgaaag cgagcugcac cugcgcgccg ccgcgaucga caacagcggc 5100

ggcagccugc gcgcccucgg ccgcagcggc agcacgcggu uggucgcugg cggccugaac 5160

aacgccuacg gcgugcugga aagcgccaac caggaccucg accugcaacu gggcagccug 5220

gccaacgccg gugggcgcau ccuccacacc ggcaauggca ccuucggccu ggauuccggg 5280

caggugaucc gcgccggcgg cgaacugacc accaauggcc ugcuggacau ccgcgccagc 5340

gaauggacca acagcagcgu gcugcaagcc ggacgccuga accuggacau cggcaccuuc 5400

cgccagacgg ccgagggcaa gcuguuggcg gugcaguccu ucacuggccg cggcggcgac 5460

uggagcaacg acggccugcu ggccagcgac ggcagcuucc gccucgaccu gagcggcggc 5520

uaccguggca acggccgcgc caccagccuc ggcgacuucg cccugaacgc cgccagccuc 5580

gaccucggca acgccgccag ccucgccggc ggugccaaug ucacgcucgg cgccggcaac 5640

cugcugguca accgugggcg gaucaccgcc gccggcgacc ucguggccag cgccgcgagc 5700

cugaacaacu acggcacccu gggcggcggc ggcaaccugc gauugaacgc gcccgcccug 5760

cucaacgagc gcggguugcu guucaguggc gccgacauga cccugcgcgc cggcgacauc 5820

accaaccucu acggggaugu guacagccuc ggcaggcugg auaucgcccg cgacgaugcg 5880

ggcaaccgug ccgccagccu gcgcaaccuu uccgggguga ucgagagcgg caaggacuuc 5940

agccugcgug ccagccugau cgagaaccgu cgcgccgugc uggaaagcaa gucgggccug 6000

uacaccgcga agauggagca gaccgccugc aucgaaggcg ucaacgcggg cgacugcagc 6060

ggcaagcgca acgccaucug gaccaucacc cagcgcgaca agaccgaggu caccgccagc 6120

agcgccaugg ggcaacugcu ggccggaggc gacuucgcca ucgacggcgg cacccugaac 6180

aaccuuucca gucugaucgg cagcggcggc aaccucaccg ccaaccucga aguccucgac 6240

aaccagggcc uggaaaccgg cgagcuggaa accauccgcg ugcugcguac cgcucgcggc 6300

ggcgauaucg gcggcaucga ccagaagucg cgcaacuuca ccaaccucua cugguaccag 6360

agcgccaauu ucgacccggc gcgcgcgggc gagauccccg ccgcgcucaa cgcgauccuc 6420

agcgacuggu ccuucgagua cgaauucccg agcaaggggc cgaccccgau cagcaguggc 6480

gaccaguccu acgcagcggu gauccaggcc gccggcgacg ucacggucaa ugccagcacg 6540

cgcaucgaca acggcgucac ccgccccggc uacaccuucg ucggcagcgg ccgccaggug 6600

ggcgacagcg cggugggcgg cagcgggguu ucgguggucg ugccgcugac cucgcaacug 6660

ccgcccgacc uggcgcggcg ccaggucaac ccgguuaccc ugcccggcuu cagccugccc 6720

cagggugaca acggccuguu ccgucucagc ucgcgcuuug ccgaggacgg caauggcagc 6780

gccgcgcucg gugccggcgc cgaccgcacc cagggcggua gcggcgucuc ggucggccag 6840

caaggcgccg gcaacgccgc cgguaccugg cagggccagg gcgugcgagu cgacggccug 6900

-continued

gcuggcgcgg ccaacgucca gggucagggc ggcagcacgc ucggcgguag ccugccgggc 6960

gucgcccggg uccagggcgu gcccggcaac gccacgccga gcgccagcca caaguaccug 7020

aucgagacca acccggcgcu caccgaacug aagcaguucc ucaacucgga cuaccugcuc 7080

agcggccugg gcaugaaccc ggacgauagc aagaagcguc ucggcgacgg ucucuacgag 7140

cagcggcuga uccgcgacgc gguggugggcg cgcaccggcc agcgcuacau cgacgggcug 7200

agcagcgacg aggcgcuguu ccgcuaccug auggacaacg ccaucgcuua caaggaccaa 7260

cugcaccugc aacugggugu gggccugagc gcggagcaga uggcggcgcu gacccacgac 7320

aucgucuggc uggaagaggu cgaggugaac ggcgagaagg uccucgcgcc gguggucuac 7380

cuggcccagg cggagggucg gcuggcaccc aacggugcgc ugauccaggg ccgcgacgug 7440

aagcugguga gcggcggcga ccugcauaac gucggcaccc ugcgcgcgcg gaacgaccuc 7500

ucggcgacgg ccgacaaccu cgacaacagc ggccugaucg aggccggcaa gcgccucgac 7560

cugcucgccg gcgacucgau ccgcaaccgc cagggcgggg ucaucgccgg gcgugacgug 7620

agccucaccg cgcugaccgg cgacguaauc aacgaacgca gcgugacccg cuacgacagc 7680

gcgcucgacg gccgcaccug ggaacgcagc uucgccgaca gcgccgcgcg gguggaggcg 7740

gcgaacagcc ugaacgucca ggccggacgc gacaucgcca accucggcgg ggugcugcag 7800

agccgcggcg accucagccu cgacgccgga cgcgacguca ccgucgccgc cgucgaggac 7860

cgccagggcc agacccgcug gagcacgucg cggcuccaga gcgugaccca gcucggcgcc 7920

gaagucagcg ccgggcggga ccugaacguc agcgccggcc gcgacuugac ggcgguggcc 7980

agcacccucg aagcgcgccg cgacaucgcc cucuccgccg ggcgcgacgu gacccuggcg 8040

gcggcggcga acgaggagca ugccuacagc aagaccagga aggucaccua ccaggaagac 8100

aaggucgccc agcaaggcac ccgcguggac gccggcggcg accuggcgau caaugccgga 8160

caggaccugc gccugaucgc gagccaggcc agcgccggcg acgaggccua ccugguggcc 8220

ggcgacaagc uggaacugcu ggccgccaac gacagcaacu acuaccugua cgacaagaag 8280

aagaaaggcg acuucggccg caaggaaacc cggcgcgacg aagucaccga cgucaaggcg 8340

gugggcagcc agaucagcag cggcggcgac cucacccugc ucagcggcgg cgaccagacc 8400

uaccagggcg cgaagcugga aucgggcaac gaccuggcca ucgucagcgg cggcgcggug 8460

accuucgagg cggugaagga ccugcaccag gaaagccacg agaagagcaa gggcgaccug 8520

gcguggaaca gcgccaaggg gaaagggcag accgaugaaa cgcuucggca gacccagauc 8580

guggcccagg ggaaucuggc gaucaaggcc guggaagggc ugaagaucga ccucaagcau 8640

aucgaccaga agaccguaag ccagaccauc gacgcgaugg ugcaggcgga uccgcaacug 8700

gcguggcuga aggaggccga gcagcgcggg gauguggacu ggcgcauggu gcaggaggug 8760

cacgauagcu ggaaguacag caacucgggc auggggccgg cgacgcagau cgcugucgcc 8820

aucgcggcgg cagccaucgg uggcauggcg gcagcgggag cgcucagugg ugcaggagug 8880

ggugccagua gcuucgccau gggcgcagga guuggugcgg caggaagccu gucgggcacg 8940

gcagcgguca gccugaucaa caacaagggc gaucucggga aggugcugaa agacagcuuc 9000

aguagugaca gucugaagca gauugcuauu gcgagccuga ccgggggcu gacggcugag 9060

uacuucgacg ggauucuuca gaccaagacu gauccgcuua cuggaaaggu cacgguagac 9120

cucagcagcc uaucuggugu uggucgcuuc gcugccaauc aggcgaugca gaacgcuaca 9180

-continued

uccacuguac ugagccaggc cuugggccag ggcgggagcc ugaacgaggc gcugaagagc 9240

gcgcucuaca acaguuucgc ggcggcaggu uucaacuucg ucggcgauau cggccaggaa 9300

uacagccuga agccaggcga uccuucgaug gugaccaugc acgcccugau ggguggccug 9360

gcggcgcagg ucagcggugg cgauuucgcc acgggcgccg cggcggcugg cgccaaugaa 9420

gcgcuggugg ccaagcuaga ccaggccuuc aagagcuuga gcccugagaa ccgugaagcc 9480

auggucacua uggggucgca auugguuggu guucuggcug cggcgguacg cgauccugau 9540

gugacaggca aagcucugga aagcgcugcu ugguagcga agaacucgac gcaauacaac 9600

uuccucaacc aucaggaugu ggccgaucug gauaaugccu ugcagaaaug caagucccag 9660

ggaaauugcc gucagguaga ggaagaguuc aaggcgcgua gcgacgagaa ccggcggagg 9720

uugaauggcu gcguggcugu ggguaauugc gcggagauuc gugcggagau cgaugcgggg 9780

ucuacggcuc ucaacgagcu gguggcccgg caggaaacag cuaauccggg aggaagugac 9840

agcgauauag ccuacgguuu ccugaugggc cgaaauguug ucgacuggac gacggcuggu 9900

caguugcacc uggagcagac cgccaaccuc ugguggaacg guaauccaca guggcagaag 9960

gaagucggug cauaccuaga ccagacgggg uucaauccgu ucggaaucgg cguuccggca 10020

augggcggug ccgcuggcaa gguaacggcc aaggcgcuca ugaaugcgcu gaaggcggga 10080

gaguugccca aggagaggu ggccccagga aaggcuaauc ugccuaccau uggggcguug 10140

gcggaugcug aggcgggaau gccuuauacc cauccaguua agcucgccgc aaaagcgacu 10200

gggacagcag ggaagauuaa gauugaagcc ggcgcaauac cugacgcaaa ugaaguacgu 10260

gcaggacaag gguuaucugg ucuuggguac gauguuacgc accaaaccac ugcgucagcu 10320

aaagguauuc aagggcagcg aacugcggac uugcauguug auggacucgg uuccauugau 10380

guguauacgc cgaagaaucu ugauccgaca aagauaguuc gagcgauaga gaagaagucg 10440

aaucaagccg gcggagucuu ggugcaggcg gacuugccaa gcacugacau gucguccauu 10500

gcugcucgua uguggggaa gacuaacgcg cagaguauaa aaacuauauu uuuccagaaa 10560

ccagacggau cauugguccg auuugaucga ccugcuggag gaggcuga 10608

<210> SEQ ID NO 90
<211> LENGTH: 16884
<212> TYPE: RNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 90

