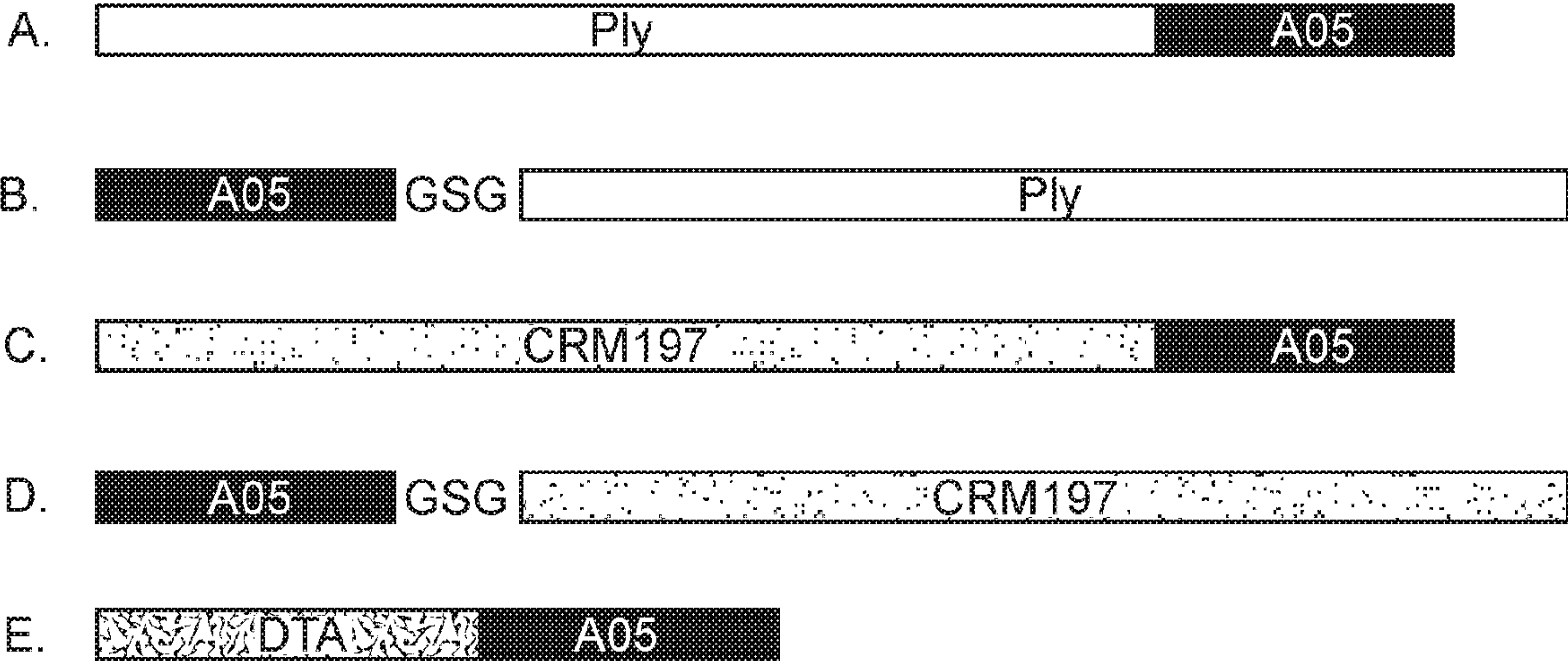




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(54) **Titre : POLYPEPTIDES IMMUNOGENES DE FUSION**
(54) **Title: IMMUNOGENIC FUSION POLYPEPTIDES**



(57) **Abrégé/Abstract:**
In one aspect, the invention relates to an isolated polypeptide including the amino acid sequence of a carrier polypeptide and the amino acid sequence of an ORF2086 polypeptide. In another aspect, the invention relates to an immunogenic conjugate including ORF2086 polypeptide and a carrier polypeptide. The invention further includes immunogenic compositions and methods for inducing an immune response against Neisseria meningitidis in a mammal.

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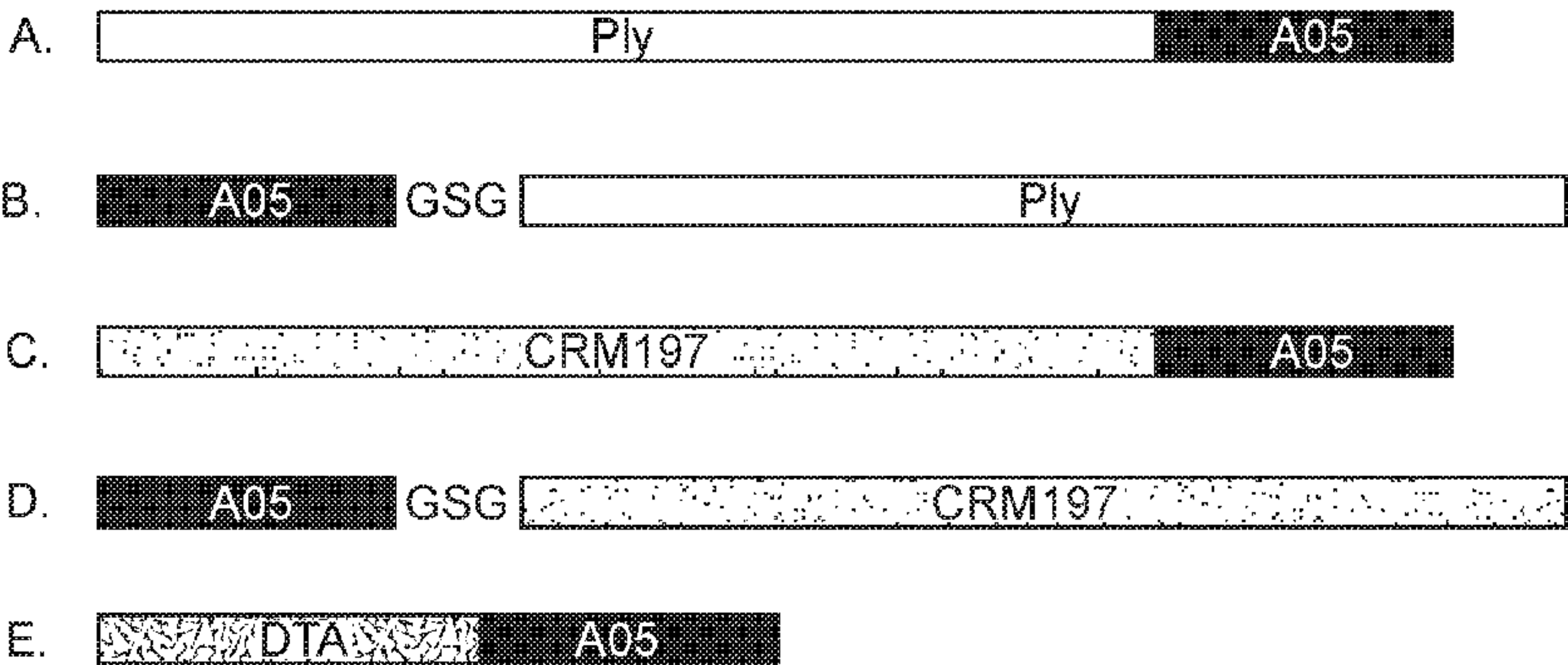
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[Continued on next page]

(54) Title: IMMUNOGENIC FUSION POLYPEPTIDES

FIG. 1



(57) Abstract: In one aspect, the invention relates to an isolated polypeptide including the amino acid sequence of a carrier polypeptide and the amino acid sequence of an ORF2086 polypeptide. In another aspect, the invention relates to an immunogenic conjugate including ORF2086 polypeptide and a carrier polypeptide. The invention further includes immunogenic compositions and methods for inducing an immune response against *Neisseria meningitidis* in a mammal.

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IMMUNOGENIC FUSION POLYPEPTIDES

CROSS REFERENCE TO RELATED APPLICATIONS

This application claims the benefit of U.S. provisional patent application Serial Number 61/775,478, filed March 8, 2013.

5 FIELD OF THE INVENTION

The present invention relates to *Neisseria meningitidis* compositions and methods thereof.

BACKGROUND OF THE INVENTION

Neisseria meningitidis is a Gram-negative encapsulated bacterium that can cause
10 sepsis, meningitis and death. *N. meningitidis* can be classified into about 13 serogroups based on chemically and antigenically distinctive polysaccharide capsules. Five of the serogroups (A, B, C, Y, and W135) are responsible for the majority of disease. Meningococcal meningitis is a devastating disease that can kill children and young adults within hours despite the availability of antibiotics. There is a need for improved immunogenic compositions against meningococcal meningitis.

15 SUMMARY OF THE INVENTION

To meet these and other needs, the present invention relates to molecules, compositions, and methods that include *Neisseria meningitidis* polypeptides and carrier polypeptides.

In one aspect, the invention relates to an isolated polypeptide including the amino acid sequence of a carrier polypeptide and the amino acid sequence of an ORF2086 polypeptide. In one
20 embodiment, the isolated polypeptide is a fusion polypeptide. In one embodiment, the ORF2086 polypeptide is a subfamily A polypeptide. In one embodiment, the ORF2086 polypeptide is a subfamily B polypeptide. In one embodiment, the ORF2086 polypeptide is lipidated. In one embodiment, the ORF2086 polypeptide is non-lipidated. In one embodiment, the ORF2086 polypeptide is A05. In one embodiment, the ORF2086 polypeptide is A12. In one embodiment, the
25 ORF2086 polypeptide is A22. In one embodiment, the ORF2086 polypeptide is B01. In one embodiment, the ORF2086 polypeptide is B09. In one embodiment, the ORF2086 polypeptide is B15. In one embodiment, the ORF2086 polypeptide is B16. In one embodiment, the ORF2086 polypeptide is B22. In one embodiment, the ORF2086 polypeptide is B24. In one embodiment, the ORF2086

polypeptide is B44. In one embodiment, the ORF2086 polypeptide is A62. In one embodiment, the ORF2086 polypeptide is A04. In one embodiment, the ORF2086 polypeptide is A01. In one embodiment, the ORF2086 polypeptide is A06. In one embodiment, the ORF2086 polypeptide is A07. In one embodiment, the ORF2086 polypeptide is A15. In one embodiment, the ORF2086 polypeptide is A19. In one embodiment, the ORF2086 polypeptide is A20. In one embodiment, the ORF2086 polypeptide is A29. In one embodiment, the ORF2086 polypeptide is B02. In one embodiment, the ORF2086 polypeptide includes the amino acid sequence selected from the group consisting of SEQ ID NOs: 5, 19, and 22-65.

In one embodiment, the carrier polypeptide is a cytolysoin. In one embodiment, the cytolysoin is derived from a pneumolysin polypeptide from *Streptococcus pneumoniae*, a perfringolysin O polypeptide from *Clostridium perfringens*, a intermediolysin polypeptide from *Streptococcus intermedius*, a alveolysin polypeptide from *Bacillus alvei*, a anthrolysin polypeptide from *Bacillus anthracis*, a putative cereolysin polypeptide from *Bacillus cereus*, a ivanolysin O polypeptide from *Listeria ivanovii*, a pyolysin polypeptide from *Arcanobacterium pyogenes*, a seeligeriolysin O polypeptide from *Listeria seeligeri*, a streptolysin O polypeptide from *S. pyogenes*, a suilysin polypeptide from *Streptococcus suis*, a tetanolysin polypeptide from *Clostridium tetani*, a listeriolysin O polypeptide from *Listeria monocytogenes*, a streptolysin O polypeptide from *Streptococcus equisimilis*, a streptolysin O polypeptide from *S. canis*, a thuringiolysin O polypeptide from *Bacillus thuringiensis*, a laterosporolysin O polypeptide from *B. laterosporus*, a botulinolysin polypeptide from *Clostridium botulinum*, a chauveolysin polypeptide from *C. chauvoei*, a bifermentolysin polypeptide from *C. bifermentans*, a sordellilysin polypeptide from *C. sordellii*, a histolyticolysin polypeptide from *Clostridium histolyticum*, a novylisin polypeptide from *Clostridium novyi*, or a septicolysin O polypeptide from *Clostridium septicum*. In one embodiment, the cytolysoin is derived from a pneumolysin polypeptide from *Streptococcus pneumoniae*. In one embodiment, the cytolysoin includes a sequence having at least 90% sequence identity to SEQ ID NO: 1.

In one embodiment, the carrier polypeptide is detoxified as compared to the corresponding wild-type carrier polypeptide and is selected from the group consisting of tetanus toxin (TT), *Plasmodium falciparum* circumsporozoite protein, hepatitis B surface antigen, hepatitis B nuclear core polypeptide, *H. influenzae* matrix polypeptide, *H. influenzae* haemagglutinin, diphtheria toxoid, diphtheria toxoid mutant CRM₁₉₇, group B *N. meningitidis* outer membrane polypeptide complex (OMPC), a cytolysoin,

pneumococcal toxin pneumolysin, heat shock polypeptide from *Mycobacterium bovis*, heat shock polypeptide from *M. leprae*, cholera toxoid, *E. coli* LT, *E. coli* ST, exotoxin A from *Pseudomonas aeruginosa*, pneumococcal surface polypeptide A, pneumococcal adhesin polypeptide (PsaA), C5a peptidase from Group A or Group B streptococcus, *Haemophilus influenzae* polypeptide D, ovalbumin, keyhole limpet hemocyanin (KLH), bovine serum albumin (BSA), purified polypeptide derivative of tuberculin (PPD), PorB (from *N. meningitidis*), and derivatives, variants, or fragments thereof. In one embodiment, carrier polypeptide is not CRM₁₉₇.

In one embodiment, the polypeptide further includes a polypeptide sequence derived from pneumococcal bacteria. In one embodiment, isolated polypeptide does not include a polypeptide sequence derived from pneumococcal bacteria.

In one embodiment, the isolated polypeptide elicits a bactericidal antibody against a *N. meningitidis* serogroup B variant that is homologous with the ORF2086 polypeptide. In one embodiment, the isolated polypeptide elicits a bactericidal antibody against a *N. meningitidis* serogroup B variant that is heterologous to the ORF2086 polypeptide.

In one embodiment, the fusion polypeptide includes in the following order: the carrier polypeptide operably linked to the ORF2086 polypeptide. In one embodiment, the fusion polypeptide includes in the following order: an ORF2086 polypeptide operably linked to a carrier polypeptide. In one embodiment, the carrier polypeptide includes SEQ ID NO: 1 and the ORF2086 polypeptide includes SEQ ID NO: 5. In one embodiment, the isolated polypeptide includes SEQ ID NO: 2.

In a second aspect, the invention relates to an isolated polynucleotide that encodes a polypeptide according to any one of inventive polypeptides described herein.

In a third aspect, the invention relates to an immunogenic composition including a polypeptide according to any one of the inventive polypeptides described herein and a pharmaceutically acceptable excipient. In one embodiment, the immunogenic composition further includes at least one conjugate selected from: a) a conjugate of a capsular polysaccharide of *Neisseria meningitidis* serogroup A; b) a conjugate of a capsular polysaccharide of *Neisseria meningitidis* serogroup C; c) a conjugate of a capsular polysaccharide of *Neisseria meningitidis* serogroup W135; and d) a conjugate of a capsular polysaccharide of *Neisseria meningitidis* serogroup Y.

In a fourth aspect, the invention relates to a method for inducing an immune response against *Neisseria meningitidis* in a mammal. The method includes administering to the mammal an effective amount of the isolated polypeptide according

to any of the embodiments described herein. In one embodiment, the immune response includes a bactericidal antibody. In one embodiment, the immune response is equal to an immune response of a mammal administered with a corresponding non-lipidated ORF2086 polypeptide in the absence of a carrier polypeptide, when assessed under identical conditions. In one embodiment, the immune response is greater than an immune response of a mammal administered with a corresponding non-lipidated ORF2086 polypeptide in the absence of a carrier polypeptide, when assessed under identical conditions. In one embodiment, the immune response is at most 10% less than an immune response of a mammal administered with a corresponding lipidated ORF2086 polypeptide in the absence of a carrier polypeptide, when assessed under identical conditions. In one embodiment, the immune response is at most 20% less than an immune response of a mammal administered with a corresponding lipidated ORF2086 polypeptide in the absence of a carrier polypeptide, when assessed under identical conditions.

In a fifth aspect, the invention relates to a method for inducing an immune response against *Neisseria meningitidis* in a mammal. The method includes administering to the mammal an effective amount of the immunogenic composition described herein. In one embodiment, the immune response includes a bactericidal antibody. In one embodiment, the immune response is equal to an immune response of a mammal administered with a corresponding lipidated ORF2086 polypeptide in the absence of a carrier polypeptide, when assessed under identical conditions. In one embodiment, the immune response is greater than an immune response of a mammal administered with a corresponding non-lipidated ORF2086 polypeptide in the absence of a carrier polypeptide, when assessed under identical conditions. In one embodiment, the immune response is at most 10% less than an immune response of a mammal administered with a corresponding lipidated ORF2086 polypeptide in the absence of a carrier polypeptide, when assessed under identical conditions. In one embodiment, the immune response is at most 20% less than an immune response of a mammal administered with a corresponding lipidated ORF2086 polypeptide in the absence of a carrier polypeptide, when assessed under identical conditions.

In a sixth aspect, the invention relates to an immunogenic composition including an ORF2086 polypeptide and a carrier polypeptide. In one embodiment, the composition is a conjugate. In one embodiment, the ORF2086 polypeptide is a subfamily A polypeptide. In one embodiment, the ORF2086 polypeptide is a subfamily B polypeptide. In one embodiment, the ORF2086 polypeptide is lipidated. In one

embodiment, the ORF2086 polypeptide is non-lipidated. In one embodiment, the ORF2086 polypeptide is non-lipidated and non-pyruvylated. In one embodiment, the ORF2086 polypeptide is A05. In one embodiment, the ORF2086 polypeptide is A12. In one embodiment, the ORF2086 polypeptide is A22. In one embodiment, the ORF2086 polypeptide is B01. In one embodiment, the ORF2086 polypeptide is B09. In one embodiment, the ORF2086 polypeptide is B15. In one embodiment, the ORF2086 polypeptide is B16. In one embodiment, the ORF2086 polypeptide is B22. In one embodiment, the ORF2086 polypeptide is B24. In one embodiment, the ORF2086 polypeptide is B44. In one embodiment, the ORF2086 polypeptide is A62. In one embodiment, the ORF2086 polypeptide is A04. In one embodiment, the ORF2086 polypeptide is A01. In one embodiment, the ORF2086 polypeptide is A06. In one embodiment, the ORF2086 polypeptide is A07. In one embodiment, the ORF2086 polypeptide is A15. In one embodiment, the ORF2086 polypeptide is A19. In one embodiment, the ORF2086 polypeptide is A20. In one embodiment, the ORF2086 polypeptide is A29. In one embodiment, the ORF2086 polypeptide is B02. In one embodiment, the ORF2086 polypeptide includes the amino acid sequence selected from the group consisting of SEQ ID NOs: 5, 19, and 22-65.

In one embodiment, the carrier polypeptide is a cytolysoid. In one embodiment, the cytolysoid is derived from a pneumolysin polypeptide from *Streptococcus pneumoniae*, a perfringolysin O polypeptide from *Clostridium perfringens*, a intermediolysin polypeptide from *Streptococcus intermedius*, a alveolysin polypeptide from *Bacillus alvei*, a anthrolysin polypeptide from *Bacillus anthracis*, a putative cereolysin polypeptide from *Bacillus cereus*, a ivanolysin O polypeptide from *Listeria ivanovii*, a pyolysin polypeptide from *Arcanobacterium pyogenes*, a seeligeriolysin O polypeptide from *Listeria seeligeri*, a streptolysin O polypeptide from *S. pyogenes*, a suilysin polypeptide from *Streptococcus suis*, a tetanolysin polypeptide from *Clostridium tetani*, a listeriolysin O polypeptide from *Listeria monocytogenes*, a streptolysin O polypeptide from *Streptococcus equisimilis*, a streptolysin O polypeptide from *S. canis*, a thuringiolysin O polypeptide from *Bacillus thuringiensis*, a laterosporolysin O polypeptide from *B. laterosporus*, a botulinolysin polypeptide from *Clostridium botulinum*, a chauveolysin polypeptide from *C. chauvoei*, a bifermentolysin polypeptide from *C. bifermentans*, a sordellilysin polypeptide from *C. sordellii*, a histolyticolysin polypeptide from *Clostridium histiolyticum*, a novylisin polypeptide from *Clostridium novyi*, or a septicolysin O polypeptide from *Clostridium septicum*. In one embodiment, the cytolysoid is derived from a pneumolysin polypeptide from *Streptococcus*

pneumoniae. In one embodiment, the cytolsoid includes a sequence having at least 90% sequence identity to SEQ ID NO: 1.

In one embodiment, the carrier polypeptide is detoxified as compared to the corresponding wild-type carrier polypeptide and is selected from the group consisting of tetanus toxin (TT), *Plasmodium falciparum* circumsporozoite protein, hepatitis B surface antigen, hepatitis B nuclear core polypeptide, *H. influenzae* matrix polypeptide, *H. influenzae* haemagglutinin, diphtheria toxoid, diphtheria toxoid mutant CRM₁₉₇, group B *N. meningitidis* outer membrane polypeptide complex (OMPC), a cytolsoid, pneumococcal toxin pneumolysin, heat shock polypeptide from *Mycobacterium bovis*, heat shock polypeptide from *M. leprae*, cholera toxoid, *E. coli* LT, *E. coli* ST, exotoxin A from *Pseudomonas aeruginosa*, pneumococcal surface polypeptide A, pneumococcal adhesin polypeptide (PsaA), C5a peptidase from Group A or Group B streptococcus, *Haemophilus influenzae* polypeptide D, ovalbumin, keyhole limpet hemocyanin (KLH), bovine serum albumin (BSA), purified polypeptide derivative of tuberculin (PPD), PorB (from *N. meningitidis*), and derivatives, variants, or fragments thereof. In one embodiment, carrier polypeptide is CRM₁₉₇. In one embodiment, the carrier polypeptide is heterologous to the ORF2086 polypeptide.

In one embodiment, the composition further includes a polypeptide sequence derived from pneumococcal bacteria. In one embodiment, the composition does not include a polypeptide sequence derived from pneumococcal bacteria.

In one embodiment, the composition elicits a bactericidal antibody response against a *N. meningitidis* serogroup B strain expressing an ORF2086 variant that is homologous to the ORF2086 polypeptide. In one embodiment, the composition elicits a bactericidal antibody response against a *N. meningitidis* serogroup B strain expressing an ORF2086 variant that is heterologous to the ORF2086 polypeptide.

In one embodiment, the composition further includes at least one conjugate selected from: a) a conjugate of a capsular saccharide of *Neisseria meningitidis* serogroup A; b) a conjugate of a capsular saccharide of *Neisseria meningitidis* serogroup C; c) a conjugate of a capsular saccharide of *Neisseria meningitidis* serogroup W135; and d) a conjugate of a capsular saccharide of *Neisseria meningitidis* serogroup Y. In one embodiment, the composition further includes a pharmaceutically acceptable excipient.

In a seventh aspect, the invention relates to a method for inducing an immune response against *Neisseria meningitidis* in a mammal. The method includes administering to the mammal an effective amount of the composition described herein.

In one embodiment, the immune response includes a bactericidal antibody. In one embodiment, the immune response is equal to an immune response of a mammal administered with a corresponding lipidated ORF2086 polypeptide in the absence of a carrier polypeptide, when assessed under identical conditions. In one embodiment, the immune response is greater than an immune response of a

5 mammal administered with a corresponding non-lipidated ORF2086 polypeptide in the absence of a carrier polypeptide, when assessed under identical conditions. In one embodiment, the immune response is at most 10% less than an immune response of a mammal administered with a corresponding lipidated ORF2086 polypeptide in the absence of a carrier polypeptide, when assessed under identical conditions. In one embodiment, the immune response is at most 20% less than an

10 immune response of a mammal administered with a corresponding lipidated ORF2086 polypeptide in the absence of a carrier polypeptide, when assessed under identical conditions.

The present invention as claimed relates to an isolated polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 2; or SEQ ID NO: 8, 14, 16 or 18.

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BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A-E: Diagrammatic description of fusion polypeptides. A. Ply-A05 fusion; B. A05-Ply fusion; C. CRM₁₉₇-A05 fusion; D. A05-CRM₁₉₇ fusion; E. DTA-A05 fusion.

Figure 2: Expression of Ply-A05 fusion proteins at 30°C in small scale flask cultures. T0, preinduction sample; T3 3 hours post induction; T21, 21 hours post induction; S, soluble fraction; I, insoluble fraction; (-), prior to induction; (+), post-induction.

Figure 3: Expression of Ply-A05 fusion proteins at 20°C in small scale flask cultures. Panel A: cells harvested prior to induction (0) and at 17 and 41h post-induction. Panel B: Solubility assessment of pDD20 at 17h post-induction. Lanes: 1. T0 whole cell lysate (WCL); 2. T17 WCL; 3. T17 BUGBUSTER™ supernatant; 4. T17 BUGBUSTER™ pellet; 5. T17 sonication supernatant; 6. T17 sonication pellet.

Figure 4: Six 1 liter flask induction of pDD20/BD686. Lanes: 0, preinduction; 18, hours post-induction; S, soluble fraction; I insoluble fraction.

SEQUENCE IDENTIFIERS

SEQ ID NO: 1 sets forth the amino acid sequence for a pneumolysoid.

SEQ ID NO: 2 sets forth the amino acid sequence for a pneumolysoid and non-lipidated A05 polypeptide (PLY-A05).

SEQ ID NO: 3 sets forth a DNA sequence encoding the pneumolysoid of SEQ ID NO: 1.

SEQ ID NO: 4 sets forth a DNA sequence encoding the polypeptide of SEQ ID NO: 2.

SEQ ID NO: 5 sets forth the amino acid sequence for a A05 polypeptide.

SEQ ID NO: 6 sets forth a DNA sequence encoding an A05 polypeptide.

SEQ ID NO: 7 sets forth a DNA sequence encoding the polypeptide of SEQ ID NO: 8.

SEQ ID NO: 8 sets forth the amino acid sequence for a non-lipidated A05 polypeptide and pneumolysoid (A05-PLY).

SEQ ID NO: 9 sets forth a DNA sequence encoding for CRM₁₉₇.

SEQ ID NO: 10 sets forth the amino acid sequence for CRM₁₉₇.

SEQ ID NO: 11 sets forth a DNA sequence encoding amino acid residues 1-193 of CRM₁₉₇ (DT-A).

SEQ ID NO: 12 sets forth the amino acid sequence for residues 1-193 of CRM₁₉₇ (DT-A).

SEQ ID NO: 13 sets forth a DNA sequence encoding the polypeptide of SEQ ID NO: 14.

SEQ ID NO: 14 sets forth the amino acid sequence for CRM₁₉₇ and a non-lipidated A05 polypeptide (CRM₁₉₇-A05).

SEQ ID NO: 15 sets forth a DNA sequence encoding the polypeptide of SEQ ID NO: 16.

SEQ ID NO: 16 sets forth the amino acid sequence for a non-lipidated A05 polypeptide and CRM₁₉₇ (A05-CRM₁₉₇).

SEQ ID NO: 17 sets forth a DNA sequence encoding the polypeptide of SEQ ID NO: 18.

SEQ ID NO: 18 sets forth the amino acid sequence for a fragment of CRM₁₉₇ and a non-lipidated A05 polypeptide (DT-A-A05).

SEQ ID NO: 19: sets forth the amino acid sequence for a *N. meningitidis*, serogroup B, 2086 variant A05. In comparison to a wild-type A05, SEQ ID NO: 19 includes a glycine after an initial cysteine and a deletion of four amino acids at the N-terminus.

SEQ ID NO: 20 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant B01, which includes an N-terminal Cys at amino acid position 1.

SEQ ID NO: 21 sets forth the amino acid sequence for a wild-type pneumolysin from *Streptococcus pneumoniae*.

SEQ ID NO: 22 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant A22, which includes an N-terminal Cys at amino acid position 1.

SEQ ID NO: 23 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant A05, which includes an N-terminal Cys at amino acid position 1.

SEQ ID NO: 24 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant A04, which includes an N-terminal Cys at amino acid position 1.

SEQ ID NO: 25 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant A01, which includes an N-terminal Cys at amino acid position 1.

SEQ ID NO: 26 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant A06, which includes an N-terminal Cys at amino acid position 1.

SEQ ID NO: 27 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant A07, which includes an N-terminal Cys at amino acid position 1.

SEQ ID NO: 28 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant A12, which includes an N-terminal Cys at amino acid position 1.

SEQ ID NO: 29 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant A15, which includes an N-terminal Cys at amino acid position 1.

SEQ ID NO: 30 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant A19, which includes an N-terminal Cys at amino acid position 1.

SEQ ID NO: 31 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant A20, which includes an N-terminal Cys at amino acid position 1.

SEQ ID NO: 32 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant A29, which includes an N-terminal Cys at amino acid position 1.

SEQ ID NO: 33 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant B03, which includes an N-terminal Cys at amino acid position 1.

SEQ ID NO: 34 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant B02, which includes an N-terminal Cys at amino acid position 1.

SEQ ID NO: 35 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant B09, which includes an N-terminal Cys at amino acid position 1.

SEQ ID NO: 36 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant B15, which includes an N-terminal Cys at amino acid position 1.

SEQ ID NO: 37 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant B16, which includes an N-terminal Cys at amino acid position 1.

SEQ ID NO: 38 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant B22, which includes an N-terminal Cys at amino acid position 1.

SEQ ID NO: 39 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant B24, which includes an N-terminal Cys at amino acid position 1.

SEQ ID NO: 40 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant B44, which includes an N-terminal Cys at amino acid position 1.

SEQ ID NO: 41 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant A62, which includes an N-terminal Cys at amino acid position 1.

N-terminal Cys is not present

SEQ ID NO: 42 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant A01, which does not include an N-terminal Cys at amino acid position 1.

SEQ ID NO: 43 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant A04, which does not include an N-terminal Cys at amino acid position 1.

SEQ ID NO: 44 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant A05, which does not include an N-terminal Cys at amino acid position 1.

SEQ ID NO: 45 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant A06, which does not include an N-terminal Cys at amino acid position 1.

SEQ ID NO: 46 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant A07, which does not include an N-terminal Cys at amino acid position 1.

SEQ ID NO: 47 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant A12, which does not include an N-terminal Cys at amino acid position 1.

SEQ ID NO: 48 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant A15, which does not include an N-terminal Cys at amino acid position 1.

SEQ ID NO: 49 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant A19, which does not include an N-terminal Cys at amino acid position 1.

SEQ ID NO: 50 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant A20, which does not include an N-terminal Cys at amino acid position 1.

SEQ ID NO: 51 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant A22, which does not include an N-terminal Cys at amino acid position 1.

SEQ ID NO: 52 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant A29, which does not include an N-terminal Cys at amino acid position 1.

SEQ ID NO: 53 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant B01, which does not include an N-terminal Cys at amino acid position 1.

SEQ ID NO: 54 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant B02, which does not include an N-terminal Cys at amino acid position 1.

SEQ ID NO: 55 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant B09, which does not include an N-terminal Cys at amino acid position 1.

SEQ ID NO: 56 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant B15, which does not include an N-terminal Cys at amino acid position 1.

SEQ ID NO: 57 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant B16, which does not include an N-terminal Cys at amino acid position 1.

SEQ ID NO: 58 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant B22, which does not include an N-terminal Cys at amino acid position 1.

SEQ ID NO: 59 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant B24, which does not include an N-terminal Cys at amino acid position 1.

SEQ ID NO: 60 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant B44, which does not include an N-terminal Cys at amino acid position 1.

SEQ ID NO: 61 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant A62, which does not include an N-terminal Cys at amino acid position 1.

Modifications:

SEQ ID NO: 62 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant B09, wherein an N-terminal cysteine is not present and the sequence includes an additional Gly/Ser region, as compared to SEQ ID NO: 35.

SEQ ID NO: 63 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant B22, in which the N-terminal Cys at amino acid position 1 of SEQ ID NO: 38 is replaced with a Glycine.

SEQ ID NO: 64 sets forth the amino acid sequence for the *N. meningitidis*, serogroup B, 2086 variant A22, in which the N-terminal Cys at amino acid position 1 of SEQ ID NO: 22 is replaced with a Glycine.

SEQ ID NO: 65 sets forth a DNA sequence for a B22 gene, in which the codon for the N-terminal Cys at amino acid position 1 of SEQ ID NO: 38 is replaced with a codon for a Glycine.

Exemplary DNA sequences encoding ORF2086 polypeptides

SEQ ID NO: 66 sets forth a DNA sequence for the *N. meningitidis*, serogroup B, 2086 variant A01 gene, which includes a codon encoding an N-terminal Cys.

SEQ ID NO: 67 sets forth a DNA sequence for the *N. meningitidis*, serogroup B, 2086 variant A29 gene, which includes a codon encoding an N-terminal Cys.

SEQ ID NO: 68 sets forth a DNA sequence for the *N. meningitidis*, serogroup B, 2086 variant A04 gene, which includes a codon encoding an N-terminal Cys.

SEQ ID NO: 69 sets forth a DNA sequence for the *N. meningitidis*, serogroup B, 2086 variant A05 gene, which includes a codon encoding an N-terminal Cys.

SEQ ID NO: 70 sets forth a DNA sequence for the *N. meningitidis*, serogroup B, 2086 variant A06 gene, which includes a codon encoding an N-terminal Cys.

SEQ ID NO: 71 sets forth a DNA sequence for the *N. meningitidis*, serogroup B, 2086 variant A07 gene, which includes a codon encoding an N-terminal Cys.

SEQ ID NO: 72 sets forth a DNA sequence for the *N. meningitidis*, serogroup B, 2086 variant A12 gene, which includes a codon encoding an N-terminal Cys.

SEQ ID NO: 73 sets forth a DNA sequence for the *N. meningitidis*, serogroup B, 2086 variant A15 gene, which includes a codon encoding an N-terminal Cys.

SEQ ID NO: 74 sets forth a DNA sequence for the *N. meningitidis*, serogroup B, 2086 variant A19 gene, which includes a codon encoding an N-terminal Cys.

SEQ ID NO: 75 sets forth a DNA sequence for the *N. meningitidis*, serogroup B, 2086 variant A20 gene, which includes a codon encoding an N-terminal Cys.

SEQ ID NO: 76 sets forth a DNA sequence for the *N. meningitidis*, serogroup B, 2086 variant A22 gene, which includes a codon encoding an N-terminal Cys.

SEQ ID NO: 77 sets forth a DNA sequence for the *N. meningitidis*, serogroup B, 2086 variant B01 gene, which includes a codon encoding an N-terminal Cys.

SEQ ID NO: 78 sets forth a DNA sequence for the *N. meningitidis*, serogroup B, 2086 variant B02 gene, which includes a codon encoding an N-terminal Cys.

SEQ ID NO: 79 sets forth a DNA sequence for the *N. meningitidis*, serogroup B, 2086 variant B44 gene, which includes a codon encoding an N-terminal Cys.

SEQ ID NO: 80 sets forth a DNA sequence for the *N. meningitidis*, serogroup B, 2086 variant B03 gene, which includes a codon encoding an N-terminal Cys.

SEQ ID NO: 81 sets forth a DNA sequence for the *N. meningitidis*, serogroup B, 2086 variant B09 gene, which includes a codon encoding an N-terminal Cys.

SEQ ID NO: 82 sets forth a DNA sequence for the *N. meningitidis*, serogroup B, 2086 variant B15 gene, which includes a codon encoding an N-terminal Cys.

SEQ ID NO: 83 sets forth a DNA sequence for the *N. meningitidis*, serogroup B, 2086 variant B16 gene, which includes a codon encoding an N-terminal Cys.

SEQ ID NO: 84 sets forth a DNA sequence for the *N. meningitidis*, serogroup B, 2086 variant B22 gene, which includes a codon encoding an N-terminal Cys.

SEQ ID NO: 85 sets forth a DNA sequence for the *N. meningitidis*, serogroup B, 2086 variant B24 gene, which includes a codon encoding an N-terminal Cys.

SEQ ID NO: 86 sets forth a DNA sequence for a *N. meningitidis*, serogroup B, 2086 variant A05 gene, wherein the codon encoding an N-terminal cysteine is deleted, as compared to SEQ ID NO: 69.

SEQ ID NO: 87 sets forth a DNA sequence for the *N. meningitidis*, serogroup B, 2086 variant A12-2 gene, which includes a codon encoding an N-terminal Cys.

Carrier polypeptides

SEQ ID NO: 88 sets forth the amino acid sequence for a wild-type Pneumolysin from *Streptococcus pneumoniae*.

SEQ ID NO: 89 sets forth the amino acid sequence for a wild-type Perfringolysin O from *Clostridium perfringens*.

SEQ ID NO: 90 sets forth the amino acid sequence for a wild-type Intermedilysin from *Streptococcus intermedius*.

SEQ ID NO: 91 sets forth the amino acid sequence for a wild-type Alveolysin from *Bacillus alvei*.

SEQ ID NO: 92 sets forth the amino acid sequence for a wild-type Anthrolysin from *Bacillus anthracis*.

SEQ ID NO: 93 sets forth the amino acid sequence for a wild-type Putative Cereolysin from *Bacillus cereus*.

SEQ ID NO: 94 sets forth the amino acid sequence for a wild-type Ivanolysin O from *Listeria ivanovii*.

SEQ ID NO: 95 sets forth the amino acid sequence for a wild-type Pyolysin from *Arcanobacterium pyogenes*.

SEQ ID NO: 96 sets forth the amino acid sequence for a wild-type Seeligeriolysin O from *Listeria seeligeri*.

SEQ ID NO: 97 sets forth the amino acid sequence for a wild-type Streptolysin O from *Streptococcus pyogenes*.

SEQ ID NO: 98 sets forth the amino acid sequence for a wild-type Suilysin from *Streptococcus suis*.

SEQ ID NO: 99 sets forth the amino acid sequence for a wild-type Tetanolysin from *Clostridium tetani*.

SEQ ID NO: 100 sets forth the amino acid sequence for a wild-type Listeriolysin O from *Listeria monocytogenes*.

SEQ ID NO: 101 sets forth the amino acid sequence for a wild-type Thuringiolysin from *Bacillus thuringiensis* (previously annotated as perfringolysin).

SEQ ID NO: 102 sets forth the amino acid sequence for a region of the wild-type Pneumolysin from *Streptococcus pneumoniae* that includes a consensus sequence corresponding to residues 144 to 161 of wild-type pneumolysin.

SEQ ID NO: 103 sets forth the amino acid sequence for a region of the wild-type Perfringolysin O from *Clostridium perfringens* that includes a consensus sequence corresponding to residues 144 to 161 of wild-type pneumolysin.

SEQ ID NO: 104 sets forth the amino acid sequence for a region of the wild-type Intermedilysin from *Streptococcus intermedius* that includes a consensus sequence corresponding to residues 144 to 161 of wild-type pneumolysin.

SEQ ID NO: 105 sets forth the amino acid sequence for a region of the wild-type Alveolysin from *Bacillus alvei* that includes a consensus sequence corresponding to residues 144 to 161 of wild-type pneumolysin.

SEQ ID NO: 106 sets forth the amino acid sequence for a region of the wild-type Anthrolysin from *Bacillus anthracis* that includes a consensus sequence corresponding to residues 144 to 161 of wild-type pneumolysin.

SEQ ID NO: 107 sets forth the amino acid sequence for a region of the wild-type Putative Cereolysin from *Bacillus cereus* that includes a consensus sequence corresponding to residues 144 to 161 of wild-type pneumolysin.

SEQ ID NO: 108 sets forth the amino acid sequence for a region of the wild-type Ivanolysin O from *Listeria ivanovii* that includes a consensus sequence corresponding to residues 144 to 161 of wild-type pneumolysin.

SEQ ID NO: 109 sets forth the amino acid sequence for a region of the wild-type Perfringolysin O from *Clostridium perfringens* that includes a consensus sequence corresponding to residues 144 to 161 of wild-type pneumolysin.

SEQ ID NO: 110 sets forth the amino acid sequence for a region of the wild-type Seeligeriolysin O from *Listeria seeligeri* that includes a consensus sequence corresponding to residues 144 to 161 of wild-type pneumolysin.

SEQ ID NO: 111 sets forth the amino acid sequence for a region of the wild-type Streptolysin O from *Streptococcus pyogenes* that includes a consensus sequence corresponding to residues 144 to 161 of wild-type pneumolysin.

SEQ ID NO: 112 sets forth the amino acid sequence for a region of the wild-type suilysin from *Streptococcus suis* that includes a consensus sequence corresponding to residues 144 to 161 of wild-type pneumolysin.

SEQ ID NO: 113 sets forth the amino acid sequence for a region of the wild-type Tetanolysin from *Clostridium tetani* that includes a consensus sequence corresponding to residues 144 to 161 of wild-type pneumolysin.

SEQ ID NO: 114 sets forth the amino acid sequence for a region of the wild-type Listeriolysin O from *Listeria monocytogenes* that includes a consensus sequence corresponding to residues 144 to 161 of wild-type pneumolysin.

SEQ ID NO: 115 sets forth the amino acid sequence for a region of the wild-type Thuringiolysin from *Bacillus thuringiensis* (previously annotated as perfringolysin) that includes a consensus sequence corresponding to residues 144 to 161 of wild-type pneumolysin.

SEQ ID NO: 116 sets forth the amino acid sequence for a wild-type Perfringolysin O from *Clostridium perfringens*.

SEQ ID NO: 117 sets forth the amino acid sequence for a variant of the pneumolysoid that includes a mutation of the lysine at amino acid position 460 to an aspartic acid residue.

SEQ ID NO: 118 sets forth the amino acid sequence for a variant of a pneumolysoid. When compared to SEQ ID NO: 117, SEQ ID NO: 118 has an amino acid change from Lysine at position 208 to Arginine.

SEQ ID NO: 119 sets forth the amino acid sequence for an exemplary pneumolysoid that includes a substitution of asparagine in place of aspartic acid at amino acid position 385 and deletion of alanine 146 and arginine 147 of the wild-type pneumolysin sequence.

SEQ ID NO: 120 sets forth the amino acid sequence for an exemplary pneumolysoid that includes a substitution of phenylalanine in place of tryptophan at amino acid position 433 of the wild-type pneumolysin sequence.

Codon-optimized sequences

SEQ ID NO: 121 sets forth a codon-optimized DNA sequence for a B44 gene.

SEQ ID NO: 122 sets forth a codon-optimized DNA sequence for a B09 gene, wherein an N-terminal cysteine is not encoded, and wherein the sequence includes codons encoding an additional Gly/Ser region, as compared to SEQ ID NO: 81.

SEQ ID NO: 123 sets forth a codon-optimized DNA sequence for a B09 gene, wherein an N-terminal cysteine is not encoded.

SEQ ID NO: 124 sets forth a codon-optimized DNA sequence for a B09 gene, wherein an N-terminal cysteine is not encoded.

SEQ ID NO: 125 sets forth a codon-optimized DNA sequence encoding an A05 polypeptide.

SEQ ID NO: 126 sets forth a codon-optimized DNA sequence encoding an A05 polypeptide.