auggacaucc gcagcccgcu gaaccagugc aucgcccugu cccuggccgg cauccuguuc 60

cucaacccga ucgucgccgc ggcggcgggg cuggcgcugg acaaggccgc cggcggcaac 120

accggccugg gccaggcggg caacggcgug cccaucguca auaucgccac gcccaacggc 180

gccgggcugu cgaacaacca uuuccgcgac uacaacgucg gcgccaacgg gcugauccuc 240

aacaacgcca ccggcaagac ccaggguacc cagcucggcg ggaucauccu cggcaacccc 300

aaccucaagg gccaggcggc gcaggugauc cucaaccagg ucaccggcgg caaccgcagc 360

acccuggccg gcuacaccga gguggccggg cagucggcgc gggugaucgu cgccaacccg 420

cacggcauca ccugccaggg cugcggcuuc aucaacacgc cgcgcgcgac ccucaccacc 480

ggcaagccga ucauggacgg ccagcgccug gagcgcuucc agguggacgg cggcgacauc 540

gucgucgaag gcgccgaacu gaacgucggc aaccucgaac aguucgaccu gaucacccgc 600

-continued

agcgccaagc ucaacgccaa gcucuacgcg aagaaccuca acaucgucac cggccgcaac 660

gacguccagg ccgacagccu gcaggccacg ccgcgcgccg ccgauggcag cgagaagcca 720

caacuggcga ucgacagcuc ggcgcugggc gggauguacg ccggggcgau ccgccugguc 780

ggcaccgagc agggcguggg ggugaagcug gccggcgaca uggccgccag cggcggcgac 840

auccgcaucg acgccagcgg caagcugagc cuggcccagg ccuccagcca gggcgaccug 900

aagaucgcgg cccaggccgu ggagcugaac ggcaagaccu acgccggcgg cagcgccgag 960

auucgcagcg cggaggaacu ggucaaccgg cagagccugg cggcgcgcga acgcaucgcg 1020

cuggaggcgg cgcauaucga caacgccggg gugaucgaag ccggcgucga gccagacgag 1080

cgacgcaacg cgcguggcga ccucgagcug cgcagcggca cccugcgcaa cgccggcagc 1140

cugguggcca gccgcgcgcu ggaagcgaag gcgagccagg cgcuggacaa ccagggcggc 1200

agccugaagg gggcgaccgu ccgggucgac ggcggacacc uggacaaccg uggcggcaag 1260

cugcucgccg agggcgaacu gcgggucgag gcgagcagcc uggacaaccg ccaggacggc 1320

cuguugcaga gccgggaccg cgccgugguc aagacccgug gcgaucucga caaccguggc 1380

ggccaggucg ucggucugaa cgaacugcag guccaggcug ccgcacugga caaucgcagu 1440

gccggucucc uuuccagcaa gggagacaug gacaucgagu ucgcucgucu ggacaacagu 1500

gcgggcggca agcuggucag cgagcgccgu acgcuccuga aggcggaucg gcucgauaau 1560

cgcagcgguc gcauugucgc cggccaggau cucgacuuga gcucucgguu gaucgacaac 1620

cgagcgggcg auaucuccag cacgucgagg gugguggcga gcgcucgcga acaguuggac 1680

aaccgcggug gcaagaucgu cggugacagu ggccuggaca ucacaacgcc acgcaugcuc 1740

aaccaggaca aggggguacu cgccagccgc gaugggcugc gccugagugc uacggaguug 1800

uucaacggcg cgggggccu gcuguccagc cagaagggua ucgacgucuc ccuggccggu 1860

gcguucgaua accaggccgg cagccuggac agccggggcu uccugacggu gaagucagcc 1920

uggcucgaca accagggcgg uacgcuaucc agcgcagggg cauuggcagu gaccagccag 1980

ggcgcccuga acaaucaggg cggcagacug gcgagcgacg ccggacuuag cuugagcagc 2040

gccagccucg acaacagcca ggccggugcg aucaguggca agggggccgu ggagauucgu 2100

accggcaacc ugaacaacag ccggaaagcc aguaucggca gcgaugcggg acucacccug 2160

gucgccgcuc ggguagacaa cagccaggcg ggccggaucg ccgccaaggg ugugaucgau 2220

gcggaucucc aagggcugga ccagcaugac aggggcaacc uggucagcga uaccggcauc 2280

acgcucgauc ugaacaaggg aagccugguc aaucgcgcuc aaggccugau cgccacgccu 2340

ggcaccuugc uccugcgcca acucggcgug guggacaaca gcgguggga aaucuccagc 2400

gaccgcgcgu ucacucuugc caccuccgcg uugaacaacc agggggacg ccugcucagc 2460

ggcggagccc ugaccuugcg uaucgcgcag gcccuggaca acagccucga ggggauuguc 2520

uccggugcug gaggucugga uauccaggca uucguccugg acaaccguag uggcuccauc 2580

ggcagcaagg gcgccaucga uaucggugug acccgccugg aaaacgacgc uggcacacug 2640

aucgcugaac gcggccugaa gcugguagcc gaugaggcga acaguuccaa ggggcguauc 2700

gccgccaaug guagccugca ugccaagguu ggcacgcuga gccagaaggg aggagaacug 2760

accagucagg acucgcugac ucucgaccug ggcauccuaa acaauaacgc uggccguauc 2820

gcuggcaacc agggcgugga caucacggcc cggcaggugg acaacagcgu cggcgagauu 2880

-continued

gccagccagg gcgugguggc gcugaaccuc acugagcagc uggacaaccg uggcggcaag 2940

aucgucggug acaguggucu gggcaucacc gcgccgcacg ugcucaacca ggacaagggg 3000

guacucgcca gccgcgaugg gcugcgccug agugcuacgg aguuguucaa cggcgcgggg 3060

ggccugcugu ccagccagaa ggguaucgac gucucccugg ccggugcguu cgauaaccag 3120

gccggcagcc uggacagccg gggcuuccug acggugaagu cagccuggcu cgacaaccag 3180

ggcgguacgc uauccagcgc aggggcauug gcagugacca gccagggcgc ccugaacaau 3240

cagggcggca gacuggcgag cgacgccgga cuuagcuuga gcagcgccag ccucgacaac 3300

agccaggccg gugcgaucag uggcaagggg gccguggaga uucguaccgg caaccugaac 3360

aacagccgga aagccaguau cggcagcgau gcgggacuca cccuggucgc cgcucgggua 3420

gacaacagcc aggcgggccg gaucgcugcc aagggugcga ucgaugcggc ucuccaaggg 3480

uuggaccagc augacagggg cagccugguc agcgauaccg gcaucacgcu cgaucugaac 3540

aagggaagcc uggucaaucg cgcucaaggc cugaucgcca cgccuggcac cuugcuucug 3600

cgccaacucg gcguggugga caacagcggu ggggaaaucu ccagcgaccg cgcguucacu 3660

cuugccaccu ccgcguugaa caaccagggu ggacgccugc ucagcggugg agcccugacc 3720

uugcguaucg cgcaggcccu ggacaacagc cucgagggga uugucuccgg cgccggaggu 3780

cuggauaucc aggcauucgu ccuggacaac cguaguggcu ccaucggcag caagggcgcc 3840

aucgauaucg gugugacccg ccuggaaaac gacgcuggca cgcugaucgc cgaacgcggc 3900

cugaagcugg cggccgauga ggcgaacaac uccaaggggc guaucgucgc caaggaugaa 3960

cugcgugcca aacucggugc gcuggugcag aacgggggag agcugacgac ucagggcgcg 4020

cuggcccucg acgccgacaa agucgacaac ggcgcugguc gcaucgccgg caaccgaggu 4080

guggucaucg augcccggca gguggacaac cgugccggcg agauugccag ccagggcgug 4140

gcgacgcuga aucucacuga gcaacuggac aaccguggcg gcaaagucgu ugcugacagu 4200

ggucugggca ucaccgcgcc acgcgugcuc aaccaggaca agggaguaau cgccagccgc 4260

gaugggcugc gccugagugg uaccgaauug uucaauggca augccggacu gcucagcagu 4320

cagagacaua uagaggucac ucuggacggc gugcuggaca aucagggcaa gggcgcgcug 4380

cucagcgacg guacccugac ggugagcgcc gggcgcauac acaaccagga cgccacucug 4440

uccagcgccg gugcgcugag acugagcagc caggaggcgg uggacaaccg uggcggcaag 4500

uuggugacgg acuccagccu gcgccugacc agcgccagcc uggacaacag ccgaucaggg 4560

aucaucagug ccaacgcugc ggcggagauc cauaccgggg uucugaacaa cagccagaaa 4620

ggcaaucuug gcaguaauga cgggcucggc cugauugcua cugaggugga uaacagccag 4680

gaaggucgga ucacugccaa aggcaugauc gacgcaaaua ucaagggacu cgaucagcag 4740

ggcaaagggc ggcuggucag uaaugccggc aucauacucg accugaacga gggaacccug 4800

gccaauggcg cucagggccu gaucgccacg ccuggaaccu ugcuccugcg ccaacucggc 4860

augguggaca acagcggcgg ggaaauuucc agcgaccgag ccuucacacu caccaccucc 4920

gcgcugacca accagggugg ccgccugcgc agcggcggug uacugacguu gcgcaucgcc 4980

caggcucugg acaacagccu cgaagguguu cucuccggca ccggaggccu ggauauccgg 5040

gcgcuugccc uggacaaccg caguggcucc aucggcagca agggcgccgu cgauaucgac 5100

gugucccguu uggaaaacga ugacggcgac cugcuuagcg aaggucgucu gaaacugacu 5160

-continued

gccgagcgag cgaacagugu caggggacgg aucgcggcca ggggugaccu gcacgccagc 5220

gugacagccu uuaaccaggc ggguggcgaa uugagcagcg agggugcgcu gaugcucgag 5280

gccgauagcc ucgacaaccg cagcggcggu cuggucagug cugauggcaa ccugaccguu 5340

uccgcccgga ggaucgacaa ccgugcgggc gaaaucgcca gcccgggcca ggugacacug 5400

gacgucgccg agcaguugga caaccgaggc ggcaaggcca ucggcgauag cggacuucgc 5460

cucgccgcgc cacggguacu caaccaggac ggcgggguac ucgccagucg ugaugggcug 5520

cgccugaaug gcgccgaacu guucaauggc aacggcggcc ugcucagcag ccagcaaagc 5580

aucgacguca uucuggacgg cguauugggc aaucaggcag gcagcuugag cagccaggga 5640

cgccugagcg ugaagagcgg ucggcuggac aaccagggcg gugcagucuc cagcgccggg 5700

accuugucgc uuuccagcca gggugcguug aacaaccagg ggggcagggu ggucaccgac 5760

gccggugccg uccugcgcag cgccagccuc gacaauagcc agggcggcau cgucagcgcc 5820

aagggggccg cggagauccg uacuggcagc cucaacaaua gccagaaggg cggcauaggc 5880

agcggugccg ggcucgcgcu ggucgcggac cugguggaca acagccagaa cggccggauc 5940

acugccaagg gugcgaucga ugccaaccug aaggggcugg aucagcaggg cagcggcagg 6000

cuggucagcg auacggccau cgcgcucgau cugcgcgggg gagaacuggu caaccgugcu 6060

cagggccuga ucgccacgcc uggagccuug cugcugcggc aacugggugu cguggacaac 6120

aguggcggug gcgagaucuc cagcgaucga agcuuuaccc ucgccgcgac cgcgcugagc 6180

aaccggggug gccgcgugau cagcggcgac ucccugaccc ugcgcaucgc ccaggcacug 6240

gacaacagcc uccaaggcgu ucuuuccgca agcggagggc uggaugucgc ugcacucguc 6300

uucgacaacc auagcggcau cguugcuagc aagggcgaua cacacaucgg ggugaaccgc 6360

cuggagaacg aggcaggccg cguggucagc gaaggcgccc uggaucugac cgccaagcag 6420

gugagcagcg ccaaggggcg cauugccgcg aagggcgauc ugcaggucac gguuggcacc 6480

cuggagcagc aggguggaga acuggccagu caggggacgc ugacucucga cgccgauagc 6540

cuggauaacc gcaauggcgg ccuggugagc gccgauggcg gggucaccgc cgaggcacgc 6600

cagaucgaua accgcggugg ggaaauaucc agcguggcca agguggcucu ggcuguccgg 6660

gaacaacugg acaaccgggg gggcaaggug aucggcgaca gugagcugag ccuaaccgug 6720

cagcgccugc ugaaccaggc caagggugug cucgccaguc gcgauggauu gcaccuggac 6780

ggcgcggaac ugcucaaugg cgauggcggc cugcucagca gccaacgccu gguggaugua 6840

acgcucagug gugcauugga caaccagggg agcggugcac uggucagcga agagucgcug 6900

acagugaagg ccgaccaggu caauaaccag gcggggacuu ucuccagugc ggguagccug 6960

cucguuacca gccggggcga guugaacaac cagggugggca gguuggugac cgaugcugga 7020

gccacccuga acagcacugg cuucgacaac agccgugcgg gccuggucag ugcgaaaggg 7080

gcuguggcca uucguaccgg agcccugaac aacagucaga agggauccau uggcggcaau 7140

acgggcguca cccuggucgc cggguugguc gacaacggcc gggaaggacg gaucagcacc 7200