SEQ ID NO: 127 sets forth a codon-optimized DNA sequence encoding an A22 polypeptide.

SEQ ID NO: 128 sets forth a codon-optimized DNA sequence encoding an A62 polypeptide.

SEQ ID NO: 129 sets forth a codon-optimized DNA sequence encoding an A12 polypeptide.

Additional sequences

SEQ ID NO: 130 sets forth the amino acid sequence for a B24 polypeptide. SEQ ID NO: 130 is identical to SEQ ID NO: 39 wherein the residues at positions 1-3 of SEQ ID NO: 39 are deleted.

SEQ ID NO: 131 sets forth a DNA sequence for an A22 polypeptide, in which the codon for the N-terminal Cys at amino acid position 1 of SEQ ID NO: 22 is replaced with a codon for a Glycine.

SEQ ID NO: 132 sets forth the amino acid sequence for an A22, in which the N-terminal Cys at amino acid position 1 of SEQ ID NO: 22 is replaced with a Glycine.

SEQ ID NO: 133 sets forth a DNA sequence for a B09 gene, wherein the codon encoding an N-terminal cysteine is not present.

SEQ ID NO: 134 sets forth a DNA sequence for a B44 gene, wherein the codon encoding an N-terminal cysteine is not present.

SEQ ID NO: 135 sets forth the amino acid sequence for a *N. meningitidis*, serogroup B, 2086 variant A05, wherein an N-terminal cysteine is not present.

SEQ ID NO: 136 sets forth the amino acid sequence for a pneumolysoid and non-lipidated A12 polypeptide (PLY-A12).

SEQ ID NO: 137 sets forth the amino acid sequence for a pneumolysoid and non-lipidated A12 polypeptide (PLY-A12), wherein the N-terminal methionine at position 1 of SEQ ID NO: 136 is removed.

SEQ ID NO: 138 sets forth the amino acid sequence for a pneumolysoid and non-lipidated B01 polypeptide (PLY-B01).

SEQ ID NO: 139 sets forth the amino acid sequence for a pneumolysoid and non-lipidated B01 polypeptide (PLY-B01), wherein the N-terminal methionine at position 1 of SEQ ID NO: 138 is removed.

SEQ ID NO: 140 sets forth the amino acid sequence for a pneumolysoid and non-lipidated B09 polypeptide (PLY-B09).

SEQ ID NO: 141 sets forth the amino acid sequence for a pneumolysoid and non-lipidated B09 polypeptide (PLY-B09), wherein the N-terminal methionine at position 1 of SEQ ID NO: 140 is removed.

SEQ ID NO: 142 sets forth the amino acid sequence for a pneumolysoid and non-lipidated B24 polypeptide (PLY-B24).

SEQ ID NO: 143 sets forth the amino acid sequence for a pneumolysoid and non-lipidated B24 polypeptide (PLY-B24), wherein the N-terminal methionine at position 1 of SEQ ID NO: 142 is removed.

SEQ ID NO: 144 sets forth the amino acid sequence for a pneumolysoid and non-lipidated B44 polypeptide (PLY-B44).

SEQ ID NO: 145 sets forth the amino acid sequence for a pneumolysoid and non-lipidated B44 polypeptide (PLY-B44), wherein the N-terminal methionine at position 1 of SEQ ID NO: 144 is removed.

SEQ ID NO: 146 sets forth the amino acid sequence for a GNA2091 polypeptide.

SEQ ID NO: 147 sets forth the amino acid sequence for a GNA2091 polypeptide, wherein the N-terminal methionine at position 1 of SEQ ID NO: 146 is removed.

SEQ ID NO: 148 sets forth the amino acid sequence for a GNA2091 and non-lipidated A05 polypeptide (GNA2091-A05).

SEQ ID NO: 149 sets forth the amino acid sequence for a GNA2091 and non-lipidated A05 polypeptide (GNA2091-A05), wherein the N-terminal methionine at position 1 of SEQ ID NO: 148 is removed.

SEQ ID NO: 150 sets forth the amino acid sequence for a streptococcal C5a peptidase (SCP) from *Streptococcus pyogenes*.

SEQ ID NO: 151 sets forth the amino acid sequence for an SCP, wherein the N-terminal methionine at position 1 of SEQ ID NO: 150 is removed.

SEQ ID NO: 152 sets forth the amino acid sequence for an SCP and non-lipidated A05 polypeptide (SCP-A05).

SEQ ID NO: 153 sets forth the amino acid sequence for an SCP and non-lipidated A05 polypeptide (SCP-A05), wherein the N-terminal methionine at position 1 of SEQ ID NO: 152 is removed.

SEQ ID NO: 154 sets forth the amino acid sequence for a CRM₁₉₇.

SEQ ID NO: 155 sets forth the amino acid sequence for a CRM₁₉₇, wherein the N-terminal methionine at position 1 of SEQ ID NO: 154 is removed.

SEQ ID NO: 156 sets forth the amino acid sequence for an A05 polypeptide as in SEQ ID NO: 5, wherein a cysteine is present at position 1.

SEQ ID NO: 157 sets forth the amino acid sequence for an A05 polypeptide as in SEQ ID NO: 5, wherein a cysteine is present at position 2.

SEQ ID NO: 158 sets forth the amino acid sequence for an A05 polypeptide as in SEQ ID NO: 5, wherein a cysteine is present at position 6.

DETAILED DESCRIPTION OF THE INVENTION

The inventors discovered, among other things, molecules and/or compositions including an ORF2086 polypeptide and a carrier polypeptide. The molecules and/or compositions may be made by genetic fusion or by conjugation or made synthetically.

The inventive polypeptides and conjugates of the invention surprisingly allow for effective induction of a broad immune response against *N. meningitidis*. In some embodiments, the fusion polypeptides and conjugates of the invention exhibit enhanced effectiveness in induction of an immune response against *N. meningitidis*, as compared to compositions including ORF2086 polypeptides in the absence of a carrier polypeptide. For example, the inventors discovered that the fusion polypeptides may provide broad coverage, e.g., eliciting bactericidal antibodies against multiple LP2086 variant strains even when the fusion polypeptide includes a ORF2086 polypeptide from one *N. meningitidis* strain. The enhanced effectiveness of the inventive compositions may allow for reduced doses or concentrations of ORF2086 polypeptides to be administered to a subject, as compared to compositions including ORF2086 polypeptides in the absence of a carrier polypeptide. The enhanced effectiveness of the inventive compositions also aids in minimizing cost of vaccine production, and allows for designs that provide efficacy to a broad range of serotypes.

A) Isolated polypeptides and Fusion polypeptides

In one aspect, the invention relates to an isolated polypeptide that includes the amino acid sequence of a carrier polypeptide and the amino acid sequence of an ORF2086 polypeptide. In one embodiment, the isolated polypeptide is a synthetically constructed polypeptide. In a preferred embodiment, the isolated polypeptide is a fusion polypeptide that includes operably linked polypeptides. At least one polypeptide component of a given isolated and/or fusion polypeptide includes a carrier polypeptide, or an active variant or fragment thereof, which is operably linked to an ORF2086 polypeptide or an active variant or fragment thereof.

As used herein, a "fusion polypeptide" or "fusion protein" refers to a polypeptide having an in-frame genetic linkage of at least two polypeptides. Upon transcription/translation, a single polypeptide is made. Accordingly, multiple polypeptides, or fragments thereof, may be incorporated into a single polypeptide. Multiple forms of fusion polypeptides are disclosed herein and discussed in detail below.

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“Operably linked” refers to a functional linkage between two or more elements. For example, an operable linkage between two polypeptides may fuse both polypeptides together in-frame to produce a single fusion polypeptide. In one embodiment, the ORF2086 polypeptide and the carrier polypeptide are fused in-frame to each other.

- 5 **1) ORF2086 polypeptide.** The isolated polypeptide may include any ORF2086 polypeptide. In one embodiment, the ORF2086 polypeptide is a subfamily A polypeptide. In one embodiment, the ORF2086 polypeptide is a subfamily B polypeptide. In one embodiment, the ORF2086 polypeptide is lipidated. In one embodiment, the ORF2086 polypeptide is non-lipidated. In one embodiment, the ORF2086 polypeptide is non-lipidated and non-pyruvylated. In one
- 10 embodiment, the ORF2086 polypeptide is A04. In one embodiment, the ORF2086 polypeptide is A05. In one embodiment, the ORF2086 polypeptide is A06. In one embodiment, the ORF2086 polypeptide is A07. In one embodiment, the ORF2086 polypeptide is A12. In one embodiment, the ORF2086 polypeptide is A15. In one embodiment, the ORF2086 polypeptide is A19. In one embodiment, the ORF2086 polypeptide is A20. In one embodiment, the ORF2086 polypeptide is
- 15 A01. In one embodiment, the ORF2086 polypeptide is A22. In one embodiment, the ORF2086 polypeptide is A29. In one embodiment, the ORF2086 polypeptide is B01. In one embodiment, the ORF2086 polypeptide is B02. In one embodiment, the ORF2086 polypeptide is B09. In one embodiment, the ORF2086 polypeptide is B15. In one embodiment, the ORF2086 polypeptide is B16. In one embodiment, the ORF2086 polypeptide is B22. In one embodiment, the ORF2086 polypeptide
- 20 is B24. In one embodiment, the ORF2086 polypeptide is B44. In one embodiment, the ORF2086 polypeptide is A62. Preferably, the ORF2086 polypeptide is A05. ORF2086 polypeptides are described in more detail below. ORF2086 polypeptides are described in WO2012032489 and US patent publication number US20120093852. ORF2086 polypeptides are also described in WO2013132452 and US patent publication number US20130243807.

2) Carrier polypeptide. The isolated polypeptide may include any carrier polypeptide. Preferably, the carrier polypeptide is detoxified or exhibits decreased toxicity as compared to the corresponding wild-type carrier polypeptide. In one embodiment, the carrier polypeptide is a cytolysoin. In a preferred embodiment, the cytolysoin is derived from a pneumolysin polypeptide from *Streptococcus pneumoniae*, a perfringolysin O polypeptide from *Clostridium perfringens*, an intermedilysin polypeptide from *Streptococcus intermedius*, an alveolysin polypeptide from *Bacillus alvei*, an anthrolysin polypeptide from *Bacillus anthracis*, a putative cereolysin polypeptide from *Bacillus cereus*, an ivanolysin O polypeptide from *Listeria ivanovii*, a pyolysin polypeptide from *Arcanobacterium pyogenes*, a seeligeriolysin O polypeptide from *Listeria seeligeri*, a streptolysin O polypeptide from *Streptococcus pyogenes*, a suilysin polypeptide from *Streptococcus suis*, a tetanolysin polypeptide from *Clostridium tetani*, a listeriolysin O polypeptide from *Listeria monocytogenes*, a streptolysin O polypeptide from *Streptococcus equisimilis*, a streptolysin O polypeptide from *S. canis*, a thuringiolysin O polypeptide from *Bacillus thuringiensis*, a laterosporolysin O polypeptide from *B. laterosporus*, a botulinolysin polypeptide from *Clostridium botulinum*, a chauveolysin polypeptide from *Clostridium chauvoei*, a bifermentolysin polypeptide from *C. bifermentans*, a sordellilysin polypeptide from *Clostridium sordellii*, a histolyticolysin polypeptide from *Clostridium histolyticum*, a novylisin polypeptide from *Clostridium novyi*, or a septicolysin O polypeptide from *Clostridium septicum*.

Additional examples of a carrier protein include streptococcal C5a peptidase (SCP) from *Streptococcus pyogenes*, GNA2091 (also known as accessory protein 936) from *Neisseria*, and CRM₁₉₇. Further examples and descriptions of carrier proteins are provided below in section C.

In a preferred embodiment, the cytolysoin is derived from a pneumolysin polypeptide from *Streptococcus pneumoniae*. In a more preferred embodiment, the cytolysoin includes a sequence having at least 50%, 60%, 70%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or greater sequence identity to SEQ ID NO: 1. In a most preferred embodiment, the cytolysoin includes SEQ ID NO: 1.

In another embodiment, the carrier polypeptide is detoxified or exhibits decreased toxicity as compared to the corresponding wild-type carrier polypeptide, and is selected from the group consisting of tetanus toxin (TT), *Plasmodium falciparum* circumsporozoite protein, hepatitis B surface antigen, hepatitis B nuclear core polypeptide, *H. influenzae* matrix polypeptide, *H. influenzae* haemagglutinin, diphtheria toxoid, diphtheria toxoid mutant CRM₁₉₇, group B *N. meningitidis* outer membrane

polypeptide complex (OMPC), a cytolysoid, pneumococcal toxin pneumolysin, heat shock polypeptide from *Mycobacterium bovis*, heat shock polypeptide from *M. leprae*, cholera toxoid, *E. coli* LT, *E. coli* ST, exotoxin A from *Pseudomonas aeruginosa*, pneumococcal surface polypeptide A, pneumococcal adhesin polypeptide (PsaA), C5a peptidase from Group A or Group B streptococcus, *Haemophilus influenzae* polypeptide D, ovalbumin, keyhole limpet hemocyanin (KLH), bovine serum albumin (BSA), purified polypeptide derivative of tuberculin (PPD), PorB (from *N. meningitidis*), and derivatives, variants, or fragments thereof.

In one embodiment, the fusion polypeptide does not include CRM₁₉₇. Carrier polypeptides are described in more detail below.

3) Assembly: The fusion polypeptide may be direct, *i.e.*, in the absence of an empirical linker molecule, or the fusion may be through a linker molecule. For example, the fusion polypeptide may include polypeptide components such as a linker peptide between the polypeptides of the fusion polypeptide, or a peptide tag for affinity purification (for example at the N- or C-terminus). Exemplary linker peptides include a Gly-Ser-Gly (GSG) linker. A linker molecule may include one or more amino acid residues, typically from about 2 to about 30 amino acid residues, preferably 3 to 25 residues. In a preferred embodiment, the fusion polypeptide does not include a linker peptide. An exemplary fusion polypeptide that does not include a linker is a fusion polypeptide that includes in the following order a carrier polypeptide and an ORF2086 polypeptide, such as, for example, in SEQ ID NO: 2. Additional examples include PLY-A12 (SEQ ID NO: 127), PLY-B01 (SEQ ID NO: 139), PLY-B09 (SEQ ID NO: 141), PLY-B24 (SEQ ID NO: 143), PLY-B44 (SEQ ID NO: 145), GNA2091-A05 (SEQ ID NO: 149), and SCP-A05 (SEQ ID NO: 153).

The fusion polypeptide may be assembled in various combinations. The carrier polypeptide may be at either at the N-terminal or C-terminal end of the fusion polypeptide, or it may be flanked by immunogenic bacterial polypeptides, *e.g.*, flanked by ORF2086 polypeptides. The ORF2086 polypeptide may be fused to the N-terminus or C-terminus of the carrier polypeptide. For example, in one embodiment, the fusion polypeptide includes in the following order: the carrier polypeptide operably linked to the ORF2086 polypeptide. In a preferred embodiment, the fusion polypeptide does not include a linker when the carrier polypeptide is operably linked to the ORF2086 polypeptide in said order. In such preferred embodiments, the native stalk region of the ORF2086 polypeptide may serve as a linker between the polypeptides. Stalk regions of

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an ORF2086 polypeptide are described in WO2012032489 and US Patent Publication No. US20120093852.

5 In another embodiment, the fusion polypeptide includes in the following order: an ORF2086 polypeptide operably linked to a carrier polypeptide. In a preferred embodiment, the fusion polypeptide includes a linker when the carrier polypeptide is operably linked to the ORF2086 polypeptide in said order.

10 In one embodiment, the fusion polypeptide includes one ORF2086 polypeptide linked to one carrier polypeptide, but other conformations are within the scope of the invention. For example, in another embodiment, the fusion polypeptide includes at most 1, 2, 3, 4, or 5 immunogenic bacterial polypeptides. In another embodiment, the fusion polypeptide includes at most 1, 2, 3, 4, or 5 carrier polypeptides.

15 In some embodiments, the fusion polypeptide further comprises a third or additional polypeptides. The source of the third or additional polypeptides may include, but is not limited to, *N. meningitidis*. In one embodiment, a third polypeptide is fused in-frame to the ORF2086 polypeptide or to the carrier polypeptide. In another embodiment, when multiple carrier polypeptides or variants or fragments thereof are included in the fusion polypeptide, the third polypeptide may be located at the N-terminal or C-terminal end of the fusion polypeptide, or it may be located internally in the fusion polypeptide so that it is flanked by carrier protein polypeptides. In one embodiment, the fusion polypeptide includes a polypeptide sequence derived from pneumococcal bacteria. In another
20 embodiment, the fusion polypeptide does not include a polypeptide sequence derived from pneumococcal bacteria.

25 Preferably, the fusion polypeptide includes polypeptides that are derived from bacterial species that are different from the bacterial species from which the carrier polypeptide is derived. Accordingly, in one embodiment, the carrier protein is heterologous to the ORF2086 polypeptide and to any additional polypeptides included in the fusion polypeptide. "Heterologous" in reference to a polypeptide is a polypeptide that originates from a different protein and/or from a different bacterial species.

4) Exemplary isolated and/or fusion polypeptides-

In one aspect, the invention relates to an isolated polypeptide that includes the amino acid sequence for a pneumolysoid (such as, e.g., SEQ ID NO: 1) and a non-lipidated ORF2086 polypeptide (such as, e.g., any one polypeptide having the amino acid sequence selected from SEQ ID NO: 42-61, and any one polypeptide described in section D “ORF Polypeptides” below). For example, in one embodiment, the isolated polypeptide includes a pneumolysoid (SEQ ID NO: 1) and a non-lipidated A12 (SEQ ID NO: 47) to produce PLY-A12 (SEQ ID NO: 136). In another embodiment, the isolated polypeptide includes a pneumolysoid (SEQ ID NO: 1) and a non-lipidated B01 (SEQ ID NO: 53) to produce PLY-B01 (SEQ ID NO: 138). In another embodiment, the isolated polypeptide includes a pneumolysoid (SEQ ID NO: 1) and a non-lipidated B09 (SEQ ID NO: 55) to produce PLY-B09 (SEQ ID NO: 140). In another embodiment, the isolated polypeptide includes a pneumolysoid (SEQ ID NO: 1) and a non-lipidated B24 (SEQ ID NO: 59) to produce PLY-B24 (SEQ ID NO: 142). In another embodiment, the isolated polypeptide includes a pneumolysoid (SEQ ID NO: 1) and a non-lipidated B44 (SEQ ID NO: 60) to produce PLY-B44 SEQ ID NO: 144).

a) PLY and A05: In one aspect, the invention relates to an isolated polypeptide that includes the amino acid sequence for a pneumolysoid and a non-lipidated A05 polypeptide. In one embodiment, the pneumolysoid includes the amino acid sequence set forth in SEQ ID NO: 1. Preferably, the pneumolysoid is encoded by a DNA sequence set forth in SEQ ID NO: 3. In one embodiment, the A05 polypeptide includes the amino acid sequence set forth in SEQ ID NO: 5. In one embodiment, the isolated polypeptide is a fusion polypeptide.

In one embodiment, the fusion polypeptide includes in the following order: the carrier polypeptide operably linked to the ORF2086 polypeptide. For example, in one embodiment, the fusion polypeptide includes the amino acid sequence set forth in SEQ ID NO: 2 (PLY-A05). In one embodiment, the fusion polypeptide is encoded by a DNA sequence set forth in SEQ ID NO: 4.

In another embodiment, the fusion polypeptide includes in the following order: the ORF2086 polypeptide operably linked to the carrier polypeptide. For example, in one embodiment, the fusion polypeptide includes the amino acid sequence set forth in SEQ ID NO: 8 (A05-PLY). In one embodiment, the fusion polypeptide is encoded by a DNA sequence set forth in SEQ ID NO: 7.

In another embodiment, the fusion polypeptide further includes a linker peptide. In one embodiment, the linker includes a Gly-Ser-Gly (GSG) peptide. The fusion

polypeptide having the amino acid sequence set forth in SEQ ID NO: 8 includes a GSG linker.

b) CRM₁₉₇ and A05:

In one aspect, the invention relates to an isolated polypeptide that includes the amino acid sequence for CRM₁₉₇ (such as, e.g., SEQ ID NO: 155) and a non-lipidated ORF2086 polypeptide (such as, e.g., any one polypeptide having the amino acid sequence selected from SEQ ID NO: 42-61, and any one polypeptide described in section D “ORF Polypeptides” below).

In one aspect, the invention relates to an isolated polypeptide that includes the amino acid sequence for CRM₁₉₇ and a non-lipidated A05 polypeptide. In one embodiment, CRM₁₉₇ includes the amino acid sequence set forth in SEQ ID NO: 10. In another embodiment, CRM₁₉₇ includes the amino acid sequence set forth in SEQ ID NO: 155. Preferably, CRM₁₉₇ is encoded by a DNA sequence set forth in SEQ ID NO: 9. In one embodiment, the A05 polypeptide includes the amino acid sequence set forth in SEQ ID NO: 5. In one embodiment, the isolated polypeptide is a fusion polypeptide.

In one embodiment, the fusion polypeptide includes in the following order: the carrier polypeptide operably linked to the ORF2086 polypeptide. For example, in one embodiment, the fusion polypeptide includes the amino acid sequence set forth in SEQ ID NO: 14 (CRM₁₉₇-A05). In one embodiment, the fusion polypeptide is encoded by a DNA sequence set forth in SEQ ID NO: 13.

In another embodiment, the fusion polypeptide includes in the following order: the ORF2086 polypeptide operably linked to the carrier polypeptide. For example, in one embodiment, the fusion polypeptide includes the amino acid sequence set forth in SEQ ID NO: 16 (A05- CRM₁₉₇). In one embodiment, the fusion polypeptide is encoded by a DNA sequence set forth in SEQ ID NO: 15.

In a further embodiment, the fusion polypeptide further includes a linker peptide. In one embodiment, the linker includes a Gly-Ser-Gly (GSG) peptide. The fusion polypeptide having the amino acid sequence set forth in SEQ ID NO: 16 includes a GSG linker.

In one aspect, the invention relates to an isolated polypeptide that includes the amino acid sequence for a fragment of CRM₁₉₇ and a non-lipidated A05 polypeptide. In one embodiment, the fragment of CRM₁₉₇ (e.g., amino acid residues 1-193 of CRM₁₉₇ shown in SEQ ID NO: 10; DT-A region) includes the amino acid sequence set forth in SEQ ID NO: 12. Preferably, the fragment of CRM₁₉₇ is encoded by a DNA sequence

set forth in SEQ ID NO: 11. In one embodiment, the A05 polypeptide includes the amino acid sequence set forth in SEQ ID NO: 5. In one embodiment, the isolated polypeptide is a fusion polypeptide.

In one embodiment, the fusion polypeptide includes in the following order: the fragment of CRM₁₉₇ operably linked to the ORF2086 polypeptide. For example, in one embodiment, the fusion polypeptide includes the amino acid sequence set forth in SEQ ID NO: 18 (DT-A-A05). In one embodiment, the fusion polypeptide is encoded by a DNA sequence set forth in SEQ ID NO: 17.

c) GNA2091 and A05:

In one aspect, the invention relates to an isolated polypeptide that includes the amino acid sequence for GNA2091 (such as, e.g., SEQ ID NO: 147) and a non-lipidated ORF2086 polypeptide (such as, e.g., any one polypeptide having the amino acid sequence selected from SEQ ID NO: 42-61, and any one polypeptide described in section D “ORF Polypeptides” below).

In one aspect, the invention relates to an isolated polypeptide that includes the amino acid sequence for GNA2091 and a non-lipidated A05 polypeptide. In one embodiment, GNA2091 includes the amino acid sequence set forth in SEQ ID NO: 147. In one embodiment, the A05 polypeptide includes the amino acid sequence set forth in SEQ ID NO: 5. In one embodiment, the isolated polypeptide is a fusion polypeptide.

In one embodiment, the fusion polypeptide includes in the following order: the GNA2091 operably linked to the ORF2086 polypeptide. For example, in one embodiment, the fusion polypeptide includes the amino acid sequence set forth in SEQ ID NO: 149 (GNA2091-A05).

d) SCP and A05:

In one aspect, the invention relates to an isolated polypeptide that includes the amino acid sequence for SCP (such as, e.g., SEQ ID NO: 151) and a non-lipidated ORF2086 polypeptide (such as, e.g., any one polypeptide having the amino acid sequence selected from SEQ ID NO: 42-61, and any one polypeptide described in section D “ORF Polypeptides” below).

In one aspect, the invention relates to an isolated polypeptide that includes the amino acid sequence for SCP and a non-lipidated A05 polypeptide. In one embodiment, SCP includes the amino acid sequence set forth in SEQ ID NO: 151. In one embodiment, the A05 polypeptide includes the amino acid sequence set forth in SEQ ID NO: 5. In one embodiment, the isolated polypeptide is a fusion polypeptide.

In one embodiment, the fusion polypeptide includes in the following order: the SCP operably linked to the ORF2086 polypeptide. For example, in one embodiment, the fusion polypeptide includes the amino acid sequence set forth in SEQ ID NO: 153 (SCP-A05).

5) Immunogenic compositions including a fusion polypeptide:

In one aspect, the invention relates to an immunogenic composition including an isolated and/or fusion polypeptide as described above. The immunogenic composition further includes a pharmaceutically acceptable excipient.

In one embodiment, the immunogenic composition further includes at least one conjugate selected from: a) a conjugate of a capsular saccharide of *Neisseria meningitidis* serogroup A; b) a conjugate of a capsular saccharide of *Neisseria meningitidis* serogroup C; c) a conjugate of a capsular saccharide of *Neisseria meningitidis* serogroup W135; and d) a conjugate of a capsular saccharide of *Neisseria meningitidis* serogroup Y. Such conjugates of a capsular saccharide of *Neisseria meningitidis* are known in the art. Descriptions of *N. meningitidis* capsular saccharide conjugates and polysaccharide conjugates are described below.

6) Immune responses: In one aspect, the fusion polypeptide induces an immune response against *N. meningitidis* in a mammal. In one embodiment, the fusion polypeptide induces a bactericidal antibody against a *N. meningitidis* serogroup B strain expressing an ORF2086 variant that is homologous to the ORF2086 polypeptide. For example, a fusion polypeptide including a carrier protein and an A05 polypeptide may induce a bactericidal antibody against an *N. meningitidis* serogroup B A05-expressing strain. In another embodiment, the fusion polypeptide induces a bactericidal antibody response against a *N. meningitidis* serogroup B strain expressing an ORF2086 variant that is heterologous to the ORF2086 polypeptide. For example, a fusion polypeptide including a carrier protein and an A05 polypeptide may induce a bactericidal antibody response against an *N. meningitidis* serogroup B A22-expressing strain.

Surprisingly, the inventors discovered that a fusion polypeptide that includes a non-lipidated ORF2086 polypeptide and a carrier polypeptide may induce an immune response in a mammal that is better than the immune response induced by a composition that includes a non-lipidated form of the same ORF2086 polypeptide in the absence of the carrier polypeptide, when assessed under identical conditions.

In one embodiment, the immune response induced by the fusion polypeptide is equal to the immune response in a mammal administered with a corresponding non-lipidated ORF2086 polypeptide in the absence of a carrier polypeptide, when assessed under identical conditions.

In another embodiment, the immune response induced by the fusion polypeptide is equal to the immune response in a mammal administered with a corresponding lipidated ORF2086 polypeptide in the absence of a carrier polypeptide, when assessed under identical conditions.

In one embodiment, the immune response induced by the fusion polypeptide is greater than the immune response in a mammal administered with a corresponding non-lipidated ORF2086 polypeptide in the absence of a carrier polypeptide, when assessed under identical conditions. For example, the immune response induced by the inventive polypeptide may be greater by at least 1%, 5%, 10%, 20%, 30%, 40%, 50%, or more.

In another embodiment, the immune response induced by the fusion polypeptide is greater than the immune response in a mammal administered with a corresponding lipidated ORF2086 polypeptide in the absence of a carrier polypeptide, when assessed under identical conditions. For example, the immune response induced by the inventive polypeptide may be greater by at least 1%, 5%, 10%, 20%, 30%, 40%, 50%, or more.

In another embodiment, the immune response to the fusion polypeptide is at most 30%, 25%, 20%, 15%, 10%, or 5% less than the immune response in a mammal administered with a corresponding lipidated ORF2086 polypeptide in the absence of a carrier polypeptide, when assessed under identical conditions.

In a further aspect, the invention relates to a method for inducing an immune response against *Neisseria meningitidis* in a mammal. The immune response may be against any one *N. meningitidis* serogroup or a combination of *N. meningitidis* serogroups (e.g., A, B, C, W135, X, and/or Y). The method includes administering to the mammal an effective amount of the isolated polypeptide as described. In one embodiment, the isolated polypeptide includes a fusion polypeptide as described above. In another embodiment, the method includes administering to the mammal an effective amount of an immunogenic composition that includes an isolated and/or fusion polypeptide as described. The immune response induced by the method may include a bactericidal antibody. Bactericidal antibody responses are described below.

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B) Conjugates

In one aspect, the invention relates to an immunogenic composition including an ORF2086 polypeptide and a carrier polypeptide. In one embodiment, the immunogenic composition includes a conjugate of an ORF2086 polypeptide linked to a carrier polypeptide. The polypeptides
 5 may be linked via any bond such that the polypeptides are stable under physiological conditions. In one embodiment, the polypeptides are linked by covalent bonds. In another embodiment, the polypeptides are linked by non-covalent bonds. The conjugates may be prepared using methods known in the art.

1) ORF2086 polypeptide. The conjugate may include any ORF2086 polypeptide.
 10 In one embodiment, the ORF2086 polypeptide is a subfamily A polypeptide. In one embodiment, the ORF2086 polypeptide is a subfamily B polypeptide. In one embodiment, the ORF2086 polypeptide is lipidated. In one embodiment, the ORF2086 polypeptide is non-lipidated. In one embodiment, the ORF2086 polypeptide is non-lipidated and non-pyruvylated. In one embodiment, the ORF2086 polypeptide is A04. In one embodiment, the ORF2086 polypeptide is A05. In one embodiment, the
 15 ORF2086 polypeptide is A06. In one embodiment, the ORF2086 polypeptide is A07. In one embodiment, the ORF2086 polypeptide is A12. In one embodiment, the ORF2086 polypeptide is A15. In one embodiment, the ORF2086 polypeptide is A19. In one embodiment, the ORF2086 polypeptide is A20. In one embodiment, the ORF2086 polypeptide is A01. In one embodiment, the ORF2086 polypeptide is A22. In one embodiment, the ORF2086 polypeptide is A29. In one
 20 embodiment, the ORF2086 polypeptide is B01. In one embodiment, the ORF2086 polypeptide is B02. In one embodiment, the ORF2086 polypeptide is B09. In one embodiment, the ORF2086 polypeptide is B15. In one embodiment, the ORF2086 polypeptide is B16. In one embodiment, the ORF2086 polypeptide is B22. In one embodiment, the ORF2086 polypeptide is B24. In one embodiment, the ORF2086 polypeptide is B44. In one embodiment, the ORF2086 polypeptide is A62. Preferably, the
 25 ORF2086 polypeptide is A05. ORF2086 polypeptides are described in more detail below.

In a preferred embodiment, the ORF2086 polypeptide is a non-pyruvylated, non-lipidated ORF2086 polypeptide, as described in WO2013132452 and US patent publication number US20130243807. The term “non-pyruvylated” refers to a polypeptide having no pyruvate content. Non-lipidated ORF2086 polypeptides having a pyruvate content typically exhibited a mass
 30 shift of +70 or +71, as compared to the corresponding wild-type

polypeptide. In one embodiment, the inventive polypeptide does not exhibit a mass shift of +70 or +71 as compared to the corresponding wild-type non-lipidated polypeptide when measured by mass spectrometry. In another embodiment, the inventive polypeptide does not exhibit a mass shift of +70 or +71 as compared to the corresponding non-lipidated polypeptide that has an initial cysteine at position 1 of the N-terminus when measured by mass spectrometry.

2) Carrier polypeptide. The conjugate may include any carrier polypeptide. Preferably, the carrier polypeptide is detoxified or exhibits decreased toxicity as compared to the corresponding wild-type carrier polypeptide. In one embodiment, the carrier polypeptide is a cytolysoin. In a preferred embodiment, the cytolysoin is derived from a pneumolysin polypeptide from *Streptococcus pneumoniae*, a perfringolysin O polypeptide from *Clostridium perfringens*, an intermediolysin polypeptide from *Streptococcus intermedius*, a alveolysin polypeptide from *Bacillus alvei*, a anthrolysin polypeptide from *Bacillus anthracis*, a putative cereolysin polypeptide from *Bacillus cereus*, a ivanolysin O polypeptide from *Listeria ivanovii*, a pyolysin polypeptide from *Arcanobacterium pyogenes*, a seeligeriolysin O polypeptide from *Listeria seeligeri*, a streptolysin O polypeptide from *Streptococcus pyogenes*, a suilysin polypeptide from *Streptococcus suis*, a tetanolysin polypeptide from *Clostridium tetani*, a listeriolysin O polypeptide from *Listeria monocytogenes*, a streptolysin O polypeptide from *Streptococcus equisimilis*, a streptolysin O polypeptide from *Streptococcus canis*, a thuringiolysin O polypeptide from *Bacillus thuringiensis*, a laterosporolysin O polypeptide from *Brevibacillus laterosporus*, a botulinolysin polypeptide from *Clostridium botulinum*, a chauveolysin polypeptide from *C Clostridium chauvoei*, a bifermentolysin polypeptide from *Clostridium bifermentans*, a sordellilysin polypeptide from *Clostridium sordellii*, a histolyticolysin polypeptide from *Clostridium histiolyticum*, a novylisin polypeptide from *Clostridium novyi*, or a septicolysin O polypeptide from *Clostridium septicum*.

In a preferred embodiment, the cytolysoin is derived from a pneumolysin polypeptide from *Streptococcus pneumoniae*. In a more preferred embodiment, the cytolysoin includes a sequence having at least 90% sequence identity to SEQ ID NO: 1.

In another embodiment, the carrier polypeptide is detoxified or exhibits decreased toxicity as compared to the corresponding wild-type carrier polypeptide, and is selected from the group consisting of tetanus toxin (TT), *Plasmodium falciparum* circumsporozoite protein, hepatitis B surface antigen, hepatitis B nuclear core polypeptide, *H. influenzae* matrix polypeptide, *H. influenzae* haemagglutinin, diphtheria toxoid, diphtheria toxoid mutant CRM₁₉₇, group B *N. meningitidis* outer membrane

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polypeptide complex (OMPC), a cytolysoid, pneumococcal toxin pneumolysin, heat shock polypeptide from *Mycobacterium bovis*, heat shock polypeptide from *M. leprae*, cholera toxoid, *E. coli* LT, *E. coli* ST, exotoxin A from *Pseudomonas aeruginosa*, pneumococcal surface polypeptide A, pneumococcal adhesin polypeptide (PsaA), C5a peptidase from Group A or Group B *Streptococcus* spp.,

- 5 *Haemophilus influenzae* polypeptide D, ovalbumin, keyhole limpet hemocyanin (KLH), bovine serum albumin (BSA), purified polypeptide derivative of tuberculin (PPD), PorB from *N. meningitidis*, and derivatives, variants, or fragments thereof. In a preferred embodiment, the conjugate includes CRM₁₉₇. Carrier polypeptides are described in more detail below.

- Additional examples of a carrier protein include streptococcal C5a peptidase (SCP)
 10 from *Streptococcus pyogenes*, GNA2091 (also known as accessory protein 936) from *Neisseria*, and CRM₁₉₇. Further examples and descriptions of carrier proteins are provided below in section C.

- 3) **Assembly:** In one embodiment, the conjugate includes an ORF2086 polypeptide directly linked to the carrier polypeptide. For example, the polypeptides of the conjugate are coupled in the absence of a linker molecule. In another embodiment, the conjugate includes an ORF2086
 15 polypeptide indirectly linked to the carrier polypeptide. For example, the carrier polypeptide may be linked to an intermediate and that intermediate is linked to the ORF2086 polypeptide.

- In one embodiment, the conjugate includes one ORF2086 polypeptide linked to one carrier polypeptide, but other conformations are within the scope of the invention. For example, in another embodiment, the conjugate includes at most 1, 2, 3, 4, or 5, 6, 7, 8, 9, or 10 immunogenic
 20 bacterial polypeptides. In one embodiment, the conjugate includes at most 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 ORF2086 polypeptides. In another embodiment, the conjugate includes at most 1, 2, 3, 4, or 5 carrier polypeptides.

- In some embodiments, the conjugate further comprises a third or subsequent additional polypeptides. The source of the third or additional polypeptides may include, but is not
 25 limited to, *N. meningitidis*. In one embodiment, a third polypeptide is fused in-frame to the ORF2086 polypeptide or to the carrier polypeptide. In one embodiment, the conjugate includes a polypeptide sequence derived from pneumococcal bacteria. In another embodiment, the conjugate does not include a polypeptide sequence derived from pneumococcal bacteria.

- Non-pyruvylated non-lipidated ORF2086 proteins are described in WO2013132452
 30 and US patent publication number US20130243807. Methods of removing or reducing the

likelihood of pyruvylation modification following expression of non-lipidated ORF2086 proteins are also described therein.

An additional method for removing pyruvylation includes treatment of the protein with zinc sulfate.

Yet another method includes genetic modifications to the non-lipidated ORF2086 protein to delete the initial cysteine at position 1 of the N-terminus and replacing any amino acid residue at the N-terminus with a cysteine residue. For example, in one embodiment, the non-lipidated ORF2086 protein includes an amino acid sequence wherein a cysteine residue is not at position 1 of the N-terminus of the ORF2086 protein and wherein a serine residue is replaced with a cysteine residue, as compared to the corresponding wild-type non-lipidated ORF2086 protein.

Preferably, the amino acid residue to be replaced by a cysteine residue is at most 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, or 5 amino acids from the initial residue of the N-terminus.

For example, in one embodiment, the non-lipidated ORF2086 protein includes an amino acid sequence wherein a cysteine residue is not at position 1 of the N-terminus of the ORF2086 protein and wherein a residue at position 2 is replaced with a cysteine residue, as compared to the corresponding wild-type non-lipidated ORF2086 protein.

Preferably, the amino acid residue to be replaced by a cysteine residue is serine residue located at most 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, or 5 amino acids from the initial residue of the N-terminus. For example, the non-lipidated ORF2086 protein includes an amino acid sequence wherein a cysteine residue is not at position 1 of the N-terminus of the ORF2086 protein and wherein a serine residue at position 2 is replaced with a cysteine residue, as compared to the corresponding wild-type non-lipidated ORF2086 protein. Compare, for example, SEQ ID NO: 5, SEQ ID NO: 156, and SEQ ID NO: 157.

In another embodiment, the non-lipidated ORF2086 protein includes an amino acid sequence wherein a cysteine residue is not at position 1 of the N-terminus of the ORF2086 protein and wherein a serine residue at position 6 is replaced with a cysteine residue, as compared to the corresponding wild-type non-lipidated ORF2086 protein. Compare, for example, SEQ ID NO: 5, SEQ ID NO: 156, and SEQ ID NO: 158.

Preferably, the conjugate includes polypeptides that are derived from bacterial species that are different from the bacterial species from which the carrier polypeptide is derived. Accordingly, in one embodiment, the carrier protein is heterologous to the ORF2086 polypeptide and to any additional polypeptides included in the conjugate.

"Heterologous" in reference to a polypeptide is a polypeptide that originates from a different protein and/or from a different bacteria species.

The conjugation between the carrier polypeptide and the ORF2086 polypeptide, optionally through a cross-linker, may be done according to methods known in the art. Preferably, a bond between a carrier polypeptide and the ORF2086 polypeptide is accomplished using an activated carrier polypeptide having at least one activated terminus suitable for reaction with a nucleophilic center (e.g., lysine or cysteine residue of a protein).

In one embodiment, the carrier protein is maleimide-activated through a non-specific NHS-ester reaction to lysine residues. The single N-terminal cysteine of the ORF2086 polypeptide is then conjugated to a maleimide of the carrier protein.

As is known in the art, maleimides react with sulfhydryl groups to form stable thioether bonds. N-ethyl maleimide (NEM) is one example of a thiol-reactive reagent. For example, a pneumolysin protein may be prepared for conjugation by derivatization of the protein with NEM followed by activation with SM(PEG)₄.

In another embodiment, the carrier polypeptide is activated with sulfosuccinimidyl-4-(N-maleimidomethyl)cyclohexane-1-carboxylate (Sulfo-SMCC). Sulfo-SMCC is a water-soluble amine-to-sulfhydryl crosslinker. It contains an amine-reactive N-hydroxysuccinimide (NHS ester) and a sulfhydryl-reactive maleimide group. In one example, an SCP protein may be activated with Sulfo-SMCC.

4) Immunogenic compositions including a conjugate: In one aspect, the invention relates to an immunogenic composition including a conjugate as described above. The immunogenic composition further includes a pharmaceutically acceptable excipient.

In one embodiment, the immunogenic composition includes at least one conjugate selected from: a) a conjugate of a capsular saccharide of *Neisseria meningitidis* serogroup A; b) a conjugate of a capsular saccharide of *Neisseria meningitidis* serogroup C; c) a conjugate of a capsular saccharide of *Neisseria meningitidis* serogroup W135; and d) a conjugate of a capsular saccharide of *Neisseria meningitidis* serogroup Y. Such conjugates of a capsular saccharide of *Neisseria meningitidis* are known in the art. Descriptions of *N. meningitidis* capsular saccharide conjugates and polysaccharide conjugates are described below.

5) Immune responses: In one aspect, the conjugate induces an immune response against *N. meningitidis* in a mammal. In one embodiment, the conjugate induces a bactericidal antibody against a *N. meningitidis* serogroup B variant that is homologous to the ORF2086 polypeptide. For example, a conjugate including a carrier protein and an A05 polypeptide may induce a bactericidal antibody against an *N. meningitidis* serogroup B A05-expressing strain. In another embodiment, the conjugate induces a bactericidal antibody against a *N. meningitidis* serogroup B variant that is heterologous to the ORF2086 polypeptide. For example, a conjugate including a carrier protein and an A05 polypeptide may induce a bactericidal antibody against an *N. meningitidis* serogroup B A22-expressing strain.

In one embodiment, a conjugate that includes a non-lipidated ORF2086 polypeptide and a carrier polypeptide may induce an immune response in a mammal that is comparable to the immune response induced by a composition that includes a lipidated form of the same ORF2086 polypeptide in the absence of the carrier polypeptide, when assessed under identical conditions.

In one embodiment, the immune response induced by the conjugate is equal to the immune response of a mammal administered with a composition including a corresponding non-lipidated ORF2086 polypeptide in the absence of a carrier polypeptide, when assessed under identical conditions.

In another embodiment, the immune response induced by the conjugate is equal to the immune response of a mammal administered with a composition including a corresponding lipidated ORF2086 polypeptide in the absence of a carrier polypeptide, when assessed under identical conditions.

In another embodiment, the immune response induced by the conjugate is greater than the immune response of a mammal administered with a composition including a corresponding lipidated ORF2086 polypeptide in the absence of a carrier polypeptide, when assessed under identical conditions. For example, the immune response induced by the conjugate may be greater by at least 1%, 5%, 10%, 20%, 30%, 40%, 50%, or more.