aaggguacgc ucgacgccaa ccugaaaggg uugcuucagc aggggggagg cucgcugguc 7260

ggcgagcgcg gugucacccu cgaccucaac gguggcaccc uggacaacca cgaccucggu 7320

cugguuucaa cgccuggcgc gcuccugcug cgccaacucg gcauggugga caacagcguc 7380

ggcggagaga uauccagcga ccgugcuuuu acccucgccg ccaacacacu gaacaaucag 7440

-continued

```
ggcgggcggc ugaucagcag cgaagcuuug acccugcgca ucgccaagac acuggacaac   7500

agucucaagg ggcagguccu ggcgaccgac ggacuggcca ucgagucuca ggucuuggac   7560

aaccgugcgg gaaccaucgg cagcaagggu gaugcccgua ucagcgugac cagccuggac   7620

aacgccgaac aaggcagccu ggugagugaa ggccgccugg agcuuguagc cgaccaggug   7680

agcaacggca accaaggccg uaucgccgcc agaggcgugc uggaggcggc ggucgguacg   7740

cugcuccagc aaggcggcga acuggucagc caggggagcc uggaccuucg cgccgacacg   7800

cucgacaaca gccaguccgg gcugaucgcc gcgaauggcg gcaucgcuau cgaggcgcgg   7860

caggucgaca accgcgccgg cgagauuucc agcaccucga aggucgccgu gaacgcccgc   7920

gagcaacugg acaaccgcgg cggcaagguc aucggcgaca gcggccugcg ccucaccgug   7980

cagcgccugc ugaaccaggc caagggggug cuggccgggc gcgacggccu gagccuggac   8040

ggcggcgaac uguucaacgg cgacggcggu cggcucgaca gccagaacag ccugagcgug   8100

agccucggcg gcgugcugga caaccagggc ggcgcgcugg ucagcgaagg cagccugacg   8160

gcgcgcgccg cgcgccugga caaccguggc gggaccuucu ccagcgccgg ugcgcuggcg   8220

cugaccagcc aggccgugcu ggacaaccag ggcggcaggc ugcucagcga ugccggugug   8280

acgcugaagg gcgccagccu cgacaacagc cguuccggcg ugaucagcgc caagggagcg   8340

guggauaucc gcaccggcgu acuggacaac agccgcaacg gcggcaucgg cagcaacgcc   8400

ggcaucaccc ugguggccgc ccggcuggac aacggccagc agggccgggu cagcgccaag   8460

ggccugcucg acgccaaccu gaaaggccuc gaccagcgcg gaggcggcgu ucuggucagc   8520

gaaaccggcg ucacccucga ccucaauggc ggcacgcugg ucaaccgcga cggcggcuug   8580

aucgccacgc ccggcgcgcu gcugcugcgc cagcucggcg cgguggacaa cggcgccggc   8640

ggggaaaucu ccagcgaccg cgccuucacc cucgccgccg ccagccugga caaccgcggc   8700

gggcgccuga ucggcgccga cagccugacc cugcgcaucg cccaggcccu ggacaacagc   8760

cuggccgggg ugaucuccgg cgccgccggc cuggacaucg cggccgcucg ccuggacaac   8820

agcgccaagg gcacccuggc cagucgcgcc ggcaucgacc ugcgcgucga cggcgcgcug   8880

gacaaccacg ccgaaggcac cgucuccggc gcccgccuga cgcucgccag cgccucgcug   8940

gacaacagcg gcaagggccu gcucuccggc aacgccggcc ugagcgucgc cacuggcgcg   9000

cuggacaacg ccgagggugg ccaguugauc agccagggcg uccuggacgu cagcagcgcc   9060

gaccucgaca accguggcgg cgcccucagu ggcaagcagu cgcugcgccu gagcgccgcc   9120

aaccuggaca accguggcgg ccugcucacc agcgacggcg aacuggaacu gacggcaggg   9180

cgcgucgauu ccgccgacgg cggcgaaauc uccgcccggg gcgaccugcg ccugacgguc   9240

gagcgccugg ugcaacgcca gggccggcug auuggcgagc gcggcgucag ucucgaccug   9300

cggggcggcg accuggacaa ccagggcggc cugaucagug cccgcggccc gcugagcauc   9360

gagcggcuga acguccucga caaccgccag ggcggcgaga uuuacagcca gcagggcuuc   9420

gagcugcugg ccaggcgcau cgacaacggc cagcaggggc gcaucaucag cgccgggaaa   9480

cugcgccugg acgccgacgc gcugggcaac gccggcgccg gccugcucuc cggauggcag   9540

ggccugacgg ugacaggcgg gagccuggac aacagcgccg gcggcacccu uucgagcaag   9600

gacggcgagc uggccaucag ccucggcggc gcgcuggaca accacggcca gggcgcgcug   9660

gucagcaagg gcgcgcaacg gaucgacgcc gccagccugg auaacgccca gggcaucguc   9720
```

-continued

uccggcgaaa gcgacgugac ccugagcauc gccgggaagc uggacaacgg ccagggcggc 9780

cuggucucgg cgcagcgcgc gcugagcuuc gagcgcgacg auacgcugcu gaacaacgcc 9840

ggcggccgga ucaacggcgg cagccugcug cucaagggcg ccagccugga uaacagcgac 9900

ggccaguuga ucagccaggg ccggcucgac gccauccucg gcggcgcccu ggucaacgcc 9960

ggcgcggcgc gccuggccag cggcggcgac cugcugcugc gcagcgccag cgucgacaac 10020

cgcggcggca agcuggucag ccaggggcug cuggagauca gcgccggcag ccucgacaac 10080

agcgccuccg gcacccucgc cagccaggcc gacaugagcc ugcgccuggg cggcggcgcc 10140

cugcgcaacc agcaggacgg ccugaucuuc agccaggccg gcgcccucga ggugcaggcc 10200

ggcagccugg acaaccgcca gggcacgcuc caggcccagg gcgacaaccg gcugcguauc 10260

gguggcgcgc uggacaacca ggccggccgc cuggacagcc gggccggcaa ccucgaccug 10320

cagagcggca gccucgacaa cggcgccggc ggcgugcuca acagcgccaa ggguuggcug 10380

aagcugguca ccgggcuguu cgacaacagc gccggcguca cccaggcgca gucgcuggag 10440

auucgcgccg ggcaaggcgu gcgcaaccag cagggccauc ucucggcgcu gggcggcgac 10500

aaccgcaucg ucaccgccga cuucgacaac cagggcggcg gccucuacgc cagcggccug 10560

cucagccucg acggccagcg cuuccucaac cagggcgcgg cggcgggcca gggcggcaag 10620

gucggcgccg ggcgcaucga cuucagccug gccggcgcgc uggccaaccg cuucggccag 10680

uuggaaagcg agagcgagcu gcaccugcgc gccgccgcga ucgacaacag cggcggcagc 10740

cugcgcgccc ucggccgcag cggcagcacg cggcuggucg cuggcgaccu gaacaacgcc 10800

uacggcgugc uggaaagcgc caaccaggac cucgaccugc aacugggcag ccuggccaac 10860

gccggcgggc gcauccucca cacuggcaac ggcaccuucg gccuggauuc cgggcaggug 10920

auccgcgccg gcggcgaacu gaccaccaau ggccugcugg acauccgugc cagcgaaugg 10980

accaacagca gcgugcugca agccggacgc cugaaccugg acaucggcac cuuccgccag 11040

acggccgagg gcaagcugcu ggcggugcag uccuucacug gccgcggcgg cgacuggagc 11100

aacgacggcc ugcuggccag caacggcagc uugcgacucg agcugagcgg cggcuaccgu 11160

ggcaacggcc gcgccaccag ccucggcgac uucgcccuga acgccgccag ccucgaccuc 11220

ggcaaugccg ccagccucgc cggcggcgcc aaugucacgc uuggcgccgg caaccugcug 11280

gucaaccgug ggcggaucac cgcugccggc gaccucgugg ccagcgccgc gagccugaac 11340

aacuacggca cccugggcgg cggcggcaac cugcgauuga acgcgcccgc ccugcucaac 11400

gagcgcgggu ugcuguucag uggcgccgac augacccugc gcgccggcga caucaccaac 11460

cucuacgggg auguguacag ccucggcagg cuggauaucg cccgcgacga ugcgggggc 11520

ugggcaaauc gcuuggagaa cauuuccggg aauuuagaga gcacagguga uaugcguuuc 11580

uccgugaguu cacuucucaa uagaagggaa acucuagaga uugaagguga cuugcagaau 11640

agcgcuauug gcguccgcug uacggggugu cagcuuucug agaggugggg aaaaacuagg 11700

ucuucgagcg agcuugucug gaucagggaa uauaagucua cauugggaga uucuucugcc 11760

gcugcuucaa uuacggcugg ucgagaucug cuuguuguag gugcaagccu gcagaauauu 11820

gcuucuaaua uaagugcugu aagagacgcc acgcuaucuc ugaguaauuu cgaaaacaaa 11880

gguuaugcgu uaggggaaua ugcggucagg ggcguuuauu cgccgccgag uaaauuuggc 11940

gaagaauugc uuaugcgcau auuggcguau aacgcuguca acgaucccag uuaugggag 12000

-continued

```
ggauaugcga gcacaggggg gagacuuccg aauauucauu auuucgacaa gaauuuuaau  12060
gaaaaagucu cuccgcugga ggucauucau ggaaacggga aaaauggugg gccggguugg  12120
caccuguacu ucgguaccuu agauguugag uauccggaca cagaucgcug gaauaaggcu  12180
auuggacgaa uaccggcgcc gaauuauuca ucgaaaaaaa cggaugcuau uccagaucua  12240
cuuaagggau uggcuccucu cgaugaguug acgauuaaca aaggggcgaa cucaacgguu  12300
ggugcugucg ugcaagcugg cggucgugua acggugaaug cugcggagag uuucaauaau  12360
ucuguccuac agggauuuca ggccguucag gaaacccagu uaccucauca ggacauagcu  12420
guuucaagca cgacgagcgc cguagugacu cugaagaguc aacugccagc ggauuuggca  12480
aggcaacaga ucaauccucu cacccugccg ggcuucagcc ugccucaagg ccagaauggg  12540
cucuuccgcc uggcguccca aggagcccag gugaaccagg caaguggugc ucugaaaucc  12600
gccagcgauc ucacccagag cggccauggc guaucuguau ccgcacagac aggcaguggc  12660
gcaaguggcu ggaguaccca ggcgcgucgu gucggcgaug aucgggucac cucgcuugcc  12720
gguuccgccu aucaaggccg gguagcugag gcuaucgaug cgcuacgggc uuccgcgcca  12780
aucucgggcg acgggggaaa cacuggccgu uuccaggccg gugagcacca ggcgaccacg  12840
ggacugggug gacucgucga gggcaaugca ucgggucaca gcggcaaugg cgucauccuc  12900
gccgaucugc gcgguggucu acccucguuc ucaagccuuc ccgcgucuga ucauguucaa  12960
ggcacagugc ccggucacga ugggaaugga acuauucucg ccaauuggca gggugcgcag  13020
gcgacggucc aggccucgcc uucgacagug cguguagagg ggguagucuc caguccaggu  13080
ggcaauggca gcauccuugc cgaucugccg gcugaacagu cgucggugca ggcacugccu  13140
ucggccguua gggcucaggg cagccugccu cgccucgaag agcggagcgc ccuucuugcc  13200
gagccuccgg uugggcagcc ggcguugcaa acccugccgu cgguugcgcg cguugagggc  13260
gugcccagca augccacacc gagcaacagc cacaaguauc ugaucgagac caacccggcg  13320
cucaccgagc ugaagcaguu ccucaacucg gacuaccugc ucgguggucu ggguaucaau  13380
ccggacgaua gcaagaagcg ccugggugac ggucuauacg agcagcgccu gguacgcgaa  13440
gcgaucgucc agcguacggg gcagcgcuuc aucgccggau ugaacagcga cgaagcgaug  13500
uuccgcuauc ugauggacaa cgccaucgcc agcaaggacg uauugggacu gaccccuggc  13560
gucacccuca gcgccgccca gguggcggcg cugacccacg auaucguuug gcuggaagaa  13620
gucgagguga auggcgaaaa gguccucgcc cccguggucu accuggccca ggccgagggg  13680
cgguugggcc cgaacggcgc gcugauccag ggcgcgacg ugaaccugau caccggcggg  13740
gaccugagga acgccgguac ccugcgcgcg cagaacgacc ucagcgcgac agccggcaac  13800
aucgacaaca gcggccugau cgaggccggc aaccgccucg accugcuggc cagcggcucc  13860
auccgcaaug accagggcgg caucauugcc gggcgcgagg uaagccucuc ugcccuuacc  13920
ggagacguca ucaaugaacg gacggugacc cagcaccagu ccuccuacag gggaaccggu  13980
accacugagg cauuugccga uagcgccgcg cguaucgagg cugcgcagaa gcugaccguu  14040
ucggcaggac gcgauguagc caauauuggc ggugucaucg acagcaaggg cgaccucgcc  14100
uugcaaggcg gcagggaugu ccugguuucg gcugcgguag cggagcgggg cuggacggca  14160
ggaagccagg cauaccagac ccagacgacc cagaugggcg ccgaggucgu ggcggggcgc  14220
gauaucagcg ucagcgccgg acgcgauauc agcgucgugg gcagccgcau cgacgcucgu  14280
```