In another embodiment, the immune response induced by the conjugate is greater than the immune response of a mammal administered with a composition including a corresponding non-lipidated ORF2086 polypeptide in the absence of a carrier polypeptide, when assessed under identical conditions. For example, the immune response induced by the conjugate may be greater by at least 1%, 5%, 10%, 20%, 30%, 40%, 50%, or more.

In a further embodiment, the immune response of the conjugate is at most 30%, 25%, 20%, 15%, 10%, or 5% less than an immune response of a mammal administered with a composition including the corresponding lipidated ORF2086 polypeptide in the absence of a carrier polypeptide, when assessed under identical conditions.

In another aspect, the invention relates to a method for inducing an immune response against *Neisseria meningitidis* in a mammal. The immune response may be against any one *N. meningitidis* serogroup or a combination of *N. meningitidis* serogroups (e.g., A, B, C, W135, X, and/or Y). The method includes administering to the mammal an effective amount of the isolated polypeptide as described. In one embodiment, the isolated polypeptide includes a conjugate as described above. In another embodiment, the method includes administering to the mammal an effective amount of an immunogenic composition that includes an isolated polypeptide and/or conjugate as described. The immune response induced by the method may include a bactericidal antibody. Bactericidal antibody responses are described below.

C) Carrier polypeptide

A carrier protein or polypeptide is a polypeptide entity that induces an immune response directed against a molecule linked to the carrier polypeptide. By linking a carrier polypeptide to a molecule (e.g., to an ORF2086 polypeptide), it is possible to increase the immunogenicity of the antigenic polypeptide.

Exemplary carrier polypeptides include detoxified forms of the following: tetanus toxin (TT), *Plasmodium falciparum* circumsporozoite protein, hepatitis B surface antigen, hepatitis B nuclear core protein, *H. influenzae* matrix protein, *H. influenzae* haemagglutinin, diphtheria toxoid, diphtheria toxoid mutant CRM₁₉₇, group B *N. meningitidis* outer membrane protein complex (OMPC), a cytolysoid, pneumococcal toxin pneumolysin, heat shock protein from *Mycobacterium bovis*, heat shock protein from *M. leprae*, cholera toxoid, *E. coli* LT, *E. coli* ST, exotoxin A from *Pseudomonas aeruginosa*, pneumococcal surface protein A, pneumococcal adhesin protein (PsaA), C5a peptidase from Group A or Group B streptococcus, *Haemophilus influenzae* protein D, ovalbumin, keyhole limpet hemocyanin (KLH), bovine serum albumin (BSA), purified protein derivative of tuberculin (PPD), PorB (from *N. meningitidis*), and derivatives, variants, or fragments thereof. The carrier polypeptide preferably exhibits less toxicity than the corresponding wild-type form of the carrier polypeptide.

Diphtheria toxoids: In a preferred embodiment, the carrier polypeptide is a diphtheria toxoid or a variant or fragment thereof, more preferably, CRM₁₉₇. CRM₁₉₇ is a non-toxic variant (*i.e.*, toxoid) of diphtheria toxin. In one embodiment, CRM₁₉₇ is isolated from cultures of *Corynebacterium diphtheriae* strain C7 (β 197) grown in casamino acids and yeast extract-based medium. In another embodiment, CRM₁₉₇ is prepared recombinantly in accordance with the methods described in U.S. Pat. No. 5,614,382. In some embodiments, CRM₁₉₇ is prepared in *Pseudomonas fluorescens*. Other diphtheria toxoids known in the art may be used, such as, for example, CRM₁₇₆, CRM₂₂₈, CRM₄₅, CRM₉, CRM₁₀₂, CRM₁₀₃ and CRM₁₀₇.

The diphtheria toxoid may include a full length diphtheria toxoid polypeptide, active variants or fragments thereof, or any immunogenic fragment of the diphtheria toxoid. Exemplary diphtheria toxoids include toxoids that have a deletion or mutation of Glu 148 to Asp, Gln or Ser and/or Ala 158 to Gly and other mutations, as compared to the corresponding wild-type diphtheria toxin, as disclosed in U.S. Pat. No. 4,709,017 or U.S. Pat. No. 4,950,740; mutation of at least one or more of the residues Lys 516, Lys 526, Phe 530 and/or Lys 534 and other mutations disclosed in U.S. Pat. No. 5,917,017 or U.S. Pat. No. 6,455,673; or fragments disclosed in U.S. Pat. No. 5,843,711.

An additional exemplary diphtheria toxoid includes a fragment of CRM that includes amino acids 1-193 of CRM₁₉₇, as shown in SEQ ID NO: 12), known as a "DT-A" region.

In one embodiment, a CRM₁₉₇ protein includes a sequence having at least 50%, 60%, 70%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or greater sequence identity to SEQ ID NO: 10. In a most preferred embodiment, the carrier protein includes SEQ ID NO: 10.

In another preferred embodiment, the CRM₁₉₇ protein includes a sequence having at least 50%, 60%, 70%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or greater sequence identity to SEQ ID NO: 155. In a most preferred embodiment, the CRM₁₉₇ protein includes SEQ ID NO: 155.

Cytolysoids: In another preferred embodiment, the carrier polypeptide is a cytolysoid or a variant or fragment thereof. In a more preferred embodiment, the carrier polypeptide is a pneumococcal toxin pneumolysin that is detoxified or exhibits less toxicity than the corresponding wild-type form of the pneumococcal toxin pneumolysin.

As used herein, "cytolysoid" refers to a modified cytolysin, wherein modification of the protein inactivates, detoxifies, or reduces the toxicity, oligomerization and/or hemolytic properties of the cytolysoid protein while retaining immunogenic activity.

Cytolysins are associated with a family of pore-forming toxins that are produced by various species from at least the genera *Clostridium*, *Streptococcus*, *Listeria*, *Bacillus*, and *Arcanobacterium*. Cytolysins may be known as hemolytic proteins. The amino acid sequences of exemplary wild-type cytolysins are shown in SEQ ID NOs: 88-101. Such cytolysins are cholesterol-binding cytolysins.

A reduction in the toxicity of the cytolysin protein (*i.e.*, a reduction in toxicity, oligomerization, and/or hemolysis) includes at least a 1%, 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or greater statistically significant decrease relative to an appropriate control, such as compared to the corresponding wild-type cytolysin protein. Methods to assay for cytolysin activity are known in the art.

Modifications that may inactivate or reduce the toxic activity (*i.e.*, oligomerization and/or hemolysis) of cytolysins are known in the art. These modifications may be amino acid substitutions, deletions, and/or additions. Such modifications are known in the art. Some examples include, but are not limited to, those described in WO2005/108419 and WO2005/108580 which disclose cytolysoids having a mutation (*e.g.*, a substitution or deletion) within the region corresponding to amino acid residues from 144 to 161 of the wild-type pneumolysin protein. This region of pneumolysin has a consensus sequence

that is shared among the cytolysins. The mutant cytolysins have reduced oligomerization and/or hemolytic activity as compared to the wild-type cytolysin, and are therefore less toxic. The mutant may have a substitution or deletion of one or more of the amino acid residues within the regions corresponding to amino acids 144 to 161 of the wild-type pneumolysin sequence. Thus, the cytolysoid may have a mutation at one or more of the amino acids residues corresponding to amino acids 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160 or 161 of wild-type pneumolysin.

The regions of the cytolysins described by SEQ ID NOS: 88-101 corresponding to residues 144 to 161 of wild-type pneumolysin are listed below.

Cytolysin	Consensus sequence to pneumolysin aa 144-161	Amino acid position
Pneumolysin from <i>Streptococcus pneumoniae</i> (SEQ ID NO: 88)	VPARMQYEKITAHSMEQL (SEQ ID NO: 102)	V144-L161
Perfringolysin O from <i>Clostridium perfringens</i> (SEQ ID NO: 89)	LPARTQYSESMVYSKSQI (SEQ ID NO: 103)	L175-I192
Intermedilysin from <i>Streptococcus intermedius</i> (SEQ ID NO: 90)	VPARMQYESISAQSMSQL (SEQ ID NO: 104)	V202-L219
Alveolysin from <i>Bacillus alvei</i> (SEQ ID NO: 91)	LPARLQYAESMVYSQNQI (SEQ ID NO: 105)	L177-I194
Anthrolysin from <i>Bacillus anthracis</i> (SEQ ID NO: 92)	LPARTQYSESMVYSKSQI (SEQ ID NO: 106)	L188-L205
Putative Cereolysin from <i>Bacillus cereus</i> (SEQ ID NO: 93)	LPARTQYSESMVYSKSQI (SEQ ID NO: 107)	L175-I192
Ivanolysin O from <i>Listeria ivanovii</i> (SEQ ID NO: 94)	ISAKIDYDQEMAYSESQL (SEQ ID NO: 108)	I199-L216
Perfringolysin O from <i>Clostridium perfringens</i> (SEQ ID NO: 116)	LPARTQYSESMVYSKSQI (SEQ ID NO: 109)	L174-I191
Seeligeriolysin O from <i>Listeria seeligeri</i> (SEQ ID NO: 96)	INAKIDYSDEMAYSESQL (SEQ ID NO: 110)	I201-L218
Streptolysin O from <i>S. pyogenes</i> (SEQ ID NO: 97)	LPARTQYTESMVYSKSQI (SEQ ID NO: 111)	L249-I266
Suilysin from <i>Streptococcus suis</i> (SEQ ID NO: 98)	TQAELQYDETMAYSMSQL (SEQ ID NO: 112)	T172-L189

Tetanolysin from <i>Clostridium tetani</i> (SEQ ID NO: 99)	IPTRMSYSDTMVYSQSQL (SEQ ID NO: 113)	I201-L218
Listeriolysin O from <i>Listeria monocytogenes</i> (SEQ ID NO: 100)	VSAKIDYDDEMAYSESQL (SEQ ID NO: 114)	V200-L217
Thuringiolysin from <i>Bacillus thuringiensis</i> (SEQ ID NO: 101)	LPARMQYTESMVYSKSQI (SEQ ID NO: 115)	L188-I205

Certain preferred mutant cytolysin proteins differ from the wild type protein by the substitution or deletion of two adjacent amino acids within the region corresponding to amino acid residues 144 to 151 of the wild type pneumolysin sequence. Examples of such double mutants are those which contain substitutions or deletions of amino acids corresponding to valine 144 and proline 145, alanine 146 and arginine 147, methionine 148 and glutamine 149, or tyrosine 150 and glutamic acid 151, *i.e.*, the corresponding amino acids shown in the table above. In a preferred embodiment, the cytolysoid includes a deletion of alanine 146 and arginine 147 as compared to the corresponding wild-type cytolysin.

The mutant may have a substitution at a residue corresponding to Y181 of perfringolysin. This residue corresponds to Y150 of pneumolysin. Such mutants may be derived from perfringolysin, or from other cytolysin proteins.

Further mutants of cytolysins having reduced haemolytic activity are described in WO 90/06951, and contain at least one amino acid substitution or deletion in at least one of the regions corresponding to amino acids 257-297, 367-397 or 424- 437 of the wild type pneumolysin sequence, and in particular at positions corresponding to amino acids 367, 384, 385, 428, 433 and 435 of the pneumolysin sequence. Thus the cytolysin protein used in the methods and compositions described herein may include one or more such mutations in addition to, or instead of, the mutation in the region corresponding to amino acids 144-161 of the pneumolysin sequence.

The cytolysin proteins may include other mutations relative to the wild-type sequences. These mutations may themselves reduce one or more biological activities of the cytolysin protein, such as the haemolytic activity, the oligomerisation activity, or the ability to activate complement, or they may be phenotypically silent.

Deletions and substitutions are examples of mutations which may be used to provide the mutant proteins of the invention with reduced toxicity. Non-conservative substitutions may be particularly suitable for reducing toxicity of the mutant, as a mutant

having a non-conservative mutation is less likely to retain wild-type levels of function relative to one having a conservative substitution. Additional, non-limiting, examples of cytolysoids in the art are disclosed in U.S. Patent Application Publication No. 2009/0285846A1 (WO2012/134975) and U.S. Patent Application Publication No. 2010/0166795 (WO2007/144647).

Active variants or fragments of the various cytolysoids may include at least 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity to a cytolysoid polypeptide provided herein in that they maintain carrier polypeptide activity. Active variants of cytolysoids are known in the art. See, for example, SEQ ID NOs: 117-120 and SEQ ID NO: 1. See also, for example, U.S. Patent Application No. 2009/0285846A1 and U.S. Patent Application No. 2010/0166795.

Fragments of wild-type or mutant cytolysin proteins which retain carrier polypeptide activity may also be used. Such fragments may be, for example, at least 50 amino acids in length, at least 100 amino acids in length, at least 200 amino acids in length, at least 300 amino acids in length, or at least 400 amino acids in length, as long as they retain carrier polypeptide activity.

Pneumolysoids: In a preferred embodiment, the carrier polypeptide includes a pneumolysoid polypeptide or a variant or fragment thereof. Pneumolysin is a pore forming toxin and is the major cytolysin produced by *Streptococcus pneumoniae*. The amino acid sequence of wild-type or native pneumolysin is set forth in SEQ ID NO: 21.

As used herein, "pneumolysoid" refers to a modified pneumolysin (a pneumolysin toxoid), wherein the modification of the protein inactivates or reduces the toxicity, oligomerization, hemolytic and/or complement activating properties of the pneumolysoid protein while still retaining carrier polypeptide activity, as compared to the corresponding wild-type pneumolysin.

Exemplary pneumolysoids that may be employed in the various compositions provided herein are described in, for example, WO2005/108419, WO2005/108580, WO 90/06951, U.S. Patent Application No. 2009/0285846A1 and U.S. Patent Application No. 2010/0166795. WO2005/108419 and WO2005/108580 disclose pneumolysoids having a mutation (e.g., a substitution or deletion) within the region of amino acids 144 to 161 of the wild-type pneumolysin protein. These mutants have reduced toxicity, oligomerization and/or hemolytic activity as compared to the wild-type pneumolysin, and are therefore less toxic.

The mutant may have a substitution or deletion of one or more amino acids 144 to 161 of the wild-type pneumolysin sequence. Thus, the pneumolysoid may have a mutation at one or more of the amino acid residues 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160 or 161 of wild-type pneumolysin. In addition, pneumolysoids having reduced hemolytic activity and having at least one amino acid substitution or deletion in at least one of the regions corresponding to amino acids 257- 297, 367-397 or 424-437 of the wild-type pneumolysin are described in WO 90/06951.

Further examples of a pneumolysoid includes SEQ ID NO: 1, or an active variant or fragment thereof. Another example includes a pneumolysoid having a mutation of the lysine at amino acid position 460 to an aspartic acid residue (SEQ ID NO: 117) as compared to the corresponding wild-type pneumolysin (SEQ ID NO: 21). Such a variant pneumolysoid is disclosed in U.S. Patent Application No. 2009/0285846A1. A variant of SEQ ID NO: 117 is provided herein and is set forth in SEQ ID NO: 118. The active variant includes an amino acid change from Lysine at position 208 to Arginine when compared to SEQ ID NO: 117.

The pneumolysoid set forth in SEQ ID NO: 119, or an active variant or fragment thereof, includes a substitution of asparagine in place of aspartic acid at amino acid position 385 and deletion of alanine 146 and arginine 147 of the wild-type pneumolysin sequence. This pneumolysoid set forth in SEQ ID NO: 119 may be deficient in both hemolysis and complement activation and is disclosed in U.S. Patent Application No. 2010/0166795.

The pneumolysoid set forth in SEQ ID NO: 120, or an active variant or fragment thereof, includes an amino acid substitution of phenylalanine in place of tryptophan at amino acid position 433 of the wild-type pneumolysin sequence. This pneumolysoid set forth in SEQ ID NO: 120 may be deficient in hemolysis and is disclosed in U.S. Patent No. 6716432.

In a most preferred embodiment, the fusion polypeptide includes a pneumolysoid having SEQ ID NO: 1 or active variants or fragments thereof. The polypeptide of SEQ ID NO: 1 includes an A146R147 deletion, as compared to the wild-type pneumolysoid.

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Accordingly, active variants or fragments of pneumolysoids are provided herein. Such active variants may comprise at least 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity to SEQ ID NOs: 88-120 or SEQ ID NO: 21. Active variants of pneumolysin are also described, for example, in US 2010/0166795 and

5 US 2009/0285846A1. The art provides guidance regarding the preparation of such variants, as described elsewhere herein. Thus, in one embodiment, the fusion polypeptide includes the pneumolysoid set forth in any one of the amino acid sequence set forth in SEQ ID NOs: 88-101, SEQ ID NO: 21, or SEQ ID NO: 1, or an active variant thereof having at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% sequence identity to the amino acid sequence of
10 SEQ ID NO: 21.

In one embodiment, the carrier protein is derived from streptococcal C5a peptidase (SCP) from *Streptococcus pyogenes*. In a preferred embodiment, the carrier protein includes a sequence having at least 50%, 60%, 70%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or greater sequence identity to SEQ ID NO: 151. In a most preferred embodiment, the carrier
15 protein includes SEQ ID NO: 151.

In one embodiment, the carrier protein is derived from GNA2091. In a preferred embodiment, the carrier protein includes a sequence having at least 50%, 60%, 70%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or greater sequence identity to SEQ ID NO: 147. In a most preferred embodiment, the carrier protein includes SEQ ID NO: 147.

20 D) ORF2086 Polypeptides

The term "ORF2086" as used herein refers to Open Reading Frame 2086 from a *Neisseria* species bacterium. *Neisseria* ORF2086, the proteins encoded therefrom, fragments of those proteins, and immunogenic compositions comprising those proteins are known in the art and are described, e.g., in WO2003/063766, and in U.S. Patent Application Publication Nos.

25 US 20060257413, US 20090202593, WO2012032489, and US 20120093852. ORF2086 polypeptides are also described in WO2013132452 and US patent publication number US20130243807. Examples of an ORF2086 polypeptide include a polypeptide having any one of the sequences set forth in SEQ ID NOs: 22-87, such as any one of the amino acid sequences set forth in SEQ ID NOs: 5, 19, 22-65.

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The term “P2086” generally refers to the protein encoded by ORF2086. The “P” before “2086” is an abbreviation for “protein.” The P2086 proteins of the invention may be lipidated or non-lipidated. “LP2086” and “P2086” typically refer to lipidated and non-lipidated forms of a 2086 protein, respectively. The P2086 protein of the invention may be recombinant. “rLP2086” and
 5 “rP2086” typically refer to lipidated and non-lipidated forms of a recombinant 2086 protein, respectively. “2086” is also known as factor H-binding protein (fHBP).

The term “wild-type non-lipidated ORF2086 polypeptide” or “wild-type non-lipidated 2086 polypeptide” or “wild-type non-lipidated polypeptide” as used herein refers to an ORF2086 polypeptide having an amino acid sequence that is identical to the amino acid sequence of the
 10 corresponding mature lipidated ORF2086 polypeptide found in nature. The only difference between the non-lipidated and lipidated molecules is that the wild-type non-lipidated ORF2086 polypeptide is not lipidated with a tripalmitoyl lipid tail at the N-terminal cysteine.

The term “N-terminal cysteine” refers to a cysteine (Cys) residue at the N-terminus or N-terminal tail of a polypeptide. More specifically, the “N-terminal cysteine” as used herein refers to
 15 the N-terminal cysteine at which LP2086 lipoproteins are lipidated with a tripalmitoyl lipid tail, as is known in the art.

In one embodiment, the inventive polypeptides and compositions include an ORF2086 polypeptide, wherein the ORF2086 polypeptide does not include a cysteine residue at the N-terminus of the ORF2086 polypeptide. Examples of an ORF2086 polypeptide wherein an N-terminal cysteine
 20 is not present includes polypeptides described in SEQ ID NOs: 42-65 and SEQ ID NOs: 131-134.

In one embodiment, the isolated polypeptide includes an ORF2086 polypeptide, wherein a cysteine is not present at the N-terminus of the ORF2086 polypeptide.

In another embodiment, the fusion polypeptide includes an ORF2086 polypeptide, wherein a cysteine is not present at the N-terminus of the ORF2086 polypeptide.

25 In yet another embodiment, the ORF2086 polypeptide in a ORF2086 polypeptide-carrier polypeptide conjugate does not include a cysteine at the N-terminus of the ORF2086 polypeptide.

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The term "Gly/Ser stalk" as used herein refers to consecutive Gly and Ser residues at the N-terminus of an ORF2086 polypeptide. There may be at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 Gly and Ser residues, preferably between 5 and 12 Gly and Ser residues, in the Gly/Ser stalk. In one embodiment, the ORF2086 polypeptide includes at least 2 and at most 15 consecutive Gly and/or Ser residues. The native Gly/Ser stalks of ORF2086 polypeptide variants are represented by the underlined sequences in FIG. 2A-2C of WO2012032489 and US Patent Publication No. US20120093852.

In one embodiment, the Gly/Ser stalk of the ORF2086 polypeptide includes a modification as compared to the wild-type or native ORF2086 polypeptide. Examples of a modification to the native Gly/Ser stalk of an ORF2086 polypeptide includes a deletion of a Gly and/or Ser residue, a substitution of a Gly with a Ser residue or a substitution of a Ser residue with a Gly residue, an addition of a Gly and/or Ser residue, and any combination thereof. Examples of an ORF2086 polypeptide that includes a modification of the native Gly/Ser stalk region include, for example, polypeptides described by SEQ ID NOs: 62-65 and SEQ ID NOs: 131-134.

As is known in the art, the non-lipidated form of an ORF2086 polypeptide may lack the original leader sequence or may include a leader sequence that is replaced with a portion of a sequence that does not specify a site for fatty acid acylation in a host cell. See, for example, WO2003/063766, US Patent No. 8101194, WO2012032489, and US Patent Publication No. US20120093852. Examples of a non-lipidated ORF2086 polypeptide include a polypeptide having any one of the sequences set forth in SEQ ID NOs: 22-65. In a preferred embodiment, the non-lipidated ORF2086 polypeptide includes a polypeptide having any one of the sequences set forth in SEQ ID NOs: 42-65.