-continued

cgcgacguga cauucgaggc gggucgcgau gugggccugg ucgcggcugc caacgaagag 14340

caugccuaug gcaagaccaa gaaggucacu uuccaggacg acaagaucac ccagcaggcc 14400

acucgcgugg acgcuggcgg cgaccuggcg aucaaugccg gacaggaccu gcggcugguc 14460

gcgagccagg ccagcgccgg cgacgaagcc uaccuggugg ccggcgacaa gcuggagcug 14520

cuggccgcga acgacagcag uuacuaccuc uacgacaaga agagcaaagg cagcuucggu 14580

agcaagaaga cccggcgcga cgaaaucacc gaugugacgg cagugggcag ccaaauaucc 14640

agcggcggcg accucacccu gcucaguggc ggcgaccaga cuuaccaggg cgcgaagcug 14700

gaaucgggca acgaccuggc caucgucagc ggcggcgcgg ugaccuucga ggcgguaaag 14760

gaccugcacc aggaaagcca cgagaagagc aagggcgacc uggcguggca gucgucgaag 14820

ggcaagggcc agaccgacga aaccgugcgc cagagccaga ucguggccca ggggaaucug 14880

gcgaucaagg ccguggaagg gcugaagauc gaccucaagc acaucgacca gaagaccgug 14940

agccagacca ucgacgcgau ggugcaggcg gauccgcaac uggccuggcu gaagcagaug 15000

gagcagcgcg gcgaugugga uuggcggcgc gugcaggaac ugcaugacag cuggaaguac 15060

agcaacuccg ggcugggcgu cggcgcgcag uuggcgauag cgaucguugu ggccuacuuc 15120

acggcgggug cggcgagugc ggcauuggga ucgauggcgg gagugggggc gggcucagga 15180

agcaugaugg cugcugccgg uagcacugca augguccagg ccgguacagc aguaggaaca 15240

gcugccgccg gcugggcgaa ugcagcugga acugccgugg cuaugggcau ggccagcaau 15300

ggagcgauca gcaccaucaa caaccgggga aaccuggggg augucgucaa ggacgugacc 15360

uccagcgaug cgcugagggg cuauguaguc gcuggcacga cugcggggcu gacugccggc 15420

gucuacgaca aauggaccuc gacccagacc ggcaccucga ccgcucuacc gaacaccggg 15480

gccguggcgc ccgccgcagg guugggcacc uggcaaggcg ugggccaguu caccucgaac 15540

caguugcugc agaaugguac uucggugcug uuggaccggg cgcugggcgg caagggcagc 15600

cugggcgaug cguugcaaaa cagccuggca aaugccuuug cggccuacgg cuucaagcug 15660

auuggcgaca ccacccaugg cgugcuggac gacggcagcc ucggcaagau cggcuugcac 15720

gcccugaugg gaggucuggc cgccgaagcg gucgguggcg auuuccguac cggagcccug 15780

gcugcgggag ucaacgaggc gcugguggau agccucgcca agcaauacgc cagccugccc 15840

aucgaugaca agaagggccu gcugaucaug aguucgcagu ugaucggcgu gcuggcggcu 15900

ucgacgcagg gcgaugcgga cgccaagagc uugcagacgg gggccugggu ggcggggaau 15960

gccacccaac acaacuaccu cagucauugg caggaggaga agaagcggca ggaggucgau 16020

ggcugcaaag acaaacagcu cugcaaaacc ggaauagaag ccaaaugggc aauuauuucg 16080

gcccagcagg augucgguau cgucguaggu guuggaggag gcaucggucu uucgacagcu 16140

gaaaccgcag ugggguguua ugagcugguc aagaacugga gggaaaccua ugcagcucug 16200

gagcaguugg ccacuucgcc agaguuccgg cagcaauuug gcgauaacua ccugaagggg 16260

cuggaggagc gcgccgcauu cuugacccag gcauacgagg augccggcug gcaagguucg 16320

gucacagcug gugucgaggg cgguagguuc gcugcggaac uuguuggcgu ucugacggca 16380

gugaaaggug gcgcgcagau aaccgccaag cugccaacag cagccaagaa ccuggucaac 16440

gcgauugcgg agucaccugu uuccgguagu augaguucgc agcuuggggc agugggggau 16500

uugggucggc ugggugggggg agguaaaggu uaugucgaua uucuuuccca cgaagcuaaa 16560

-continued

```
cagcauauuu uguauggcga caaaccuggg aguggauggcc auuuguggcc ggggcaggca  16620

gggaagacag uuuucccuca aaacuggucg gcagauaaga uaguucacga gguuggugau  16680

auugcgacgu ccccuaguac caaaugguau gcccaaacag gaacuggugg gguuuauaca  16740

agcaagggug aucccgcuaa augguugcu uaugagguuc gugauggagu ucguaugcgc  16800

guuguuuauc agcccgcuac aggaaaggug aucacagccu uccccgacaa cgcaccuauc  16860

ccaccuuaua agcccauuaa auag                                        16884
```

1. A polypeptide comprising
a) an amino acid sequence selected from the group consisting of any one of SEQ ID NOs: 1-30, or
b) an amino acid sequence consisting of at least or exactly 35 contiguous amino acid residues from any one of SEQ ID NOs: 1-30, or
c) an amino acid sequence having a sequence identity of at least 60% with the amino acid sequence of a), or
d) an amino acid sequence having a sequence identity of at least 60% with the amino acid sequence of b),
said polypeptide being antigenic in a mammal.

2. (canceled)

3. The polypeptide according to claim 1, wherein the sequence identity with the amino acid sequence of a) is at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, and at least 99%.

4. The polypeptide according to claim 1, wherein the sequence identity with the amino acid sequence of b) is at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, and at least 99%.

5. The polypeptide according to claim 1, wherein the at least 35 contiguous amino acid residues have an N-terminal amino acid residue corresponding to any one of amino acid residues 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61 and 62 in any one of SEQ ID NOs: 1-30, or

corresponding to any one of amino acid residues 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73 and 74 in any one of SEQ ID NOs: 2-30, or

corresponding to any one of amino acid residues 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 and 100 in any one of SEQ ID NOs: 3-30, or corresponding to any one of amino acid residues 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150 and 151 in any one of SEQ ID NOs: 4-30, or

corresponding to any one of amino acid residues 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174 and 175 in any one of SEQ ID NOs: 5-30, or

corresponding to any one of amino acid residues 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299 and 300 in any one of SEQ ID NOs: 6-30, or corresponding to any one of amino acid residues 301, 302, 303, 304 and 305 in any one of SEQ ID NOs: 7-30, or

corresponding to any one of amino acid residues 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335 and 336 in any one of SEQ ID NOs: 8-30, or

corresponding to any one of amino acid residues 337, 338, 339, 340, 341, 342 and 343 in any one of SEQ ID NOs: 9-30, or

corresponding to any one of amino acid residues 344, 345, 346, 347 and 348 in any one of SEQ ID NOs: 10-30, or

corresponding to any one of amino acid residues 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415 and 416 in any one of SEQ ID NOs: 11-30, or

corresponding to any one of amino acid residues 417, 418, 419, 420, 421, 422 and 423 in any one of SEQ ID NOs: 12-30, or

corresponding to amino acid residue 424 in any one of SEQ ID NOs: 13-30, or

corresponding to any one of amino acid residues 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563 and 564 in any one of SEQ ID NOs: 14-30, or

corresponding to any one of amino acid residues 565, 566, 567, 568, 569, 570, 571, 572, 573, 574 and 575 in any one of SEQ ID NOs: 15-30, or

corresponding to any one of amino acid residues 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616 and 617 in any one of SEQ ID NOs: 16-30, or

corresponding to any one of amino acid residues 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683 and 684 in any one of SEQ ID NOs: 17-30, or

corresponding to any one of amino acid residues 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737 and 738 in any one of SEQ ID NOs: 18-30, or

corresponding to any one of amino acid residues 739, 740, 741 and 742 in any one of SEQ ID NOs: 19-30, or

corresponding to any one of amino acid residues 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779 and 780 in any one of SEQ ID NOs: 20-30, or

corresponding to any one of amino acid residues 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 845, 846 and 847 in any one of SEQ ID NOs: 21-30, or

corresponding to any one of amino acid residues 848, 849, 850, 851, 852, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, 873, 874, 875 and 876 in any one of SEQ ID NOs: 22-30, or

corresponding to any one of amino acid residues 877, 878, 879, 880, 881, 882, 883, 884, 885, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 896, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910, 911, 912, 913, 914 and 915 in any one of SEQ ID NOs: 23-30, or

corresponding to any one of amino acid residues 916, 917, 918, 919, 920, 921, 922, 923, 924, 925, 926, 927, 928, 929, 930, 931, 932, 933, 934, 935, 936, 937, 938, 939, 940, 941, 942, 943, 944, 945, 946, 947, 948, 949, 950, 951, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 965, 966, 967, 968, 969, 970, 971, 972, 973, 974, 975, 976, 977, 978, 979, 980, 981, 982, 983, 984, 985, 986, 987, 988, 989, 990 and 991 in any one of SEQ ID NOs: 24-30, or

corresponding to any one of amino acid residues 992, 993, 994, 995, 996, 997, 998, 999, 1000, 1001, 1002, 1003, 1004, 1005, 1006, 1007, 1008, 1009, 1010, 1011, 1012, 1013, 1014, 1015, 1016, 1017, 1018, 1019, 1020, 1021, 1022, 1023, 1024, 1025, 1026, 1027, 1028, 1029, 1030, 1031, 1032, 1033, 1034, 1035, 1036, 1037, 1038, 1039, 1040, 1041, 1042, 1043, 1044, 1045, 1046, 1047, 1048, 1049, 1050, 1051, 1052 and 1053 in any one of SEQ ID NOs: 25-30, or

corresponding to any one of amino acid residues 1054, 1055, 1056, 1057, 1058, 1059, 1060, 1061, 1062, 1063, 1064, 1065, 1066, 1067, 1068, 1069, 1070, 1071, 1072, 1073, 1074, 1075, 1076, 1077, 1078, 1079, 1080, 1081, 1082, 1083, 1084, 1085, 1086, 1087, 1088, 1089, 1090, 1091, 1092, 1093, 1094, 1095, 1096, 1097, 1098, 1099, 1100, 1101, 1102, 1103, 1104, 1105, 1106, 1107, 1108, 1109, 1110, 1111, 1112, 1113, 1114, 1115, 1116, 1117, 1118, 1119, 1120, 1121, 1122, 1123, 1124, 1125, 1126, 1127, 1128, 1129, 1130, 1131, 1132, 1133, 1134, 1135, 1136, 1137, 1138, 1139, 1140, 1141, 1142, 1143, 1144, 1145, 1146, 1147, 1148, 1149, 1150, 1151, 1152, 1153, 1154, 1155, 1156, and 1157 in any one of SEQ ID NOs: 26-30, or

corresponding to any one of amino acid residues 1158, 1159, 1160, 1161, 1162, 1163, 1164, 1165, 1166, 1167, 1168, 1169, 1170, 1171, 1172, 1173, 1174, 1175, 1176, 1177, 1178, 1179, 1180, 1181, 1182, 1183, 1184, 1185, 1186, 1187, 1188, 1189, 1190, 1191, 1192, 1193, 1194, 1195, 1196, 1197, 1198, 1199, 1200, 1201, 1202, 1203, 1204, 1205, 1206, and 1207 in any one of SEQ ID NOs: 27-30, or

corresponding to any one of amino acid residues 1208, 1209, 1210, 1211, 1212, 1213, 1214, 1215, 1216, 1217, 1218, 1219, 1220, 1221, 1222, 1223, 1224, 1225, 1226, 1227, 1228, 1229, 1230, 1231, 1232, 1233, 1234, 1235, 1236, 1237, 1238, 1239, 1240, 1241, 1242, 1243, 1244, 1245, 1246, 1247, 1248, 1249, 1250, 1251, 1252, 1253, 1254, 1255, 1256, 1257, 1258, 1259, 1260, 1261, 1262, 1263, 1264, 1265, 1266, 1267, 1268, 1269, 1270, 1271, 1272, 1273, 1274, 1275, 1276, 1277, 1278, 1279, 1280, 1281, 1282, 1283, 1284, 1285, 1286, 1287, 1288, 1289, 1290, 1291, 1292, 1293, 1294, 1295, 1296, 1297, 1298, 1299, 1300, 1301, 1302, 1303, 1304, 1305, 1306, 1307, 1308, 1309, 1310, 1311, 1312, 1313, 1314, 1315, 1316, 1317, 1318, 1319, 1320, 1321, 1322, 1323, 1324, 1325, 1326, 1327, 1328, 1329, 1330, 1331, 1332, 1333, 1334, 1335, 1336, 1337, 1338, 1339, 1340, 1341, 1342, 1343, 1344, 1345, 1346, 1347, 1348, 1349, 1350, 1351, 1352, 1353, 1354, 1355, 1356, 1357, 1358, 1359, 1360, 1361, 1362, 1363, 1364, 1365, 1366, 1367, 1368, 1369, 1370, 1371, 1372, 1373, 1374, 1375, 1376, 1377, 1378, 1379, 1380, 1381, 1382, 1383, 1384, 1385, 1386, 1387, 1388, 1389, 1390, 1391, 1392, 1393, 1394, 1395, 1396, 1397, 1398, 1399, 1400, 1401, 1402, 1403, 1404, 1405, 1406, 1407, 1408, 1409, 1410, 1411, 1412, 1413, 1414, 1415, 1416, 1417, 1418, 1419, 1420, 1421, 1422, 1423, 1424, 1425, 1426, 1427, 1428, 1429, 1430, 1431, 1432, 1433, 1434, 1435, 1436, 1437, 1438, 1439, 1440, 1441, 1442, 1443, 1444, 1445, 1446, 1447, 1448, 1449, 1450, 1451, 1452, 1453, 1454, 1455, 1456, 1457, 1458, 1459, 1460, 1461, 1462, 1463, 1464, 1465, 1466, 1467, 1468, 1469, 1470, 1471, 1472, 1473, 1474, 1475, 1476, 1477, 1478, 1479, 1480, 1481, 1482, 1483, 1484, 1485, 1486, 1487, 1488, 1489, 1490, 1491, 1492, 1493, 1494, 1495, 1496, 1497, 1498, 1499, 1500, 1501, 1502, 1503, 1504, 1505, 1506, 1507, 1508, 1509, 1510, 1511, 1512, 1513, 1514, 1515, 1516, 1517, 1518, 1519, 1520, 1521, 1522, 1523, 1524, 1525, 1526, 1527, 1528, 1529, 1530, 1531, 1532, 1533, 1534, 1535, 1536, 1537, 1538, 1539, 1540, 1541, 1542, 1543, 1544, 1545, 1546, 1547, 1548, 1549, 1550, 1551, 1552, 1553, 1554, 1555, 1556, 1557, 1558, 1559, 1560, 1561, 1562, 1563, 1564, 1565, 1566, 1567, 1568, 1569, 1570, 1571, 1572, 1573, 1574, 1575, 1576, 1577, 1578, 1579, 1580, 1581, 1582, 1583, 1584, 1585, 1586, 1587, 1588, 1589, 1590, 1591, 1592, 1593, 1594, 1595, 1596, 1597, 1598, 1599, 1600, 1601, 1602, 1603, 1604, 1605, 1606, 1607, 1608, 1609, 1610, 1611, 1612, 1613, 1614, 1615, 1616, 1617, 1618, 1619, 1620, 1621, 1622, 1623, 1624, 1625, 1626, 1627, 1628, 1629, 1630, 1631, 1632, 1633, 1634, 1635, 1636, 1637, 1638, 1639, 1640, 1641, 1642, 1643, 1644, 1645, 1646, 1647, 1648, 1649, 1650, 1651, 1652, 1653, 1654, 1655, 1656, 1657, 1658, 1659, 1660, 1661, 1662, 1663, 1664, 1665, 1666, 1667, 1668, 1669, 1670, 1671, 1672, 1673, 1674, 1675, 1676, 1677, 1678, 1679, 1680, 1681, 1682, 1683, 1684, 1685, 1686, 1687, 1688, 1689, 1690, 1691, 1692, 1693, 1694, 1695, 1696, 1697, 1698, 1699, 1700, 1701, 1702, 1703, 1704, 1705, 1706, 1707, 1708, 1709, 1710, 1711, 1712, 1713, 1714, 1715, 1716, 1717, 1718, 1719, 1720, 1721, 1722, 1723, 1724, 1725, 1726, 1727, 1728, 1729, 1730, 1731, 1732, 1733, 1734, 1735, 1736, 1737, 1738, 1739, 1740, 1741, 1742, 1743, 1744, 1745, 1746, 1747, 1748, 1749, 1750, 1751, 1752, 1753, 1754, 1755, 1756, 1757, 1758, 1759, 1760, 1761, 1762, 1763, 1764, 1765, 1766, 1767, 1768, 1769, 1770, 1771, 1772, 1773, 1774, 1775, 1776, 1777, 1778, 1779, 1780, 1781, 1782, 1783, 1784, 1785, 1786, 1787, 1788, 1789, 1790, 1791, 1792, 1793, 1794, 1795, 1796, 1797, 1798, 1799, 1800, 1801, 1802, 1803, 1804, 1805, 1806, 1807, 1808, 1809, 1810, 1811, 1812, 1813, 1814, 1815, 1816, 1817, 1818, 1819, 1820, 1821, 1822, 1823, 1824, 1825, 1826, 1827, 1828, 1829, 1830, 1831, 1832, 1833, 1834, 1835, 1836, 1837, 1838, 1839, 1840, 1841, 1842, 1843, 1844, 1845, 1846, 1847, 1848, 1849, 1850, 1851, 1852, 1853, 1854, 1855, 1856, 1857, 1858, 1859, 1860, 1861, 1862, 1863, 1864, 1865, 1866, 1867, 1868, 1869, 1870, 1871, 1872, 1873, 1874, 1875, 1876, 1877, 1878, 1879, 1880, 1881, 1882, 1883, 1884, 1885, 1886, 1887, 1888, 1889, 1890, 1891, 1892, 1893, 1894, 1895, 1896, 1897, 1898, 1899, 1900, 1901, 1902, 1903, 1904, 1905, 1906, 1907, 1908, 1909, 1910, 1911, 1912, 1913, 1914, 1915, 1916, 1917, 1918, 1919, 1920, 1921, 1922, 1923, 1924, 1925, 1926, 1927, 1928, 1929, 1930, 1931, 1932, 1933, 1934, 1935, 1936, 1937, 1938, 1939, 1940, 1941, 1942, 1943, 1944, 1945, 1946, 1947, 1948, 1949, 1950, 1951, 1952, 1953, 1954, 1955, 1956, 1957, 1958, 1959, 1960, 1961, 1962, 1963, 1964, 1965, 1966, 1967, 1968, 1969, 1970, 1971, 1972, 1973, 1974, 1975, 1976, 1977, 1978, 1979, 1980, 1981, 1982, 1983, 1984, 1985, 1986, 1987, 1988, 1989, 1990, 1991, 1992, 1993, 1994, 1995, 1996, 1997, 1998, 1999, 2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058, 2059, 2060, 2061, 2062, 2063, 2064, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2072, 2073, 2074, 2075, 2076, 2077, 2078, 2079, 2080, 2081, 2082, 2083, 2084, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092, 2093, 2094, 2095, 2096, 2097, 2098, 2099, 2100, 2101, 2102, 2103, 2104, 2105, 2106, 2107, 2108, 2109, 2110, 2110, 2111, 2112, 2113, 2114, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2122, 2123, 2124, 2125, 2126, 2127, 2128, 2129, 2130, 2131, 2132, 2133, 2134, 2135, 2136, 2137, 2138, 2139, 2140, 2141, 2142, 2143, 2144, 2145, 2146, 2147, 2148, 2149, 2150, 2151, 2152, 2153, 2154, 2155, 2156, 2157, 2158, 2159, 2160, 2171, 2172, 2173, 2174, 2175, 2176, 2177, 2178, 2179, 2180, 2181, 2182, 2183, 2184, 2185, 2186, 2187, 2188, 2189, 2190, 2191, 2192, 2193, 2194, 2195, 2196, 2197, 2198, 2199, 2200, 2201, 2202, 2203, 2204, 2205, 2206, 2207, 2208, 2209, 2210, 2211, 2212, 2213, 2214, 2215, 2216, 2217, 2218, 2219, 2220, 2221, 2222, 2223, 2224, 2225, 2226, 2227, 2228, 2229, 2230, 2231, 2232, 2233, 2234, 2235, 2236, 2237, 2238, 2239, 2240, 2241, 2242, 2243, 2244, 2245, 2246, 2247, 2248, 2249, 2250, 2251, 2252, 2253, 2254, 2255, 2256, 2257, 2258, 2259, 2260, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2279, 2280, 2281, 2282, 2283, 2284, 2285, 2286, 2287, 2288, 2289, 2290, 2291, 2292, 2293, 2294, 2295, 2296, 2297, 2298, 2299, 2300, 2301, 2302, 2303, 2304, 2305, 2306, 2307, 2308, 2309, 2310, 2311, 2312, 2313, 2314, 2315, 2316, 2317, 2318, 2319, 2320, 2321, 2322, 2323, 2324, 2325, 2326, 2327, 2328, 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337, 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351, 2352, 2353, 2354, 2355, 2356, 2357, 2358, 2359, 2360, 2361, 2362, 2363, 2364, 2365, 2366, 2367, 2368, 2369, 2370, 2371, 2372, 2373, 2374, 2375, 2376, 2377, 2378, 2379, 2380, 2381, 2382, 2383, 2384, 2385, 2386, 2387, 2388, 2389, 2390, 2391, 2392, 2393, 2394, 2395, 2396, 2397, 2398, 2399, 2400, 2401, 2402, 2403, 2404, 2405, 2406, 2407, 2408, 2409, 2410, 2411, 2412, 2413, 2414, 2415, 2416, 2417, 2418, 2419, 2420, 2421, 2422, 2423, 2424, 2425, 2426, 2427, 2428, 2429, 2430, 2431, 2432, 2433, 2434, 2435, 2436, 2437, 2438, 2439, 2440, 2441, 2442, 2443, 2444, 2445, 2446, 2447, 2448, 2449, 2450, 2451, 2452, 2453, 2454, 2455, 2456, 2457, 2458, 2459, 2460, 2461, 2462, 2463 and 2464 in any one of SEQ ID NOs: 28-30, or