In one embodiment, the ORF2086 polypeptide is encoded by any one of the polynucleotide sequences set forth in SEQ ID NOs: 66-87. In a preferred embodiment, the ORF2086 polypeptide is encoded by a sequence that does not encode a cysteine at the N-terminus or at amino acid residue position 1 of the ORF2086 polypeptide. Exemplary polynucleotide sequences include SEQ ID NOs: 131-134.

In another preferred embodiment, the ORF2086 polypeptide is encoded by a codon-optimized sequence of any one of the polynucleotide sequences set forth in SEQ ID NOs: 66-87. Codon-optimized sequences encoding an ORF2086 polypeptide are described in WO2012032489, US Patent Publication No. US20120093852, PCT/IB2013/051791, and US Patent Application No. 13/787594. Exemplary codon-optimized sequences include the polynucleotide sequences set forth in SEQ ID NOs: 121-129.

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The ORF2086 polypeptide may be derived from a *Neisseria* species, including strains of *Neisseria meningitidis* (serogroups A, B, C, D, W-135, X, Y, Z, and 29E), *Neisseria gonorrhoeae*, and *Neisseria lactamica*, as well as immunogenic portions and/or biological equivalents of said proteins.

5 The ORF2086 polypeptides include Subfamily A proteins and Subfamily B proteins, immunogenic portions thereof, and/or biological equivalents thereof. The ORF2086 polypeptides or equivalents thereof, etc. may be lipidated or non-lipidated. Preferably, the ORF2086 polypeptide is non-lipidated. Alternatively, the immunogenic compositions may include combinations of lipidated and non-lipidated ORF2086 polypeptides.

10 ORF2086 Subfamily A proteins and Subfamily B polypeptides are known in the art. See WO2003/063766 and US Patent No. 8101194, which disclose SEQ ID NOs: 260 to 278 therein as representing amino acid sequences associated with proteins of 2086 Subfamily A. In addition, SEQ ID NOS: 279 to 299 disclosed in WO2003/063766 and US Patent No. 8101194 represent amino acid sequences associated with proteins of 2086 Subfamily B. ORF2086 subfamily A and
15 Subfamily B polypeptides are also described in WO2012032489, US Patent Publication No. US20120093852, PCT/IB2013/051791, now WO2013132452, and US Patent Application No. 13/787594, now publication number US20130243807.

 In one embodiment, the non-lipidated polypeptide includes the amino acid sequence that is at least about 60%, 65%, 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%,
20 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence encoding the corresponding lipidated polypeptide.

 In a one embodiment, the ORF2086 polypeptide includes at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 consecutive serine and/or glycine residues at the N-terminus of the ORF2086 polypeptide. Preferably, the ORF2086 polypeptide includes at least 3, 4, 5, 6, 7, 8, 9, or 10 and at
25 most 15, 14, 13, 12, 11, or 10 consecutive serine and/or glycine residues at the N-terminus of the ORF2086 polypeptide. The presence of such residues may facilitate in construction of the fusion polypeptide.

 In an exemplary embodiment, the ORF2086 polypeptide includes its respective native Gly/Ser stalk region. For example, the B44 polypeptide includes a stalk region as shown in
30 underlining in FIG. 2C of WO2012032489 and US Patent Publication No. US20120093852.

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See, for example, residues 2-12 of SEQ ID NO: 40 and residues 1-11 of SEQ ID NO: 60. As another example, the A12 polypeptide includes a stalk region as shown in underlining in FIG. 2A of WO2012032489 and US Patent Publication No. US20120093852. See, for example, residues 2-7 of SEQ ID NO: 28 and residues 1-6 of SEQ ID NO: 47.

5 In one embodiment, the ORF2086 polypeptide includes at least about 200, 210, 220, 230, 240, 250, 255, or 260 consecutive amino acids, and at most about 270, 269, 268, 267, 266, 265, 264, 263, 260, 259, 258, 257, 256, or 255 consecutive amino acids. Any minimum value may be combined with any maximum value to define a range. More preferably, the polypeptide has at least 254 or 262 consecutive amino acids. In some embodiments, the polypeptide has at most 254
10 consecutive amino acids. In other embodiments, the polypeptide has at most 262 consecutive amino acids. In one embodiment, the ORF2086 polypeptide includes the amino acid sequence that is at least about 60%, 65%, 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence encoding the corresponding ORF2086 polypeptide. For example, in an exemplary embodiment, the A62 polypeptide includes the amino acid
15 sequence that is at least about 60%, 65%, 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 41.

As used herein, the term “non-pyruvylated” refers to a polypeptide having no pyruvate content. Non-lipidated ORF2086 polypeptides having a pyruvate content typically exhibited a mass shift of +70, as compared to the corresponding wild-type polypeptide. In one embodiment, the
20 inventive polypeptide does not exhibit a mass shift of +70 as compared to the corresponding wild-type non-lipidated polypeptide when measured by mass spectrometry. Non-pyruvylated ORF2086 polypeptides are also described in WO2012032489, US Patent Publication No. US20120093852, PCT/IB2013/051791, and US Patent Application No. 13/787594.

E) Polynucleotides

25 In one aspect, the invention relates to an isolated polynucleotide that encodes any one of the isolated polypeptides described herein. In one aspect, the invention relates to an isolated polynucleotide that encodes any one of the fusion polypeptides described herein. In one embodiment, the isolated polynucleotide sequence is a codon-optimized sequence.

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In one embodiment, the ORF2086 polypeptide is encoded by a codon-optimized polynucleotide sequence. Examples of a codon-optimized sequence encoding an ORF2086 polypeptide include sequences set forth in SEQ ID NOs: 121-129. In a preferred embodiment, the isolated polypeptide is encoded by a polynucleotide sequence that includes a codon-optimized

5 polynucleotide sequence encoding a ORF2086 polypeptide. In a more preferred embodiment, the fusion polypeptide is encoded by a polynucleotide sequence that includes a codon-optimized polynucleotide sequence encoding an ORF2086 polypeptide. In another preferred embodiment, the ORF2086 polypeptide in a carrier-ORF2086 polypeptide conjugate is encoded by a codon-optimized polynucleotide sequence.

F) Fragments of the Polynucleotides and Polypeptides

Active variants and fragments of the disclosed polynucleotides and polypeptides are also described herein. "Variants" refer to substantially similar sequences. As used herein, a "variant polypeptide" refers to a polypeptide derived from the native protein by a modification of one or more amino acid residues at any position of the native protein. The modification may include a deletion (so-called truncation) of one or more amino acid residues at the N-terminal and/or C-terminal end of the native protein, deletion and/or addition of one or more amino acid residues at one or more internal sites in the native protein, or a substitution of one or more amino acid residues at one or more sites in the native protein. Variant polypeptides continue to possess the desired biological activity of the native polypeptide, that is, they are immunogenic. A variant of a polypeptide or polynucleotide sequence disclosed herein will typically have at least about 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity with the reference sequence.

The term "fragment" refers to a portion of an amino acid or nucleotide sequence comprising a specified number of contiguous amino acid or nucleotide residues. In particular embodiments, a fragment of a polypeptide disclosed herein may retain the biological activity of the full-length polypeptide and hence be immunogenic. Fragments of a polynucleotide may encode protein fragments that retain the biological activity of the protein and hence be immunogenic. Alternatively, fragments of a polynucleotide that are useful as PCR primers generally do not encode protein fragments that retain biological activity. Thus, fragments of a nucleotide sequence disclosed herein may range from at least about 15, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 175, 200, 225, 250, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, or 1500 contiguous nucleotides or up to the full-length polynucleotide. Fragments of a polypeptide sequence disclosed herein may comprise at least 10, 15, 20, 25, 30, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, or 500 contiguous amino acids, or up to the total number of amino acids present in the full-length polypeptide.

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G) Meningococcal conjugates

In one embodiment, the immunogenic composition further includes at least one conjugate selected from the group consisting of: a conjugate of a capsular saccharide of *Neisseria meningitidis* serogroup A; a conjugate of a capsular saccharide of *Neisseria meningitidis* serogroup C; a conjugate of a capsular saccharide of *Neisseria meningitidis* serogroup W135; and a conjugate of a capsular saccharide of *Neisseria meningitidis* serogroup Y.

In a preferred embodiment, the immunogenic composition includes a conjugate of a capsular polysaccharide of *Neisseria meningitidis* and a carrier protein. Preferably, the carrier protein in the saccharide conjugate is a bacterial toxin, such as a diphtheria or tetanus toxin, or toxoids or mutants thereof. Most preferably, the carrier protein is CRM₁₉₇. For example, in one embodiment, the composition includes at least one conjugate selected from (a) a conjugate of the capsular polysaccharide of serogroup A *N. meningitidis* and CRM₁₉₇; (b) a conjugate of the capsular polysaccharide of serogroup C *N. meningitidis* and CRM₁₉₇; (c) a conjugate of the capsular polysaccharide of serogroup W135 *N. meningitidis* and CRM₁₉₇; and (d) a conjugate of the capsular polysaccharide of serogroup Y *N. meningitidis* and CRM₁₉₇.

The capsular saccharides of serogroups A, C, W135, and Y are characterized and known in the art, and are described in WO2012032489 and US Patent Publication No. US20120093852.

H) Bactericidal immune responses

In another aspect, the isolated polypeptides and compositions described herein elicit a bactericidal immune response in a mammal against an ORF2086 polypeptide from serogroup B *N. meningitidis*. The compositions have the ability to induce bactericidal anti-meningococcal antibodies after administration to a mammal, and in preferred embodiments may induce antibodies that are bactericidal against strains of *N. meningitidis* that express LP2086 variants from the respective subfamilies. Further information on bactericidal responses is given below.

In one embodiment, the isolated polypeptide and/or composition described herein elicits a bactericidal immune response against a *N. meningitidis* serogroup B strain expressing an ORF2086 variant that is homologous to the ORF2086 polypeptide. In a preferred embodiment, a composition including a subfamily A polypeptide elicits a bactericidal immune response against a strain of *N. meningitidis* serogroup B that expresses a homologous subfamily A LP2086 variant. In another preferred embodiment, a composition including a subfamily A polypeptide elicits a bactericidal

immune response against a strain of *N. meningitidis* serogroup B that expresses a heterologous subfamily A LP2086 variant.

In another preferred embodiment, the isolated polypeptide and/or composition described herein elicits a bactericidal immune response against a *N. meningitidis* serogroup B strain expressing an ORF2086 variant that is heterologous to the ORF2086 polypeptide.

In one embodiment, the compositions elicit a bactericidal immune response against a strain of *N. meningitidis* serogroup B that expresses a heterologous subfamily LP2086 variant. For example, a composition including a subfamily A polypeptide may elicit a bactericidal immune response against strains of *N. meningitidis* serogroup B that expresses either a subfamily A or a subfamily B LP2086 variant.

In a further aspect, the isolated polypeptides and compositions described herein elicit a bactericidal immune response against at least one of serogroup A, serogroup B, serogroup C, serogroup W135, serogroup X, and/or serogroup Y strains of *N. meningitidis*. In a preferred embodiment, the compositions elicit a bactericidal immune response at least against serogroup B, serogroup C, and serogroup Y of *N. meningitidis*.

Bactericidal antibodies are an indicator of protection in humans and preclinical studies serve as a surrogate. Any new immunogenic composition candidate described herein preferably elicits these functional antibodies.

In one embodiment, the immune response and/or induction of bactericidal antibodies is measured by a serum bactericidal assay (SBA). An exemplary SBA is described below.

In a preferred embodiment, the inventive polypeptide and/or composition induces an immune response in a mammal, wherein the response is at least a 1-fold rise, 2-fold rise, at least a 3-fold rise, or preferably at least a 4-fold rise or greater than the immune response in the mammal in the absence of the inventive polypeptide and/or composition. For example, in one embodiment, the inventive polypeptide and/or composition induces an immune response in a mammal, wherein the response is at least a 1-fold rise, 2-fold rise, a 3-fold rise, or preferably at least a 4-fold rise or greater than the immune response in the mammal prior to administration of the inventive polypeptide and/or composition. In an exemplary embodiment, an isolated polypeptide including SEQ ID NO: 2 induces an immune response in a mammal, wherein the response is at least 1-fold, 2-fold, 3-fold, or preferably at least 4-fold greater than the immune response in the mammal in the absence of the polypeptide.

General descriptions

The term “mammals” as used herein refers to any mammal, such as, for example, humans, mice, rabbits, or non-human primates. In a preferred embodiment, the mammal is a human.

Example 1: Cloning and expression of fusion polypeptides including A05

The fHBP A05 gene used is shown in SEQ ID NO: 6 (expression construct pEB042).

Design of PLY fusions

The version of pneumolysin (PLY) used in these studies was termed delta 6 ($\Delta 6$ PLY). It contains a deletion of amino acid residues A146R147. The resultant gene is 1410 bp (SEQ ID NO: 3) and 470 amino acids (SEQ ID NO: 1). Two $\Delta 6$ PLY fusions to A05 were designed. One had $\Delta 6$ PLY at the N terminal end of the fusion polypeptide (SEQ ID NO: 4 DNA and SEQ ID NO: 2, protein; Figure 1A). The stalk region of A05 served as a flexible linker between the proteins. In the second fusion, A05 was placed at the N-terminus followed by the Gly-Ser-Gly linker (GSG), followed by the PLY gene (SEQ ID NO: 7, DNA; SEQ ID NO: 8, protein, Figure 1B).

Several additional pneumolysin fusion protein constructs have been made and verified for expression. These additional constructs use the stalk region of the respective fHBP variants as a flexible linker. These include PLY-A12 (SEQ ID NO: 136), PLY-B01 (SEQ ID NO: 138), PLY-B09 (SEQ ID NO: 140), PLY-B24 (SEQ ID NO: 142), PLY-B44 (SEQ ID NO: 144),

Design of CRM₁₉₇-A05 fusions

CRM₁₉₇ was used both as the full length protein (536 amino acids, SEQ ID NO: 9, DNA; SEQ ID NO: 10, protein) or the DT-A region (amino acids 1-193 of CRM₁₉₇; SEQ ID NO: 11, DNA; SEQ ID NO: 12, protein). Two A05 fusions were made using the full length CRM₁₉₇, (i) N-terminal CRM₁₉₇ fused to A05 (SEQ ID NO: 13, DNA; SEQ ID NO: 14, protein Figure 1C), and (ii) N-terminal A05, followed by the GSG linker and then CRM₁₉₇ (SEQ ID NO: 15, DNA; SEQ ID NO: 16; protein, Figure 1D). One version of the DT-A-A05 fusion was made: N-terminal DT-A fused to A05 at the C terminus (SEQ ID NO: 17, DNA; SEQ ID NO: 18, protein, Figure 1E).

Design of A05 fusion protein constructs that use alternative protein carriers

Additional constructs were designed to evaluate alternative protein carriers fused with the A05 fHBP variant. These protein carriers include, (i) GNA2091 from *N. meningitidis*, and (ii) streptococcal C5a peptidase (SCP) from *Streptococcus pyogenes*. The fusion protein in the former case is composed of 180 amino acids from GNA2091 (SEQ ID NO: 146) at the N-terminal end fused to A05 at the C-terminal end, using the stalk region of A05 as the flexible linker between the proteins (GNA2091-A05 SEQ ID NO: 148). The second example is composed of 950 amino acids from SCP (SEQ ID NO: 150) at the N-terminal end fused to A05 at the C-terminal end, using the stalk region of A05 as the flexible linker between the proteins (SCP-A05 SEQ ID NO: 152),

Expression vectors used in these studies

Initial fusion proteins were cloned into pET30a at the NdeI-BamHI sites via the InFusion® (Clontech) reaction. Fusions were subsequently cloned into a panel of 6 vectors selected to evaluate different promoters in order to optimize protein expression (*rhaT*, *lac*, and the arabinose promoter). The vectors also varied in the strength of the Shine Delgarno sequences that promote translation initiation. The vectors are based on the pET30a backbone, substituting the T7 promoter and regulatory genes for these specific elements.

Cell lines and expression

All expression plasmids were transformed into *E. coli*. Expression strains were grown overnight in HySoy plus 0.5% glucose and 50 µg/ml kanamycin at 30°C. Overnight cultures were seeded in to fresh HySoy media plus 50 µg/ml kanamycin at a 1:50 dilution. Cells were grown at either 30°C or 20°C. At an OD₆₀₀ ~1.0, cultures were induced with the appropriate inducer and incubated at the same temperatures overnight. Cells were harvested and samples assessed for solubility by either adding BUGBUSTER™ (EMD) reagent or by sonication followed by centrifugation. Whole cell lysates and soluble/insoluble fractions were run on Tris-Bis 4-12% gels and stained with Coomassie stain.

Results

Table 1 shows the results of CRM₁₉₇-A05 (SEQ ID NO: 14) fusion cloning. In general, CRM₁₉₇-A05 clones gave products with multiple mutations in the open reading frame. All fusion clones produced recombinant protein that was 100% insoluble. The DT-A-A05 (SEQ ID NO: 18) fusion construct also produced insoluble protein.

Table 2 shows the results of Ply-A05 fusion proteins. While expression of Ply-A05 or A05-Ply from pET30a at 30°C produced insoluble fusion protein, the alternative vectors produced partially soluble protein. In particular, Ply-A05 fusion proteins expressed from pRHAM (pDD18), pRAME (pDD21) and pDK347 (pDD20) at 30°C were largely soluble (Figure 2). pDD18 was chosen for fermentation, however the conditions used (Apollon medium, 30°C growth, 0.2% rhamnose induction) produced insoluble protein. Small scale shake flask cultures of pDD18, pDD20 and pDD21 were grown at 20°C to determine if lower temperature might enhance the solubility of the fusion protein. Unlike pDD20, the pDD18 and pDD21 cultures did not express detectable amounts of Ply-A05 protein at 20°C (Figure 3). Therefore, six 1 liter flask cultures of

pDD20 were produced for protein purification (Figure 4). The fusion protein expressed from pDD20 has a single amino acid change (L32F) in the pneumolysin portion of the fusion protein.

Table 1. CRM₁₉₇-A05 fusion proteins produced.

Construct	Insert	Plasmid	Strain	Expression Level	Solubility	Sequence
pDD23	CRM-A05	pRHAM (rhamnose)	BD686	{+}	not tested	V543G
pDD24	CRM-A05	pRAME (rhaT w/enhancer)	BD686	{++}	insoluble	L164F, S446N, V482I, V651I
pDD25	CRM-A05	pDK329 (ara)	BD686	{+}	not tested	correct
pDD26	CRM-A05	pDK338 (lac)	BD686	{-}	not tested	N373H
pDD27	CRM-A05	pDK347 (lac w/ enhancer)	BD686	{+}	insoluble	correct
pDD28	CRM-A05	pDK363 (ara w/enhancer)	BD686	{+++}	insoluble	correct
pDD14	DTA-A05	pET30a	BD686	{+++++}	insoluble	R259K, T394S
pDD31	DTA-A05	pRAME (rhaT w/enhancer)	BD686	{-}	not tested	R259K, T394S
pDD34	DTA-A05	pDK347 (lac w/ enhancer)	BD686	{-}	not tested	R259K, T394S
pDD35	DTA-A05	pDK363 (ara w/enhancer)	BD686	{++++}	insoluble	R259K, T394S
pLN15	A05-CRM	pET30a	BD686	{+++++}	insoluble	correct

Table 2. Ply-A05 fusion proteins produced.

construct	insert	plasmid	strain	expression level	solubility	sequence
pDD15	Ply-A05	pET30a	BD686	{+++++}	insoluble	correct
pDD18	Ply-A05	pRHAM (rhamnose)	BD686	{+++}	soluble	correct
pDD19	Ply-A05	pDK329 (ara)	BD686	{+}	not tested	correct
pDD20	Ply-A05	pDK347 (lac w/ enhancer)	BD686	{++++}	soluble	L32F
pDD21	Ply-A05	pRAME (rhaT w/enhancer)	BD686	{++++}	mostly soluble	correct
pDD22	Ply-A05	pDK338 (lac)	BD686	{+}	not tested	correct
pDD29	Ply-A05	pDK363 (ara w/enhancer)	BD686	{+++++}	mostly insoluble	correct
pLN116	A05-Ply	pET30a	BD686	{+++++}	insoluble	correct

Example 2: Serum bactericidal assay

Functional antibody titers were determined by serum bactericidal assay (SBA) against *Neisseria meningitidis* strains expressing an LP2086 variant with sequence homologous or heterologous to those contained in the vaccine.

Bactericidal antibodies in serum from macaques or rabbits immunized with ORF2086 vaccine were detected using SBAs with human complement. Rabbit immune sera or macaque immune sera were heat-inactivated to remove intrinsic complement activity and subsequently serially diluted 1:2 in Dulbecco's PBS with Ca²⁺ and Mg²⁺ (D-PBS) in a 96-well microtiter plate to test for serum bactericidal activity against *N. meningitidis* strains. Bacteria used in the assay were grown in GC media supplemented with Kellogg's supplement (GCK) and 4.2% NaHCO₃ and monitored by optical density at 650 nm. Bacteria were harvested for use in the assay at a final OD₆₅₀ of 0.50-0.60, diluted in D-PBS and 1000–3000 CFU were added to the assay mixture with 20% human complement.

Human serum with no detectable bactericidal activity was used as the exogenous complement source. Complement sources were tested for suitability against each individual *N. meningitidis* test strain. A complement source was used only if the number of bacteria surviving in control reactions without added immune sera was >50% of the input.