corresponding to any one of amino acid residues 2465, 2466, 2467, 2468, 2469, 2470, 2471, 2472, 2473, 2474, 2475, 2476, 2477, 2478, 2479, 2480, 2481, 2482, 2483, 2484, 2485, 2486, 2487, 2488, 2489, 2490, 2491, 2492, 2493, 2494, 2495, 2496, 2497, 2498, 2499, 2500, 2501, 2502, 2503, 2504, 2505, 2506, 2507, 2508, 2509, 2510, 2511, 2512, 2513, 2514, 2515, 2516, 2517, 2518, 2519, 2520, 2521, 2522, 2523, 2524, 2525, 2526, 2527, 2528, 2529, 2530, 2531, 2532, 2533, 2534, 2535, 2536, 2537, 2538, 2539, 2540, 2541, 2542, 2543, 2544, 2545, 2546, 2547, 2548, 2549, 2550, 2551, 2552, 2553, 2554, 2555, 2556, 2557, 2558, 2559, 2560, 2561, 2562, 2563, 2564, 2565, 2566, 2567, 2568, 2569, 2570, 2571, 2572, 2573, 2574, 2575, 2576, 2577, 2578, 2579, 2580, 2581, 2582, 2583, 2584, 2585, 2586, 2587, 2588, 2589, 2590, 2591, 2592, 2593, 2594, 2595, 2596, 2597, 2598, 2599, 2600, 2601, 2602, 2603, 2604, 2605, 2606, 2607, 2608, 2609, 2610, 2611, 2612, 2613, 2614, 2615, 2616, 2617, 2618, 2619, 2620, 2621, 2622, 2623, 2624, 2625, 2626, 2627, 2628, 2629, 2630, 2631, 2632, 2633, 2634, 2635, 2636, 2637, 2638, 2639, 2640, 2641, 2642, 2643, 2644, 2645, 2646, 2647, 2648, 2649, 2650, 2651, 2652, 2653, 2654, 2655, 2656, 2657, 2658, 2659, 2660, 2661, 2662, 2663, 2664, 2665, 2666, 2667, 2668, 2669, 2670, 2671, 2672, 2673, 2674, 2675, 2676, 2677, 2678, 2679, 2680, 2681, 2682, 2683, 2684, 2685, 2686, 2687, 2688, 2689, 2690, 2691, 2692, 2693, 2694, 2695, 2696, 2697, 2698, 2699, 2700, 2701, 2702, 2703, 2704, 2705, 2706, 2707, 2708, 2709, 2710, 2711, 2712, 2713, 2714, 2715, 2716, 2717, 2718, 2719, 2720, 2721, 2722, 2723, 2724, 2725, 2726, 2727, 2728, 2729, 2730, 2731, 2732, 2733, 2734, 2735, 2736, 2737, 2738, 2739, 2740, 2741, 2742, 2743, 2744, 2745, 2746, 2747, 2748, 2749, 2750, 2751, 2752, 2753, 2754, 2755, 2756, 2757, 2758, 2759, 2760, 2761, 2762, 2763, 2764, 2765, 2766, 2767, 2768, 2769, 2770, 2771, 2772, 2773, 2774, 2775, 2776, 2777, 2778, 2779, 2780, 2781, 2782, 2783, 2784, 2785, 2786, 2787, 2788, 2789, 2790, 2791, 2792, 2793, 2794, 2795, 2796, 2797, 2798, 2799, 2800, 2801, 2802, 2803, 2804, 2805, 2806, 2807, 2808, 2809, 2810, 2811, 2812, 2813, 2814, 2815, 2816, 2817, 2818, 2819, 2820, 2821, 2822, 2823, 2824, 2825, 2826, 2827, 2828, 2829, 2830, 2831, 2832, 2833, 2834, 2835, 2836, 2837, 2838, 2839, 2840, 2841, 2842, 2843, 2844, 2845, 2846, 2847, 2848, 2849, 2850, 2851, 2852, 2853, 2854, 2855, 2856, 2857, 2858, 2859, 2860, 2861, 2862, 2863, 2864, 2865, 2866, 2867, 2868, 2869, 2870, 2871, 2872, 2873, 2874, 2875, 2876, 2877, 2878, 2879, 2880, 2881, 2882, 2883, 2884, 2885, 2886, 2887, 2888, 2889, 2890, 2891, 2892, 2893, 2894, 2895, 2896, 2897, 2898, 2899, 2900, 2901, 2902, 2903, 2904, 2905, 2906, 2907, 2908, 2909, 2910, 2911, 2912, 2913, 2914, 2915, 2916, 2917, 2918, 2919, 2920, 2921, 2922, 2923, 2924, 2925, 2926, 2927, 2928, 2929, 2930, 2931, 2932, 2933, 2934, 2935, 2936, 2937, 2938, 2939, 2940, 2941, 2942, 2943, 2944, 2945, 2946, 2947, 2948, 2949, 2950, 2951, 2952, 2953, 2954, 2955, 2956, 2957, 2958, 2959, 2960, 2961, 2962, 2963, 2964, 2965, 2966, 2967, 2968, 2969, 2970, 2971, 2972, 2973, 2974, 2975, 2976, 2977, 2978, 2979, 2980, 2981, 2982, 2983, 2984, 2985, 2986, 2987, 2988, 2989, 2990, 2991, 2992, 2993, 2994, 2995, 2996, 2997, 2998, 2999, 3000, 3001, 3002, 3003, 3004, 3005, 3006, 3007, 3008, 3009, 3010, 3011, 3012, 3013, 3014, 3015, 3016, 3017, 3018, 3019, 3020, 3021, 3022, 3023, 3024, 3025, 3026, 3027, 3028, 3029, 3030, 3031, 3032, 3033, 3034, 3035, 3036, 3037, 3038, 3039, 3040, 3042, 3043, 3044, 3045, 3046, 3047, 3048, 3049, 3050, 3051, 3052, 3053, 3054, 3055, 3056, 3057, 3058, 3059, 3060, 3061, 3062, 3063, 3064, 3065, 3066, 3067, 3068, 3069, 3070, 3071, 3072, 3073, 3074, 3075, 3076, 3077, 3078, 3079, 3080, 3081, 3082, 3083, 3084, 3085, 3086, 3087, 3088, 3089, 3090, 3091, 3092, 3093, 3094, 3095, 3096, 3097, 3098, 3099, 3100, 3101, 3102, 3103, 3104, 3105, 3106, 3107, 3108, 3109, 3110, 3110, 3111, 3112, 3113, 3114, 3115, 3116, 3117, 3118, 3119, 3120, 3121, 3122, 3123, 3124, 3125, 3126, 3127, 3128, 3129, 3130, 3131, 3132, 3133, 3134, 3135, 3136, 3137, 3138, 3139, 3140, 3141, 3142, 3143, 3144, 3145, 3146, 3147, 3148, 3149, 3150, 3151, 3152, 3153, 3154, 3155, 3156, 3157, 3158, 3159, 3160, 3171, 3172, 3173, 3174, 3175, 3176, 3177, 3178, 3179, 3180, 3181, 3182, 3183, 3184, 3185, 3186, 3187, 3188, 3189, 3190, 3191, 3192, 3193, 3194, 3195, 3196, 3197, 3198, 3199, 3200, 3201, 3202, 3203, 3204, 3205, 3206, 3207, 3208, 3209, 3210, 3211, 3212, 3213, 3214, 3215, 3216, 3217, 3218, 3219, 3220, 3221, 3222, 3223, 3224, 3225, 3226, 3227, 3228, 3229, 3230, 3231, 3232, 3233, 3234, 3235, 3236, 3237, 3238, 3239, 3240, 3241, 3242, 3243, 3244, 3245, 3246, 3247, 3248, 3249, 3250, 3251, 3252, 3253, 3254, 3255, 3256, 3257, 3258, 3259, 3260, 3271, 3272, 3273, 3274, 3275, 3276, 3277, 3278, 3279, 3280, 3281, 3282, 3283, 3284, 3285, 3286, 3287, 3288, 3289, 3290, 3291, 3292, 3293, 3294, 3295, 3296, 3297, 3298, 3299, 3300, 3301, 3302, 3303, 3304, 3305, 3306, 3307, 3308, 3309, 3310, 3311, 3312, 3313, 3314, 3315, 3316, 3317, 3318, 3319, 3320, 3321, 3322, 3323, 3324, 3325, 3326, 3327, 3328, 3329, 3330, 3331, 3332, 3333, 3334, 3335, 3336, 3337, 3338, 3339, 3340, 3344, 3342, 3343, 3344, 3345, 3346, 3347, 3348, 3349, 3350, 3351, 3352, 3353, 3354, 3355, 3356, 3357, 3358, 3359, 3360, 3361, 3362, 3363, 3364, 3365, 3366, 3367, 3368, 3369, 3370, 3371, 3372, 3373, 3374, 3375, 3376, 3377, 3378, 3379, 3380, 3381, 3382, 3383, 3384, 3385, 3386, 3387, 3388, 3389, 3390, 3391, 3392, 3393, 3394, 3395, 3396, 3397, 3398, 3399, 3400, 3401, 3402, 3403, 3404, 3405, 3406, 3407, 3408, 3409, 3410, 3411, 3412, 3413, 3414, 3415, 3416, 3417, 3418, 3419, 3420, 3421, 3422, 3423, 3424, 3425, 3426, 3427, 3428, 3429, 3430, 3431, 3432, 3433, 3434, 3435, 3436, 3437, 3438, 3439, 3440, 3441, 3442, 3443, 3444, 3445, 3446, 3447, 3448, 3449, 3450, 3451, 3452, 3453, 3454, 3455, 3456, 3457, 3458, 3459, 3460, 3461, 3462, 3463, 3464, 3465, 3466, 3467, 3468, 3469, 3470, 3471, 3472, 3473, 3474, 3475, 3476, 3477, 3478, 3479, 3480, 3481, 3482, 3483, 3484, 3485, 3486, 3487, 3488, 3489, 3490, 3491, 3492, 3493, 3494, 3495, 3496, 3497, 3498, 3499, 3500, 3501, 3502, 3503, 3504, 3505, 3506, 3507, 3508, 3509, 3510, 3511, 3512, 3513, 3514, 3515, 3516, 3517, 3518, 3519, 3520, 3521, 3522, 3523, 3524, 3525, 3526, 3527, 3528, 3529, 3530 and 3531 in any one of SEQ ID NOs: 29-30, or

corresponding to anyone of amino acid residues 3532, 3533, 3534, 3535, 3536, 3537, 3538, 3539, 3540, 3541, 3542, 3543, 3544, 3545, 3546, 3547, 3548, 3549, 3550, 3551, 3552, 3553, 3554, 3555, 3556, 3557, 3558, 3559, 3560, 3561, 3562, 3563, 3564, 3565, 3566, 3567, 3568, 3569, 3570, 3571, 3572, 3573, 3574, 3575, 3576, 3577, 3578, 3579, 3580, 3581, 3582, 3583, 3584, 3585, 3586, 3587, 3588, 3589, 3590, 3591, 3592, 3593, 3594, 3595, 3596, 3597, 3598, 3599, 3600, 3601, 3602, 3603, 3604, 3605, 3606, 3607, 3608, 3609, 3610, 3611, 3612, 3613, 3614, 3615, 3616, 3617, 3618, 3619, 3620, 3621, 3622, 3623, 3624, 3625, 3626, 3627, 3628, 3629, 3630, 3631, 3632, 3633, 3634, 3635, 3636, 3637, 3638, 3639, 3640, 3641, 3642, 3643, 3644, 3645, 3646, 3647, 3648, 3649, 3650, 3651, 3652, 3653, 3654, 3655, 3656, 3657, 3658, 3659, 3660, 3661, 3662, 3663, 3664, 3665, 3666, 3667, 3668, 3669, 3670, 3671, 3672, 3673, 3674, 3675, 3676, 3677, 3678, 3679, 3680, 3681, 3682, 3683, 3684, 3685, 3686, 3687, 3688, 3689, 3690, 3691, 3692, 3693, 3694, 3695, 3696, 3697, 3698, 3699, 3700, 3701, 3702, 3703, 3704, 3705, 3706, 3707, 3708, 3709, 3710, 3711, 3712, 3713, 3714, 3715, 3716, 3717, 3718, 3719, 3720, 3721, 3722, 3723, 3724, 3725, 3726, 3727, 3728, 3729, 3730, 3731, 3732, 3733, 3734, 3735, 3736, 3737, 3738, 3739, 3740, 3741, 3742, 3743, 3744, 3745, 3746, 3747, 3748, 3749, 3750, 3751, 3752, 3753, 3754, 3755, 3756, 3757, 3758, 3759, 3760, 3761, 3762, 3763, 3764, 3765, 3766, 3767, 3768, 3769, 3770, 3771, 3772, 3773, 3774, 3775, 3776, 3777, 3778, 3779, 3780, 3781, 3782, 3783, 3784, 3785, 3786, 3787, 3788, 3789, 3790, 3791, 3792, 3793, 3794, 3795, 3796, 3797, 3798, 3799, 3800, 3801, 3802, 3803, 3804, 3805, 3806, 3807, 3808, 3809, 3810, 3811, 3812, 3813, 3814, 3815, 3816, 3817, 3818, 3819, 3820, 3821, 3822, 3823, 3824, 3825, 3826, 3827, 3828, 3829, 3830, 3831, 3832, 3833, 3834, 3835, 3836, 3837, 3838, 3839, 3840, 3841, 3842, 3843, 3844, 3845, 3846, 3847, 3848, 3849, 3850, 3851, 3852, 3853, 3854, 3855, 3856, 3857, 3858, 3859, 3860, 3861, 3862, 3863, 3864, 3865, 3866, 3867, 3868, 3869, 3870, 3871, 3872, 3873, 3874, 3875, 3876, 3877, 3878, 3879, 3880, 3881, 3882, 3883, 3884, 3885, 3886, 3887, 3888, 3889, 3890, 3891, 3892, 3893, 3894, 3895, 3896, 3897, 3898, 3899, 3900, 3901, 3902, 3903, 3904, 3905, 3906, 3907, 3908, 3909, 3910, 3911, 3912, 3913, 3914, 3915, 3916, 3917, 3918, 3919, 3920, 3921, 3922, 3923, 3924, 3925, 3926, 3927, 3928, 3929, 3930, 3931, 3932, 3933, 3934, 3935, 3936, 3937, 3938, 3939, 3940, 3941, 3942, 3943, 3944, 3945, 3946, 3947, 3948, 3949, 3950, 3951, 3952, 3953, 3954, 3955, 3956, 3957, 3958, 3959, 3960, 3961, 3962, 3963, 3964, 3965, 3966, 3967, 3968, 3969, 3970, 3971, 3972, 3973, 3974, 3975, 3976, 3977, 3978, 3979, 3980, 3981, 3982, 3983, 3984, 3985, 3986, 3987, 3988, 3989, 3990, 3991, 3992, 3993, 3994, 3995, 3996, 3997, 3998, 3999, 4000, 4001, 4002, 4003, 4004, 4005, 4006, 4007, 4008, 4009, 4010, 4011, 4012, 4013, 4014, 4015, 4016, 4017, 4018, 4019, 4020, 4021, 4022, 4023, 4024, 4025, 4026, 4027, 4028, 4029, 4030, 4031, 4032, 4033, 4034, 4035, 4036, 4037, 4038, 4039, 4040, 4042, 4043, 4044, 4045, 4046, 4047, 4048, 4049, 4050, 4051, 4052, 4053, 4054, 4055, 4056, 4057, 4058, 4059, 4060, 4061, 4062, 4063, 4064, 4065, 4066, 4067, 4068, 4069, 4070, 4071, 4072, 4073, 4074, 4075, 4076, 4077, 4078, 4079, 4080, 4081, 4082, 4083, 4084, 4085, 4086, 4087, 4088, 4089, 4090, 4091, 4092, 4093, 4094, 4095, 4096, 4097, 4098, 4099, 4100, 4101, 4102, 4103, 4104, 4105, 4106, 4107, 4108, 4109, 4110, 4110, 4111, 4112, 4113, 4114, 4115, 4116, 4117, 4118, 4119, 4120, 4121, 4122, 4123, 4124, 4125, 4126, 4127, 4128, 4129, 4130, 4131, 4132, 4133, 4134, 4135, 4136, 4137, 4138, 4139, 4140, 4141, 4142, 4143, 4144, 4145, 4146, 4147, 4148, 4149, 4150, 4151, 4152, 4153, 4154, 4155, 4156, 4157, 4158, 4159, 4160, 4171, 4172, 4173, 4174, 4175, 4176, 4177, 4178, 4179, 4180, 4181, 4182, 4183, 4184, 4185, 4186, 4187, 4188, 4189, 4190, 4191, 4192, 4193, 4194, 4195, 4196, 4197, 4198, 4199, 4200, 4201, 4202, 4203, 4204, 4205, 4206, 4207, 4208, 4209, 4210, 4211, 4212, 4213, 4214, 4215, 4216, 4217, 4218, 4219, 4220, 4221, 4222, 4223, 4224, 4225, 4226, 4227, 4228, 4229, 4230, 4231, 4232, 4233, 4234, 4235, 4236, 4237, 4238, 4239, 4240, 4241, 4242, 4243, 4244, 4245, 4246, 4247, 4248, 4249, 4250, 4251, 4252, 4253, 4254, 4255, 4256, 4257, 4258, 4259, 4260, 4271, 4272, 4273, 4274, 4275, 4276, 4277, 4278, 4279, 4280, 4281, 4282, 4283, 4284, 4285, 4286, 4287, 4288, 4289, 4290, 4291, 4292, 4293, 4294, 4295, 4296, 4297, 4298, 4299, 4300, 4301, 4302, 4303, 4304, 4305, 4306, 4307, 4308, 4309, 4310, 4311, 4312, 4313, 4314, 4315, 4316, 4317, 4318, 4319, 4320, 4321, 4322, 4323, 4324, 4325, 4326, 4327, 4328, 4329, 4330, 4331, 4332, 4333, 4334, 4335, 4336, 4337, 4338, 4339, 4340, 4341, 4342, 4343, 4344, 4345, 4346, 4347, 4348, 4349, 4350, 4351, 4352, 4353, 4354, 4355, 4356, 4357, 4358, 4359, 4360, 4361, 4362, 4363, 4364, 4365, 4366, 4367, 4368, 4369, 4370, 4371, 4372, 4373, 4374, 4375, 4376, 4377, 4378, 4379, 4380, 4381, 4382, 4383, 4384, 4385, 4386, 4387, 4388, 4389, 4390, 4391, 4392, 4393, 4394, 4395, 4396, 4397, 4398, 4399, 4400, 4401, 4402, 4403, 4404, 4405, 4406, 4407, 4408, 4409, 4410, 4411, 4412, 4413, 4414, 4415, 4416, 4417, 4418, 4419, 4420, 4421, 4422, 4423, 4424, 4425, 4426, 4427, 4428, 4429, 4430, 4431, 4432, 4433, 4434, 4435, 4436, 4437, 4438, 4439, 4440, 4441, 4442, 4443, 4444, 4445, 4446, 4447, 4448, 4449, 4450, 4451, 4452, 4453, 4454, 4455, 4456, 4457, 4458, 4459, 4460, 4461, 4462, 4463, 4464, 4465, 4466, 4467, 4468, 4469, 4470, 4471, 4472, 4473, 4474, 4475, 4476, 4477, 4478, 4479, 4480, 4481, 4482, 4483, 4484, 4485, 4486, 4487, 4488, 4489, 4490, 4491, 4492, 4493, 4494, 4495, 4496, 4497, 4498, 4499, 4500, 4501, 4502, 4503, 4504, 4505, 4506, 4507, 4508, 4509, 4510, 4511, 4512, 4513, 4514, 4515, 4516, 4517, 4518, 4519, 4520, 4521, 4522, 4523, 4524, 4525, 4526, 4527, 4528, 4529, 4530, 4531, 4532, 4533, 4534, 4535, 4536, 4537, 4538, 4539, 4540, 4541, 4542, 4543, 4544, 4545, 4546, 4547, 4548, 4549, 4550, 4551, 4552, 4553, 4554, 4555, 4556, 4557, 4558, 4559, 4560, 4561, 4562, 4563, 4564, 4565, 4566, 4567, 4568, 4569, 4570, 4571, 4572, 4573, 4574, 4575, 4576, 4577, 4578, 4579, 4580, 4581, 4582, 4583, 4584, 4585, 4586, 4587, 4588, 4589, 4590, 4591, 4592, 4593, 4594, 4595, 4596, 4597, 4598, 4599, 4600, 4601, 4602, 4603, 4604, 4605, 4606, 4607, 4608, 4609, 4610, 4611, 4612, 4613, 4614, 4615, 4616, 4617, 4618, 4619, 4620, 4621, 4622, 4623, 4624, 4625, 4626, 4627, 4628, 4629, 4630, 4631, 4632, 4633, 4634, 4635, 4636, 4637, 4638, 4639, 4640, 4641, 4642, 4643, 4644, 4645, 4646, 4647, 4648, 4649, 4650, 4651, 4652, 4653, 4654, 4655, 4656, 4657, 4658, 4659, 4660, 4661, 4662, 4663, 4664, 4665, 4666, 4667, 4668, 4669, 4670, 4671, 4672, 4673, 4674, 4675, 4676, 4677, 4678, 4679, 4680, 4681, 4682, 4683, 4684, 4685, 4686, 4687, 4688, 4689, 4690, 4691, 4692, 4693, 4694, 4695, 4696, 4697, 4698, 4699, 4700, 4701, 4702, 4703, 4704, 4705, 4706, 4707, 4708, 4709, 4710, 4711, 4712, 4713, 4714, 4715, 4716, 4717, 4718, 4719, 4720, 4721, 4722, 4723, 4724, 4725, 4726, 4727, 4728, 4729, 4730, 4731, 4732, 4733, 4734, 4735, 4736, 4737, 4738, 4739, 4740, 4741, 4742, 4743, 4744, 4745, 4746, 4747, 4748, 4749, 4750, 4751, 4752, 4753, 4754, 4755, 4756, 4757, 4758, 4759, 4760, 4761, 4762, 4763, 4764, 4765, 4766, 4767, 4768, 4769, 4770, 4771, 4772, 4773, 4774, 4775, 4776, 4777, 4778, 4779, 4780, 4781, 4782, 4783, 4784, 4785, 4786, 4787, 4788, 4789, 4790, 4791, 4792, 4793, 4794, 4795, 4796, 4797, 4798, 4799, 4800, 4801, 4802, 4803, 4804, 4805, 4806, 4807, 4808, 4809, 4810, 4811, 4812, 4813, 4814, 4815, 4816, 4817, 4818, 4819, 4820, 4821, 4822, 4823, 4824, 4825, 4826, 4827, 4828, 4829, 4830, 4831, 4832, 4833, 4834, 4835, 4836, 4837, 4838, 4839, 4840, 4841, 4842, 4843, 4844, 4845, 4846, 4847, 4848, 4849, 4850, 4851, 4852, 4853, 4854, 4855, 4856, 4857, 4858, 4859, 4860, 4861, 4862, 4863, 4864, 4865, 4866, 4867, 4868, 4869, 4870, 4871, 4872, 4873, 4874, 4875, 4876, 4877, 4878, 4879, 4880, 4881, 4882, 4883, 4884, 4885, 4886, 4887, 4888, 4889, 4890, 4891, 4892, 4893, 4894, 4895, 4896, 4897, 4898, 4899, 4900, 4901, 4902, 4903, 4904, 4905, 4906, 4907, 4908, 4909, 4910, 4911, 4912, 4913, 4914, 4915, 4916, 4917, 4918, 4919, 4920, 4921, 4922, 4923, 4924, 4925, 4926, 4927, 4928, 4929, 4930, 4931, 4932, 4933, 4934, 4935, 4936, 4937, 4938, 4939, 4940, 4941, 4942, 4943, 4944, 4945, 4946, 4947, 4948, 4949, 4950, 4951, 4952, 4953, 4954, 4955, 4956.4957, 4958, 4959, 4960, 4961, 4962, 4963, 4964, 4965, 4966, 4967, 4968, 4969, 4970, 4971, 4972, 4973, 4974, 4975, 4976, 4977, 4978, 4979, 4980, 4981, 4982, 4983, 4984, 4985, 4986, 4987, 4988, 4989, 4990, 4991, 4992, 4993, 4994, 4995, 4996, 4997, 4998, 4999, 5000, 5001, 5002, 5003, 5004, 5005, 5006, 5007, 5008, 5009, 5010, 5011, 5012, 5013, 5014, 5015, 5016, 5017, 5018, 5019, 5020, 5021, 5022, 5023, 5024, 5025, 5026, 5027, 5028, 5029, 5030, 5031, 5032, 5033, 5034, 5035, 5036, 5037, 5038, 5039, 5040, 5042, 5043, 5044, 5045, 5046, 5047, 5048, 5049, 5050, 5051, 5052, 5053, 5054, 5055, 5056, 5057, 5058, 5059, 5060, 5061, 5062, 5063, 5064, 5065, 5066, 5067, 5068, 5069, 5070, 5071, 5072, 5073, 5074, 5075, 5076, 5077, 5078, 5079, 5080, 5081, 5082, 5083, 5084, 5085, 5086, 5087, 5088, 5089, 5090, 5091, 5092, 5093, 5094, 5095, 5096, 5097, 5098, 5099, 5100, 5101, 5102, 5103, 5104, 5105, 5106, 5107, 5108, 5109, 5110, 5110, 5111, 5112, 5113, 5114, 5115, 5116, 5117, 5118, 5119, 5120, 5121, 5122, 5123, 5124, 5125, 5126, 5127, 5128, 5129, 5130, 5131, 5132, 5133, 5134, 5135, 5136, 5137, 5138, 5139, 5140, 5141, 5142, 5143, 5144, 5145, 5146, 5147, 5148, 5149, 5150, 5151, 5152, 5153, 5154, 5155, 5156, 5157, 5158, 5159, 5160, 5171, 5172, 5173, 5174, 5175, 5176, 5177, 5178, 5179, 5180, 5181, 5182, 5183, 5184, 5185, 5186, 5187, 5188, 5189, 5190, 5191, 5192, 5193, 5194, 5195, 5196, 5197, 5198, 5199, 5200, 5201, 5202, 5203, 5204, 5205, 5206, 5207, 5208, 5209, 5210, 5211, 5212, 5213, 5214, 5215, 5216, 5217, 5218, 5219, 5220, 5221, 5222, 5223, 5224, 5225, 5226, 5227, 5228, 5229, 5230, 5231, 5232, 5233, 5234, 5235, 5236, 5237, 5238, 5239, 5240, 5241, 5242, 5243, 5244, 5245, 5246, 5247, 5248, 5249, 5250, 5251, 5252, 5253, 5254, 5255, 5256, 5257, 5258, 5259, 5260, 5271, 5272, 5273, 5274, 5275, 5276, 5277, 5278, 5279, 5280, 5281, 5282, 5283, 5284, 5285, 5286, 5287, 5288, 5289, 5290, 5291, 5292, 5293, 5294, 5295, 5296, 5297, 5298, 5299, 5300, 5301, 5302, 5303, 5304, 5305, 5306, 5307, 5308, 5309, 5310, 5311, 5312, 5313, 5314, 5315, 5316, 5317, 5318, 5319, 5320, 5321, 5322, 5323, 5324, 5325, 5326, 5327, 5328, 5329, 5330, 5331, 5332, 5333, 5334, 5335, 5336, 5337, 5338, 5339, 5340, 5341, 5342, 5343, 5344, 5345, 5346, 5347, 5348, 5349, 5350, 5351, 5352, 5353, 5354, 5355, 5356, 5357, 5358, 5359, 5360, 5361, 5362, 5363, 5364, 5365, 5366, 5367, 5368, 5369, 5370, 5371, 5372, 5373, 5374, 5375, 5376, 5377, 5378, 5379, 5380, 5381, 5382, 5383, 5384, 5385, 5386, 5387, 5388, 5389, 5390, 5391, 5392, 5393, 5394, 5395, 5396, 5397, 5398, 5399, 5400, 5401, 5402, 5403, 5404, 5405, 5406, 5407, 5408, 5409, 5410, 5411, 5412, 5413, 5414, 5415, 5416, 5417, 5418, 5419, 5420, 5421, 5422, 5423, 5424, 5425, 5426, 5427, 5428, 5429, 5430, 5431, 5432, 5433, 5434, 5435, 5436, 5437, 5438, 5439, 5440, 5441, 5442, 5443, 5444, 5445, 5446, 5447, 5448, 5449, 5450, 5451, 5452, 5453, 5454, 5455, 5456, 5457, 5458, 5459, 5460, 5461, 5462, 5463, 5464, 5465, 5466, 5467, 5468, 5469, 5470, 5471, 5472, 5473, 5474, 5475, 5476, 5477, 5478, 5479, 5480, 5481, 5482, 5483, 5484, 5485, 5486, 5487, 5488, 5489, 5490, 5491, 5492, 5493, 5494, 5495, 5496, 5497, 5498, 5499, 5500, 5501, 5502, 5503, 5504, 5505, 5506, 5507, 5508, 5509, 5510, 5511, 5512, 5513, 5514, 5515, 5516, 5517, 5518, 5519, 5520, 5521, 5522, 5523, 5524, 5525, 5526, 5527, 5528, 5529, 5530, 5531, 5532, 5533, 5534, 5535, 5536, 5537, 5538, 5539, 5540, 5541, 5542, 5543, 5544, 5545, 5546, 5547, 5548, 5549, 5550, 5551, 5552, 5553, 5554, 5555, 5556, 5557, 5558, 5559, 5560, 5561, 5562, 5563, 5564, 5565, 5566, 5567, 5568, 5569, 5570, 5571, 5572, 5573, 5574, 5575, 5576, 5577, 5578, 5579, 5580, 5581, 5582, 5583, 5584, 5585, 5586, 5587, 5588, 5589, 5590, 5591, 5592, 5593, 5594, 5595, 5596, 5597, 5598, 5599, 5600, 5601, 5602, 5603, 5604, 5605, 5606, 5607, 5608, 5609, 5610, 5611, 5612, 5613, 5614, 5615, 5616, 5617, 5618, 5619, 5620, 5621, 5622 and 5623 in SEQ ID NO: 30,