After a 30 min incubation with agitation at 700rpm on a shaker at 37°C with 5% CO₂, D-PBS was added to the reaction mixture and aliquots transferred to microfilter plates filled with 50% GCK media. The microfilter plates were filtered, incubated overnight at 37°C with 5% CO₂, and microcolonies were stained and quantified. The serum bactericidal titers were defined as the interpolated reciprocal serum dilution that yielded a 50% reduction in colony forming units (CFU) compared to the CFU in control wells without immune sera using these assay conditions. Enhanced susceptibility to killing with ORF2086 immune sera relative to pre-immune sera was noted if there was a 4-fold or greater rise in SBA titer. Sera that were negative against the assay strain at the starting dilution were assigned a titer of one half the limit of detection for the assay (*i.e.*, 4).

Example 3: Immunogenicity of Fusion Polypeptide (SEQ ID NO: 2)

The bactericidal activity of serum samples from mice immunized with nonlipidated versions of fHBP protein alleles is generally lower than serum samples from mice immunized with the lipidated fHBP counterparts. Similarly, the SBA response against *N. meningitidis* strains that express two distinct subfamily A fHBP variants (A05 and A22) is greater following immunization of nonhuman primates (NHPs) with lipidated A05 (SEQ ID NO: 19) than nonlipidated A05 (SEQ ID NO: 44) (Table 3).

Table 3. The bactericidal titer against *N. meningitidis* strains that express A05 and A22 fHBP variants is greater in serum from NHPs vaccinated with lipidated A05 (SEQ ID NO: 19) compared with nonlipidated A05 (SEQ ID NO: 5).

A05 Vaccine	Dose (mcg)	% Responders $\geq$ 4X rise PD3 SBA Titers	
		A05	A22
Lipidated	30	100	60
	10	70	80
Non-Lipidated	120	30	0
	60	50	20
	30	50	0
	10	40	10

Additional compositions have been evaluated to provide coverage using combinations of nonlipidated proteins. In this investigation we demonstrate that immunogenicity may be enhanced with recombinant proteins composed of nonlipidated variants of fHBP genetically fused to a carrier protein. The same findings could also be extended to fHBP variants that are conjugated to carrier proteins.

In the current example a recombinant fusion protein (SEQ ID NO: 2) composed of attenuated *Streptococcus pneumoniae* pneumolysin (Δ 6PLY) genetically fused to the *N. meningitidis* fHBP A05 variant (SEQ ID NO: 5) is tested.

The attenuated Δ 6PLY (SEQ ID NO: 1) is produced by site-directed mutagenesis. Specifically, the immunogenic Δ 6 PLY variant (deletion of the A146R147 dipeptide) eliminates both the pore forming cytolytic activity and the pro-inflammatory phenotype that is characteristic of wild type PLY (SEQ ID NO: 21).

To explore whether the attenuated $\Delta 6\text{PLY}$ could stabilize and therefore enhance the immunogenicity of the nonlipidated A05, a recombinant protein composed of *Str. pneumoniae* $\Delta 6\text{PLY}$ genetically fused to *N. meningitidis* fHBP variant A05 was constructed (SEQ ID NO: 2) for testing. In the current example, non-human primates (NHPs) were immunized with the $\Delta 6\text{PLY}$ -A05 fusion protein (SEQ ID NO: 2) or the lipidated bivalent A05 (SEQ ID NO: 19)/B01 (SEQ ID NO: 20) composition and boosted on weeks 4 and 8. Serum from animals taken at 10wks (post-dose 3, PD3) was evaluated for bactericidal activity against an A05 expressing strain of *N. meningitidis*. SBA titers in PD3 samples from both treatment groups were elevated compared to prevaccination titers (Table 4). The immune response to $\Delta 6\text{PLY}$ -A05 (SEQ ID NO: 2) was as strong as to the response to the lipidated A05 (SEQ ID NO: 19)/B01 (SEQ ID NO: 20) composition.

TABLE 4. Bactericidal activity against *N. meningitidis* serogroup B clinical isolates expressing either A05 (SEQ ID NO: 23) or A22 (SEQ ID NO: 22) fHBP protein variants using serum from NHPs vaccinated with $\Delta 6\text{PLY}$ -A05 fusion protein (SEQ ID NO: 2) or the bivalent lipidated A05 (SEQ ID NO: 19)/B01 (SEQ ID NO: 20) composition.

Antigenic Composition	Lipidated	Dose/0.5 mL	% Responders at PD3 with $\geq 4X$ rise SBA Titers	
			A05	A22
A05 (SEQ ID NO : 19) and B01 (SEQ ID NO: 20)	Yes	10 mcg each	80	60
$\Delta 6\text{PLY}$ -A05 (SEQ ID NO: 2)	No	10 mcg	100	100

The PD3 serum samples from $\Delta 6\text{PLY}$ -A05 (SEQ ID NO: 2) vaccinated NHPs also had strong bactericidal activity against a strain of *N. meningitidis* expressing the fHBP A22 (SEQ ID NO: 22) variant (Table 4). The percent of animals that respond with a $> 4X$ rise in SBA titer using the A22 target strain of *N. meningitidis* was greater in the $\Delta 6\text{PLY}$ -A05 treated NHPs than in the bivalent lipidated fHBP treatment group. In summary, the functional bactericidal activity against *N. meningitidis* strains that express two distinct subfamily A fHBP variants using serum from NHPs vaccinated with the non-lipidated $\Delta 6\text{PLY}$ -A05 fusion protein is at least as strong as the activity from the lipidated bivalent rLP2086 treatment group.

To further explore the impact of *Str. pneumoniae* Δ 6PLY relative to other carrier proteins on the immunogenicity of nonlipidated A05, a recombinant protein composed of GNA2091 from *N. meningitidis* fused with fHBP variant A05 was prepared for testing. In addition, a chemical conjugate of recombinant expressed streptococcal C5a peptidase (SCP) from *Streptococcus pyogenes* (zinc treated, see Example 4) coupled with fHBP variant A05 (SEQ ID NO: 5) was also prepared for immunogenicity assessment. In the current example, non-human primates (NHPs) were immunized with the respective A05 fusion proteins, the SCP-A05 chemical conjugate, the lipidated bivalent A05 (SEQ ID NO: 19)/B01 (SEQ ID NO: 20) composition, or the nonlipidated A05 (SEQ ID NO: 5) and boosted on weeks 4 and 8. The antigen dose was adjusted so that the equivalent of 10mcg of A05 was administered with each vaccination. Serum from animals taken at 10wks (post-dose 3, PD3) was evaluated for bactericidal activity against an A05 expressing strain of *N. meningitidis*. SBA titers in PD3 samples from the PLY-A05 (SEQ ID NO: 2) treatment group were, (i) elevated compared to prevaccination titers, (ii) comparable to the response to the lipidated bivalent A05/B01 composition, and (iii) superior to the immune response to both nonlipidated A05 and the GNA2091-A05 (SEQ ID NO: 149) fusion protein antigens (Table 5). While animals vaccinated with the SCP-A05 chemical conjugate did respond to the antigen, the magnitude of the immune response was not as robust as that detected in the PLY-A05 fusion protein treatment group.

Table 5

Antigenic Composition	Lipidated	Amount of fHBP in antigen (mcg/0.5mL)	PD3 GMT SBA Titers (A05)	% Responders >4X Rise SBA Titers (A05)
A05 (SEQ ID NO : 19) and B01 (SEQ ID NO: 20)	yes	10 of each	64	100
A05 (SEQ ID NO: 5)	no	10	19	80
PLY-A05 (SEQ ID NO: 2)	no	10	104	100
GNA2091-A05 (SEQ ID NO: 149)	no	10	16	60
SCP-A05 (SEQ ID NO: 5) Conjugate	no	10	43	80

Example 4: Post-translational modification removal

When the cysteine in rP2086-A05-cys is located on the amino terminus (SEQ ID NO: 156), a significant amount of the protein is pyruvylated during fermentation. This pyruvylation modification was removed from the proteins by treatment with zinc sulfate. Mass spectra characterized the pyruvylated rP2086-A05-cys (SEQ ID NO: 156) as exhibiting a mass shift of +71 Da, as compared to the rP2086-A05-cys protein treated with zinc sulfate, which did not exhibit a mass shift of +71 as compared to the corresponding pyruvylated rP2086-A05-cys.

Moving the cysteine residue to other positions in the protein (e.g., moving the cysteine to positions 2 or 6, see SEQ ID NO: 157 and SEQ ID NO: 158, respectively) eliminated the pyruvylation issue. A description of these constructs is provided in Example 9.

In addition to standard chromatography techniques, to separate native rP2086-A05-cys from protein containing blocked thiols, a thiol reactive resin (Thiopropyl Sepharose 6B) was used. In this technique, the native rP2086-A05-cys binds to the column and the blocked rP2086-A05-cys is eluted in the flow through. The native rP2086-A05-cys is then eluted from the column using a reducing agent (preferably DTT).

As used in the following examples, the term “rP2086-A05-cys” refers to a non-pyruvylated, non-lipidated rP2085 A05 protein, regardless of how the pyruvylation modification is not present, e.g., naturally during fermentation, by zinc sulfate treatment, by genetic modifications to the protein to delete the initial cysteine at position 1 of the N-terminus and replacing a serine residue at positions 2 or 6 with a cysteine residue.

None of the processes described below have been optimized. Accordingly, other protein concentrations, protein ratios, reaction times and temperatures than those described could be used to produce rP2086-A05 conjugates.

Example 5: Conjugation of Pneumolysin to rP2086-A05-cys using an amine-to-sulfhydryl crosslinker with soluble polyethylene glycol (PEG) spacer arm.

Preparation of SM(PEG)₄-Activated Pneumolysin-NEM intermediate:

Pneumolysin protein at approx 10 mg/ml in phosphate buffered saline is prepared for conjugation by derivatization of the protein with N-Ethyl Maleimide (NEM), followed by activation with SM(PEG)₄. A 10 fold molar excess NEM is incubated with pneumolysin at 20-25 deg C and 1mM EDTA for a time sufficient to completely block pneumolysin sulfhydryls. Typically 20 minutes is sufficient to prepare Pneumolysin-NEM intermediate. SM(PEG)₄ linker, obtained from a solution having a concentration of 100 mM and dissolved in dimethyl sulfoxide solvent, is incubated at a 10 fold molar excess over Pneumolysin-NEM intermediate for 30 minutes. The activation reaction is terminated by Size Exclusion Chromatography using a column packed with Sephadex G25 resin. The chromatographic fractions containing SM(PEG)₄-Activated Pneumolysin-NEM intermediate can be stored -80 C or immediately conjugated to Reduced MnB 2086 A05 Cysteine-stem mutant Protein intermediate.

The NEM modification is used to block the cysteine residue in pneumolysin so that it does not react with the SM(PEG) linker.

Example 6: Preparation of Reduced rP2086-A05-cys:

rP2086-A05-cys at approx 1.3 mg/ml in phosphate buffered saline is incubated with a quantity of settled immobilized TCEP resin and 1mM EDTA sufficient to completely reduce the sulfhydryls of MnB protein. Typically, a 30 minute incubation of rP2086-A05-cys with an equal volume of settled resin and 1mM EDTA is sufficient to completely reduce the sulfhydryls. Reduced MnB protein intermediate is recovered by filtration through a 0.2 micron Polyether sulfone membrane and used immediately for conjugation.

Example 7: Conjugation of SM(PEG)₄ -Activated Pneumolysin-NEM intermediate to rP2086-A05-cys:

The reduced rP2086-A05-cys intermediate is combined with SM(PEG)₄ -Activated Pneumolysin-NEM intermediate to achieve a 4:1 molar ratio at protein concentrations of approximately 1.2 and 0.6mg/mL respectively. The reaction proceeds for 2 hr at 20-25 deg C and is terminated by the addition of Cysteamine-HCl pH 5.5, to the reaction solution to a 2mM final concentration of cysteamine-HCl. The conjugation reaction product rP2086-A05-cys SM(PEG)₄ Pneumolysin-NEM conjugate reaction product is chromatographically purified from unconjugated SM(PEG)₄ -Activated Pneumolysin-NEM intermediate by Immobilized Metal Affinity Chromatography (IMAC) using Nickel Sepharose 6 fast flow resin. The reaction product binds in a buffer composed of 20mM Tris, 0.5M NaCl pH 7.7 and is eluted in 20mM Tris, 0.5M NaCl pH 7.7 40 mM Imidazole. Further purification of the conjugate is achieved by removal of Reduced MnB 2086 A05 Cysteine-stem mutant Protein intermediate by Ion Exchange Chromatography using Q Sepharose HP resin. The reaction product binds in 20mM Tris, pH 7.7 and is recovered in a salt gradient elution of 20mM Tris, 0.5M NaCl pH 7.7. The Q fractions containing the conjugate are buffer exchanged by Size Exclusion Chromatography using a column packed with Sephadex G25 resin and sterile filtered.

Example 8: Conjugation of SCP to rP2086-A05-cys using an amine-to-sulfhydryl crosslinker with a cyclohexane spacer arm

Preparation of SMCC -Activated SCP intermediate:

SCP protein at approx 12.6 mg/ml in phosphate buffered saline is incubated at 25 deg C with a 20 fold molar excess of Sulfosuccinimidyl-4-(*N*-maleimidomethyl)cyclohexane-1-carboxylate linker, (Sulfo-SMCC; obtained from a 20 mM stock prepared in 10 mM sodium phosphate pH 6.8) and 1mM EDTA for 1 hour. The activation reaction is terminated by Size Exclusion Chromatography using a column packed with Sephadex G25 resin. The chromatographic fractions containing SMCC -Activated SCP intermediate can be stored -80° C or immediately conjugated to reduced rP2086-A05-cys intermediate.

Preparation of Reduced rP2086-A05-cys intermediate:

rP2086-A05-cys at approx 3.8 mg/ml in phosphate buffered saline is incubated with 4mM TCEP and 1mM EDTA sufficient to completely reduce the sulfhydryls of MnB protein. Typically, a 1hr incubation of MnB Protein with TCEP and 1mM EDTA is sufficient to completely reduce the sulfhydryls. Reduced MnB protein is used immediately for conjugation.

Conjugation of SMCC -Activated SCP intermediate to rP2086-A05-cys:

The reduced rP2086-A05-cys is combined with SMCC -Activated SCP intermediate to achieve an equal weight ratio, (a 4:1 molar ratio), at protein concentrations of approximately 2.6mg/ml and 2.6 mg/mL respectively. The reaction proceeds for 2.5 hr at 25 deg C and is terminated by the addition of Cysteamine-HCl pH 5.5, to the reaction solution to a 2mM final concentration of cysteamine-HCl. The conjugation reaction product MnB 2086 A05 Cysteine-mutant Protein SMCC-SCP conjugate reaction product is chromatographically purified from unconjugated SMCC-SCP Activated intermediate by Immobilized Metal Affinity Chromatography (IMAC) using Nickel Sepharose 6 fast flow resin. The reaction product binds in a buffer composed of 20mM Tris, 0.5M NaCl pH 7.7 and is eluted in 20mM Tris, 0.5M NaCl pH 7.7 40 mM Imidazole. Further purification of the conjugate is achieved by removal of Reduced MnB 2086 A05 Cysteine mutant Protein intermediate by Ion Exchange Chromatography using Q Sepharose HP resin. The reaction product binds in 20mM Tris, pH 7.7 and is recovered in a salt gradient elution of 20mM Tris, 0.5M NaCl pH 7.7. The Q fractions containing the conjugate are buffer exchanged by Size Exclusion Chromatography using a column packed with Sephadex G25 resin and sterile filtered.

Example 9: Generation of rP2086-A05-cys Stalk Mutants

A Non-lipidated construct of A05 were designed to remove the lipidation signal and produce a recombinant protein with the cysteine at the N-terminus. The proteins were strongly expressed in *E. coli*. Purified proteins were analyzed using reverse-phase high performance liquid chromatography (RP-HPLC) interfaced with a quadruple time-of-flight mass spectrometer (QTOF-MS) to provide a means of monitoring formation of product related variants.

To assess whether moving the cysteine into the serine glycine stalk region of A05 would reduce the modifications on the cysteine while keeping it available for conjugation, two variants of A05 were constructed, one with the N-terminal cysteine moved to position 2 of the mature protein replacing the serine residue at this position (see SEQ ID NO: 157) and one with the cysteine moved to position 6 of the mature protein replacing the serine residue at this position (see SEQ ID NO: 158). This was accomplished by incorporating the codon changes in the 5' primer used for amplification of the gene. Both the 5' and 3' primers designed to amplify A05 had 15 base extensions with homology to pET30a cut with NdeI and BamHI. A05 and the vector were ligated using a Clontech InFusion® kit. After transformation, colonies were screened for inserts and those containing inserts were verified to contain the amino acid substitution by DNA sequencing.

The following clauses describe additional embodiments of the invention:

- C1. An isolated polypeptide comprising the amino acid sequence of a carrier polypeptide and the amino acid sequence of an ORF2086 polypeptide.
- C2. The polypeptide according to clause C1, wherein the isolated polypeptide is a fusion polypeptide.
- C3. The polypeptide according to clause C1, wherein the ORF2086 polypeptide is a subfamily A polypeptide.
- C4. The polypeptide according to clause C1, wherein the ORF2086 polypeptide is a subfamily B polypeptide.
- C5. The polypeptide according to clause C1, wherein the ORF2086 polypeptide is lipidated.
- C6. The polypeptide according to clause C1, wherein the ORF2086 polypeptide is non-lipidated.

- C7. The polypeptide according to clause C1, wherein the ORF2086 polypeptide is A05.
- C8. The polypeptide according to clause C1, wherein the ORF2086 polypeptide is A12.
- C9. The polypeptide according to clause C1, wherein the ORF2086 polypeptide is A22.
- C10. The polypeptide according to clause C1, wherein the ORF2086 polypeptide is B01.
- C11. The polypeptide according to clause C1, wherein the ORF2086 polypeptide is B09.
- C12. The polypeptide according to clause C1, wherein the ORF2086 polypeptide is B15.
- C13. The polypeptide according to clause C1, wherein the ORF2086 polypeptide is B16.
- C14. The polypeptide according to clause C1, wherein the ORF2086 polypeptide is B22.
- C15. The polypeptide according to clause C1, wherein the ORF2086 polypeptide is B24.
- C16. The polypeptide according to clause C1, wherein the ORF2086 polypeptide is B44.
- C17. The polypeptide according to clause C1, wherein the ORF2086 polypeptide is A62.
- C18. The polypeptide according to clause C1, wherein the ORF2086 polypeptide is A04.
- C19. The polypeptide according to clause C1, wherein the ORF2086 polypeptide is A01.
- C20. The polypeptide according to clause C1, wherein the ORF2086 polypeptide is A06.
- C21. The polypeptide according to clause C1, wherein the ORF2086 polypeptide is A07.
- C22. The polypeptide according to clause C1, wherein the ORF2086 polypeptide is A15.
- C23. The polypeptide according to clause C1, wherein the ORF2086 polypeptide is A19.

- C24. The polypeptide according to clause C1, wherein the ORF2086 polypeptide is A20.
- C25. The polypeptide according to clause C1, wherein the ORF2086 polypeptide is A29.
- C26. The polypeptide according to clause C1, wherein the ORF2086 polypeptide is B02.
- C27. The polypeptide according to clause C1, wherein the ORF2086 polypeptide comprises the amino acid sequence selected from the group consisting of SEQ ID NOs: 5, 19, 22-65.
- C28. The polypeptide according to clause C1, wherein the carrier polypeptide is a cytolysoid.
- C29. The polypeptide according to clause C28, wherein the cytolysoid is derived from a pneumolysin polypeptide from *Streptococcus pneumoniae*, a perfringolysin O polypeptide from *Clostridium perfringens*, a intermedilysin polypeptide from *Streptococcus intermedius*, a alveolysin polypeptide from *Bacillus alvei*, a anthrolysin polypeptide from *Bacillus anthracis*, a putative cereolysin polypeptide from *Bacillus cereus*, a ivanolysin O polypeptide from *Listeria ivanovii*, a pyolysin polypeptide from *Arcanobacterium pyogenes*, a seeligeriolysin O polypeptide from *Listeria seeligeri*, a streptolysin O polypeptide from *S. pyogenes*, a suilysin polypeptide from *Streptococcus suis*, a tetanolysin polypeptide from *Clostridium tetani*, a listeriolysin O polypeptide from *Listeria monocytogenes*, a streptolysin O polypeptide from *Streptococcus equisimilis*, a streptolysin O polypeptide from *S. canis*, a thuringiolysin O polypeptide from *Bacillus thuringiensis*, a laterosporolysin O polypeptide from *B. laterosporus*, a botulinolysin polypeptide from *Clostridium botulinum*, a chauveolysin polypeptide from *C. chauvoei*, a bifermentolysin polypeptide from *C. bifermentans*, a sordellilysin polypeptide from *C. sordellii*, a histolyticolysin polypeptide from *Clostridium histiolyticum*, a novylisin polypeptide from *Clostridium novyi*, or a septicolysin O polypeptide from *Clostridium septicum*.
- C30. The polypeptide according to clause C29, wherein the cytolysoid is derived from a pneumolysin polypeptide from *Streptococcus pneumoniae*.
- C31. The polypeptide according to clause C30, wherein the cytolysoid comprises a sequence having at least 90% sequence identity to SEQ ID NO: 1.
- C32. The polypeptide according to clause C1, wherein the carrier polypeptide is detoxified as compared to the corresponding wild-type carrier polypeptide and is selected from the group consisting of tetanus toxin (TT), *Plasmodium falciparum*

circumsporozite protein, hepatitis B surface antigen, hepatitis B nuclear core polypeptide, *H. influenzae* matrix polypeptide, *H. influenzae* haemagglutinin, diphtheria toxoid, diphtheria toxoid mutant CRM₁₉₇, group B *N. meningitidis* outer membrane polypeptide complex (OMPC), a cytolysoid, pneumococcal toxin pneumolysin, heat shock polypeptide from *Mycobacterium bovis*, heat shock polypeptide from *M. leprae*, cholera toxoid, *E. coli* LT, *E. coli* ST, exotoxin A from *Pseudomonas aeruginosa*, pneumococcal surface polypeptide A, pneumococcal adhesin polypeptide (PsaA), C5a peptidase from Group A or Group B streptococcus, *Haemophilus influenzae* polypeptide D, ovalbumin, keyhole limpet hemocyanin (KLH), bovine serum albumin (BSA), purified polypeptide derivative of tuberculin (PPD), PorB (from *N. meningitidis*), and derivatives, variants, or fragments thereof.