with the proviso that the selected amino acid residue satisfies the formula $N \leq L-n+1$, where N is the number of the selected residue, L is the number of amino acid residues in the sequence from which the residue is selected, and n is the number of consecutive amino acid residues.

6. (canceled)
7. (canceled)
8. (canceled)
9. (canceled)
10. (canceled)
11. (canceled)
12. (canceled)
13. (canceled)
14. (canceled)
15. (canceled)
16. (canceled)
17. (canceled)
18. (canceled)
19. (canceled)
20. (canceled)
21. (canceled)
22. (canceled)
23. (canceled)
24. (canceled)
25. (canceled)
26. (canceled)
27. (canceled)
28. (canceled)
29. (canceled)
30. (canceled)
31. (canceled)
32. (canceled)
33. (canceled)
34. (canceled)
35. (canceled)
36. (canceled)

37. The polypeptide according to claim **1**, which is fused or conjugated to an immunogenic carrier molecule.

38. The polypeptide according to claim **37**, wherein the immunogenic carrier molecule is a polypeptide that induces T-helper lymphocyte responses in a majority of humans, such as immunogenic carrier proteins selected from the group consisting of keyhole limpet hemocyanin or a fragment thereof, tetanus toxoid or a fragment thereof, dipththeria toxoid or a fragment thereof.

39. The polypeptide according to claim **1**, which is capable of inducing an adaptive immune response against the polypeptide in a mammal, in particular in a human being.

40. The polypeptide according to claim **39**, which is capable of inducing, in the mammal, a protective adaptive immune response against infection with *Pseudomonas aeruginosa.*

41. The polypeptide according to claim **39**, which induces a humoral and/or a cellular immune response.

An isolated nucleic acid fragment, which comprises

i) a nucleotide sequence encoding a polypeptide according to claim **1**, or

ii) a nucleotide sequence consisting of the amino acid encoding part of any one of SEQ ID NOs: 31-90.

43. The nucleic acid fragment according to claim **42**, which is a DNA or an RNA fragment.

44. The nucleic acid fragment according to claim **42**, option i), wherein the nucleotide sequence consists of at least 105, at least 106, at least 107, at least 108, at least 109, at least 110, at least 111, at least 112, at least 113, at least 114, at least 115, at least 116, at least 117, at least 118, at least 119, at least 120, at least 121, at least 122, at least 123, at least 124, at least 125, at least 126, at least 127, at least 128, at least 129, at least 130, at least 131, at least 132, at least 133, at least 134, at least 135, at least 136, at least 137, at least 138, at least 139, at least 140, at least 141, at least 142, at least 143, at least 144, at least 145, at least 146, at least 147, at least 148, at least 149, at least 150, at least 151, at least 152, at least 153, at least 154, at least 155, at least 156, at least 157, at least 158, at least 159, at least 160, at least 171, at least 172, at least 173, at least 174, at least 175, at least 176, at least 177, at least 178, at least 179, at least 180, at least 181, at least 182, at least 183, at least 184, at least 185, at least 186, at least 187, at least 188, at least 189, at least 190, at least 191, at least 192, at least 193, at least 194, at least 195, at least 196, at least 197, at least 198, at least 199, at least 200 and at least 201 consecutive nucleotides in the amino acid encoding part of any one of SEQ ID NOs: 30-90.

45. (canceled)

46. (canceled)

47. A vector comprising the nucleic acid according to claim **42** vector.

48. The vector according to claim **47**, which comprises in operable linkage and in the 5'-3' direction, an expression control region comprising an enhancer/promoter for driving expression of the nucleic acid fragment defined in claim **42**, option i), optionally a signal peptide coding sequence, a nucleotide sequence defined in claim **42**, option i), and optionally a terminator.

49. The vector according to claim **47**, wherein the expression control region drives expression in a prokaryotic cell.

50. The vector according to claim **47**, which is capable of autonomous replication.

51. The vector according to claim **47**, which is capable of being integrated into the genome of a host cell.

52. The vector according to claim **47**, which is incapable of being integrated into the genome of a mammalian host cell.

53. The vector according to claim **47**, which is selected from the group consisting of a virus, a bacteriophage, a plasmid, a minichromosome, and a cosmid.

54. A cell which is transformed to carry the vector according to claim **47**.

55. The transformed cell according to claim **54**, which is capable of replicating the nucleic acid fragment defined in claim **42**, option i).

56. The transformed cell according to claim **54**, which is capable of expressing the nucleic acid fragment defined in claim **42**, option i).

57. The transformed cell according to claim **54**, which is selected from a prokaryotic cell or a eukaryotic cell.

58. The transformed cell according to claim **54**, which is a bacterial cell selected from the group consisting of *Escherichia, Bacillus, Salmonella*, and *Mycobacterium.*

59. The transformed cell according to claim **54**, which is stably transformed by having the nucleic acid defined in claim **42**, option i), stably integrated into its genome.

60. The transformed cell according to claim **54**, which secretes or carries on its surface the polypeptide according to claim **1**.

61. The transformed cell according to claim **60**, wherein the cell is a bacterium and secretion is into the periplasmic space.

62. A cell line derived from a transformed cell according to claim **54**.

63. A pharmaceutical composition comprising a polypeptide according to claim **1**, a nucleic acid fragment according to claim **42**, a vector according to claim **47**, or a cell according to claim **54**, and a pharmaceutically acceptable carrier, vehicle or diluent.

64. The pharmaceutical composition according to claim **63**, which further comprises an immunological adjuvant.

65. The pharmaceutical composition according to claim **64**, wherein the adjuvant is an aluminium based adjuvant.

66. A method for inducing immunity in an animal by administering at least once an immunogenically effective amount of a polypeptide according to claim **1**, a nucleic acid fragment according to claim **42**, a vector according to claim **47**, a cell according to claim **54**, or a pharmaceutical composition according to claim **63** so as to induce adaptive immunity against *Pseudomonas aeruginosa* in the animal.

67. The method according to claim **66**, wherein, when the polypeptide according to claim **1** or a composition comprising said polypeptide is administered, the animal receives between 0.5 and 5,000 μg of the polypeptide according to claim **1** per administration.

68. The method according to claim **66**, wherein the animal receives a priming administration and one or more booster administrations.

69. The method according to claim **66**, wherein the animal is a human being.

70. The method according to claim **66**, wherein the administration is for the purpose of inducing protective immunity against *Pseudomonas aeruginosa.*

71. The method according to claim **70**, wherein the protective immunity is effective in reducing the risk of attracting infection with *Pseudomonas aeruginosa* or is effective in treating or ameliorating infection with *Pseudomonas aeruginosa.*

72. The method according to claim **66**, wherein the administration is for the purpose of inducing antibodies specific for *Pseudomonas aeruginosa* and wherein said antibodies or B-lymphocytes producing said antibodies are subsequently recovered from the animal.

73. The method according to claim **66**, wherein the administration is for the purpose of inducing antibodies specific for *Pseudomonas aeruginosa* and wherein B-lymphocytes producing said antibodies are subsequently recovered from the animal and used for preparation of monoclonal antibodies.

74. (canceled)

75. (canceled)

76. (canceled)

77. (canceled)

78. (canceled)

79. (canceled)

80. (canceled)

81. (canceled)

82. (canceled)
83. (canceled)
84. (canceled)
85. (canceled)
86. (canceled)
87. (canceled)
88. (canceled)
89. (canceled)
90. (canceled)
91. (canceled)
92. (canceled)
93. (canceled)

94. The vector according to claim **47** wherein the vector is a cloning vector or an expression vector.

95. The transformed cell according to claim **58** wherein the bacterial cell is non-pathogenic.

* * * * *