- C33. The polypeptide according to clause C1, wherein the carrier polypeptide is CRM₁₉₇.
- C34. The polypeptide according to clause C32, wherein the carrier polypeptide is not CRM₁₉₇.
- C35. The polypeptide according to clause C1, wherein the carrier polypeptide is streptococcal C5a peptidase (SCP) from *Streptococcus pyogenes*.
- C36. The polypeptide according to clause C1, wherein the carrier polypeptide is GNA2091.
- C37. The polypeptide according to clause C1, further comprising a polypeptide sequence derived from pneumococcal bacteria.
- C38. The polypeptide according to clause C1, wherein the isolated polypeptide does not comprise a polypeptide sequence derived from pneumococcal bacteria.
- C39. The polypeptide according to clause C1, wherein the isolated polypeptide elicits a bactericidal antibody against a *N. meningitidis* serogroup B variant that is homologous with the ORF2086 polypeptide.
- C40. The polypeptide according to clause C1, wherein the isolated polypeptide elicits a bactericidal antibody against a *N. meningitidis* serogroup B variant that is heterologous to the ORF2086 polypeptide.
- C41. The polypeptide according to clause C2, wherein the fusion polypeptide comprises in the following order: the carrier polypeptide operably linked to the ORF2086 polypeptide.
- C42. The polypeptide according to clause C2, wherein the fusion polypeptide comprises in the following order: an ORF2086 polypeptide operably linked to a carrier polypeptide.

- C43. The polypeptide according to clause C2, wherein the carrier polypeptide comprises SEQ ID NO: 1 and the ORF2086 polypeptide comprises SEQ ID NO: 5.
- C44. The polypeptide according to clause C43, wherein the isolated polypeptide comprises SEQ ID NO: 2.
- C45. An isolated polynucleotide that encodes a polypeptide according to any one of clauses CC1-CC44.
- C46. An immunogenic composition comprising a polypeptide according to any one of clauses CC1-CC44 and a pharmaceutically acceptable excipient.
- C47. The composition according to clause C46, further comprising at least one conjugate selected from: a) a conjugate of a capsular saccharide of *Neisseria meningitidis* serogroup A; b) a conjugate of a capsular saccharide of *Neisseria meningitidis* serogroup C; c) a conjugate of a capsular saccharide of *Neisseria meningitidis* serogroup W135; and d) a conjugate of a capsular saccharide of *Neisseria meningitidis* serogroup Y.
- C48. A method for inducing an immune response against *Neisseria meningitidis* in a mammal comprising administering to the mammal an effective amount of the isolated polypeptide according to any one of clauses CC1-CC44.
- C49. The method of clause C48, wherein the immune response comprises a bactericidal antibody.
- C50. The method of clause C48, wherein the immune response is equal to an immune response of a mammal administered with a corresponding lipidated ORF2086 polypeptide in the absence of a carrier polypeptide, when assessed under identical conditions.
- C51. The method of clause C48, wherein the immune response is greater than an immune response of a mammal administered with a corresponding non-lipidated ORF2086 polypeptide in the absence of a carrier polypeptide, when assessed under identical conditions.
- C52. The method of clause C48, wherein the immune response is at most 10% less than an immune response of a mammal administered with a corresponding lipidated ORF2086 polypeptide in the absence of a carrier polypeptide, when assessed under identical conditions.
- C53. The method of clause C48, wherein the immune response is at most 20% less than an immune response of a mammal administered with a corresponding lipidated ORF2086 polypeptide in the absence of a carrier polypeptide, when assessed under identical conditions.

- C54. A method for inducing an immune response against *Neisseria meningitidis* in a mammal comprising administering to the mammal an effective amount of the immunogenic composition according to any one of clauses CC46-CC47.
- C55. The method of clause C54, wherein the immune response comprises a bactericidal antibody.
- C56. The method of clause C54, wherein the immune response is equal to an immune response of a mammal administered with a corresponding lipidated ORF2086 polypeptide in the absence of a carrier polypeptide, when assessed under identical conditions.
- C57. The method of clause C54, wherein the immune response is greater than an immune response of a mammal administered with a corresponding non-lipidated ORF2086 polypeptide in the absence of a carrier polypeptide, when assessed under identical conditions.
- C58. The method of clause C54, wherein the immune response is at most 10% less than an immune response of a mammal administered with a corresponding lipidated ORF2086 polypeptide in the absence of a carrier polypeptide, when assessed under identical conditions.
- C59. The method of clause C54, wherein the immune response is at most 20% less than an immune response of a mammal administered with a corresponding lipidated ORF2086 polypeptide in the absence of a carrier polypeptide, when assessed under identical conditions.
- C60. An immunogenic composition comprising an ORF2086 polypeptide and a carrier polypeptide.
- C61. The composition according to clause C60, wherein the composition is a conjugate.
- C62. The composition according to clause C60, wherein the ORF2086 polypeptide is a subfamily A polypeptide.
- C63. The composition according to clause C60, wherein the ORF2086 polypeptide is a subfamily B polypeptide.
- C64. The composition according to clause C60, wherein the ORF2086 polypeptide is lipidated.
- C65. The composition according to clause C60, wherein the ORF2086 polypeptide is non-lipidated.
- C66. The composition according to clause C60, wherein the ORF2086 polypeptide is non-lipidated and non-pyruvylated.

- C67. The composition according to clause C60, wherein the ORF2086 polypeptide is A05.
- C68. The composition according to clause C60, wherein the ORF2086 polypeptide is A12.
- C69. The composition according to clause C60, wherein the ORF2086 polypeptide is A22.
- C70. The composition according to clause C60, wherein the ORF2086 polypeptide is B01.
- C71. The composition according to clause C60, wherein the ORF2086 polypeptide is B09.
- C72. The composition according to clause C60, wherein the ORF2086 polypeptide is B15.
- C73. The composition according to clause C60, wherein the ORF2086 polypeptide is B16.
- C74. The composition according to clause C60, wherein the ORF2086 polypeptide is B22.
- C75. The composition according to clause C60, wherein the ORF2086 polypeptide is B24.
- C76. The composition according to clause C60, wherein the ORF2086 polypeptide is B44.
- C77. The composition according to clause C60, wherein the ORF2086 polypeptide is A62.
- C78. The polypeptide according to clause C60, wherein the ORF2086 polypeptide is A04.
- C79. The polypeptide according to clause C60, wherein the ORF2086 polypeptide is A01.
- C80. The polypeptide according to clause C60, wherein the ORF2086 polypeptide is A06.
- C81. The polypeptide according to clause C60, wherein the ORF2086 polypeptide is A07.
- C82. The polypeptide according to clause C60, wherein the ORF2086 polypeptide is A15.
- C83. The polypeptide according to clause C60, wherein the ORF2086 polypeptide is A19.

- C84. The polypeptide according to clause C60, wherein the ORF2086 polypeptide is A20.
- C85. The polypeptide according to clause C60, wherein the ORF2086 polypeptide is A29.
- C86. The polypeptide according to clause C60, wherein the ORF2086 polypeptide is B02.
- C87. The composition according to clause C60, wherein the ORF2086 polypeptide comprises the amino acid sequence selected from the group consisting of SEQ ID NOs: 5, 19, 22-65.
- C88. The composition according to clause C60, wherein the carrier polypeptide is a cytolysoid.
- C89. The composition according to clause C88, wherein the cytolysoid is derived from a pneumolysin polypeptide from *Streptococcus pneumoniae*, a perfringolysin O polypeptide from *Clostridium perfringens*, a intermedilysin polypeptide from *Streptococcus intermedius*, a alveolysin polypeptide from *Bacillus alvei*, a anthrolysin polypeptide from *Bacillus anthracis*, a putative cereolysin polypeptide from *Bacillus cereus*, a ivanolysin O polypeptide from *Listeria ivanovii*, a pyolysin polypeptide from *Arcanobacterium pyogenes*, a seeligeriolysin O polypeptide from *Listeria seeligeri*, a streptolysin O polypeptide from *S. pyogenes*, a suilysin polypeptide from *Streptococcus suis*, a tetanolysin polypeptide from *Clostridium tetani*, a listeriolysin O polypeptide from *Listeria monocytogenes*, a streptolysin O polypeptide from *Streptococcus equisimilis*, a streptolysin O polypeptide from *S. canis*, a thuringiolysin O polypeptide from *Bacillus thuringiensis*, a laterosporolysin O polypeptide from *B. laterosporus*, a botulinolysin polypeptide from *Clostridium botulinum*, a chauveolysin polypeptide from *C. chauvoei*, a bifermentolysin polypeptide from *C. bifermentans*, a sordellilysin polypeptide from *C. sordellii*, a histolyticolysin polypeptide from *Clostridium histiolyticum*, a novylisin polypeptide from *Clostridium novyi*, or a septicolysin O polypeptide from *Clostridium septicum*.
- C90. The composition according to clause C89, wherein the cytolysoid is derived from a pneumolysin polypeptide from *Streptococcus pneumoniae*.
- C91. The composition according to clause C90, wherein the cytolysoid comprises a sequence having at least 90% sequence identity to SEQ ID NO: 1.
- C92. The composition according to clause C60, wherein the carrier polypeptide is detoxified as compared to the corresponding wild-type carrier polypeptide and is selected from the group consisting of tetanus toxin (TT), *Plasmodium falciparum*

circumsporozite protein, hepatitis B surface antigen, hepatitis B nuclear core polypeptide, *H. influenzae* matrix polypeptide, *H. influenzae* haemagglutinin, diphtheria toxoid, diphtheria toxoid mutant CRM₁₉₇, group B *N. meningitidis* outer membrane polypeptide complex (OMPC), a cytolysoide, pneumococcal toxin pneumolysin, heat shock polypeptide from *Mycobacterium bovis*, heat shock polypeptide from *M. leprae*, cholera toxoid, *E. coli* LT, *E. coli* ST, exotoxin A from *Pseudomonas aeruginosa*, pneumococcal surface polypeptide A, pneumococcal adhesin polypeptide (PsaA), C5a peptidase from Group A or Group B streptococcus, *Haemophilus influenzae* polypeptide D, ovalbumin, keyhole limpet hemocyanin (KLH), bovine serum albumin (BSA), purified polypeptide derivative of tuberculin (PPD), PorB (from *N. meningitidis*), and derivatives, variants, or fragments thereof.

C93. The composition according to clause C60, wherein the carrier polypeptide is CRM₁₉₇.

C94. The composition according to clause C92, wherein the carrier polypeptide is CRM₁₉₇.

C95. The composition according to clause C60, wherein the carrier polypeptide is streptococcal C5a peptidase (SCP) from *Streptococcus pyogenes*.

C96. The composition according to clause C60, wherein the carrier polypeptide is GNA2091.

C97. The composition according to clause C60, wherein the carrier polypeptide is heterologous to the ORF2086 polypeptide.

C98. The composition according to clause C60, further comprising a polypeptide sequence derived from pneumococcal bacteria.

C99. The composition according to clause C60, wherein the composition does not comprise a polypeptide sequence derived from pneumococcal bacteria.

C100. The composition according to clause C60, wherein the composition elicits a bactericidal antibody response against a *N. meningitidis* serogroup B strain expressing an ORF2086 variant that is homologous to the ORF2086 polypeptide.

C101. The composition according to clause C60, wherein the composition elicits a bactericidal antibody response against a *N. meningitidis* serogroup B strain expressing an ORF2086 variant that is heterologous to the ORF2086 polypeptide.

C102. The composition according to clause C60, further comprising at least one conjugate selected from: a) a conjugate of a capsular saccharide of *Neisseria meningitidis* serogroup A; b) a conjugate of a capsular saccharide of *Neisseria meningitidis* serogroup C; c) a conjugate of a capsular saccharide of *Neisseria*

meningitidis serogroup W135; and d) a conjugate of a capsular saccharide of *Neisseria meningitidis* serogroup Y.

- C103. The composition according to any one of clauses CC60-CC102, and a pharmaceutically acceptable excipient.
- C104. A method for inducing an immune response against *Neisseria meningitidis* in a mammal comprising administering to the mammal an effective amount of the composition according to any one of clauses CC60-CC103.
- C105. The method of clause C104, wherein the immune response comprises a bactericidal antibody.
- C106. The method of clause C104, wherein the immune response is equal to an immune response of a mammal administered with a corresponding lipidated ORF2086 polypeptide in the absence of a carrier polypeptide, when assessed under identical conditions.
- C107. The method of clause C104, wherein the immune response is greater than an immune response of a mammal administered with a corresponding non-lipidated ORF2086 polypeptide in the absence of a carrier polypeptide, when assessed under identical conditions.
- C108. The method of clause C104, wherein the immune response is at most 10% less than an immune response of a mammal administered with a corresponding lipidated ORF2086 polypeptide in the absence of a carrier polypeptide, when assessed under identical conditions.
- C109. The method of clause C104, wherein the immune response is at most 20% less than an immune response of a mammal administered with a corresponding lipidated ORF2086 polypeptide in the absence of a carrier polypeptide, when assessed under identical conditions.
- C110. An isolated polypeptide comprising SEQ ID NO: 2.
- C111. An isolated polypeptide comprising SEQ ID NO: 8.
- C112. An isolated polypeptide comprising SEQ ID NO: 14.
- C113. An isolated polypeptide comprising SEQ ID NO: 16.
- C114. An isolated polypeptide comprising SEQ ID NO: 18.
- C115. An isolated polypeptide comprising SEQ ID NO: 137.
- C116. An isolated polypeptide comprising SEQ ID NO: 139.
- C117. An isolated polypeptide comprising SEQ ID NO: 141.
- C118. An isolated polypeptide comprising SEQ ID NO: 143.
- C119. An isolated polypeptide comprising SEQ ID NO: 145.

- C120. An isolated polypeptide comprising SEQ ID NO: 149.
- C121. An isolated polypeptide comprising SEQ ID NO: 153.
- C122. A fusion polypeptide comprising SEQ ID NO: 1 operably linked to any one sequence set forth in SEQ ID NO: 42 to SEQ ID NO: 61.
- C123. A fusion polypeptide comprising SEQ ID NO: 147 operably linked to any one sequence set forth in SEQ ID NO: 42 to SEQ ID NO: 61.
- C124. A fusion polypeptide comprising SEQ ID NO: 151 operably linked to any one sequence set forth in SEQ ID NO: 42 to SEQ ID NO: 61.
- C125. A fusion polypeptide comprising SEQ ID NO: 10 operably linked to any one sequence set forth in SEQ ID NO: 42 to SEQ ID NO: 61.
- C126. A fusion polypeptide comprising SEQ ID NO: 155 operably linked to any one sequence set forth in SEQ ID NO: 42 to SEQ ID NO: 61.
- C127. A composition comprising a streptococcal C5a peptidase (SCP) from *Streptococcus pyogenes* conjugated to a polypeptide having the amino acid sequence of SEQ ID NO: 156.
- C128. A composition comprising a streptococcal C5a peptidase (SCP) from *Streptococcus pyogenes* conjugated to a polypeptide having the amino acid sequence of SEQ ID NO: 157.
- C129. A composition comprising a streptococcal C5a peptidase (SCP) from *Streptococcus pyogenes* conjugated to a polypeptide having the amino acid sequence of SEQ ID NO: 158.
- C130. A composition comprising a pneumolysoid conjugated to a polypeptide having the amino acid sequence of SEQ ID NO: 156.
- C131. A composition comprising a pneumolysoid conjugated to a polypeptide having the amino acid sequence of SEQ ID NO: 157.
- C132. A composition comprising a pneumolysoid conjugated to a polypeptide having the amino acid sequence of SEQ ID NO: 158.
- C133. A composition comprising a first fusion polypeptide comprising a pneumolysoid operably linked to a non-lipidated ORF2086 A05 and a second fusion polypeptide comprising a pneumolysoid operably linked to a non-lipidated ORF2086 B01.
- C134. A composition comprising a first fusion polypeptide comprising the amino acid sequence of SEQ ID NO: 2 and a second fusion polypeptide comprising the amino acid sequence of SEQ ID NO: 139.

C135. A composition comprising a first fusion polypeptide comprising a pneumolysoid operably linked to a non-lipidated ORF2086 B01 and a second fusion polypeptide comprising a pneumolysoid operably linked to a non-lipidated ORF2086 B24.

C136. A composition comprising a first fusion polypeptide comprising a pneumolysoid operably linked to a non-lipidated ORF2086 B09 and a second fusion polypeptide comprising a pneumolysoid operably linked to a non-lipidated ORF2086 B44.

SEQUENCE LISTING IN ELECTRONIC FORM

In accordance with Section 111(1) of the Patent Rules, this description contains a sequence listing in electronic form in ASCII text format (file: 64680-1768 Seq 01-SEP-15 v1.txt).

A copy of the sequence listing in electronic form is available from the Canadian Intellectual Property Office.

The sequences in the sequence listing in electronic form are reproduced in the following table.

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His	Ser	Ala	Val	Ala	Leu	Gln	Ile	Glu	Lys	Ile	Asn	Asn	Pro	Asp	
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Lys	Ile	Asp	Ser	Leu	Ile	Asn	Gln	Arg	Ser	Phe	Leu	Val	Ser	Gly	Leu
	595					600					605				
Gly	Gly	Glu	His	Thr	Ala	Phe	Asn	Gln	Leu	Pro	Ser	Gly	Lys	Ala	Glu
	610				615						620				
Tyr	His	Gly	Lys	Ala	Phe	Ser	Ser	Asp	Asp	Ala	Gly	Gly	Lys	Leu	Thr
625				630				635						640	
Tyr	Thr	Ile	Asp	Phe	Ala	Ala	Lys	Gln	Gly	His	Gly	Lys	Ile	Glu	His
			645					650						655	
Leu	Lys	Thr	Pro	Glu	Gln	Asn	Val	Glu	Leu	Ala	Ser	Ala	Glu	Leu	Lys
		660				665						670			
Ala	Asp	Glu	Lys	Ser	His	Ala	Val	Ile	Leu	Gly	Asp	Thr	Arg	Tyr	Gly
	675					680					685				
Ser	Glu	Glu	Lys	Gly	Thr	Tyr	His	Leu	Ala	Leu	Phe	Gly	Asp	Arg	Ala
	690				695						700				
Gln	Glu	Ile	Ala	Gly	Ser	Ala	Thr	Val	Lys	Ile	Arg	Glu	Lys	Val	His
705				710				715						720	
Glu	Ile	Gly	Ile	Ala	Gly	Lys	Gln								
			725												

<210> 3
 <211> 1410
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic sequence

<400> 3

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gatgagtttg	ttgttatcga	aagaaagaag	cggagcttgt	cgacaaatac	aagtgatatt	180
tctgtaacag	ctaccaacga	cagtcgcctc	tatcctggag	cacttctcgt	agtggatgag	240
accttgttag	agaataatcc	cactcttctt	gcggttgata	gtgctccgat	gacttatagt	300
attgattttgc	ctggttttggc	aagtagcgat	agctttctcc	aagtggaaga	ccccagcaat	360
tcaagtgttc	gcggagcggg	aaacgatttg	ttggctaagt	ggcatcaaga	ttatggtcag	420
gtcaataatg	tcccaatgca	gtatgaaaaa	ataacggctc	acagcatgga	acaactcaag	480
gtcaagtttg	gttctgactt	tgaaaagaca	gggaattctc	ttgatattga	ttttaactct	540
gtccattcag	gtgaaaagca	gattcagatt	gttaatttta	agcagattta	ttatacagtc	600
agcgtagacg	ctgttaaaaa	tccaggagat	gtgtttcaag	atactgtaac	ggtagaggat	660
ttaaaacaga	gaggaatttc	tgcagagcgt	cctttgggtct	atatttcgag	tgttgcttat	720
gggcgcccaag	tctatctcaa	gttggaacc	acgagtaaga	gtgatgaagt	agaggctgct	780
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gacaatacag	aagtgaaggc	ggttatttta	gggggcgacc	caagttcggg	tgcccagagt	900
gtaacaggca	aggtggatat	ggtagaggac	ttgattcaag	aaggcagtcg	ctttacagca	960
gatcatccag	gcttgccgat	ttcctataca	acttcttttt	tacgtgacaa	tgtagttgcg	1020
acctttcaaa	acagtacaga	ctatgttgag	actaaggtta	cagcttacag	aaacggagat	1080
ttactgctgg	atcatagtgg	tgcctatggt	gcccataatt	atattacttg	ggatgaatta	1140
tcctatgata	atcaaggtaa	ggaagtcttg	actcctaagg	cttgggacag	aaatgggcag	1200
gatttgacgg	ctcactttac	cactagtatt	cctttaaaag	ggaatgttcg	taatctctct	1260
gtcaaaaatta	gagagtgtac	cgggcttgcc	tgggaatggg	ggcgtagcgt	ttatgaaaaa	1320
accgattttgc	cactagtgcg	taagcggacg	atttctattt	ggggaacaac	tctctatcct	1380
caggtagagg	ataaggtaga	aaatgactag				1410

<210> 4

<211> 1280

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence

<400> 4

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gatgagtttg	ttgttatcga	aagaaagaag	cggagcttgt	cgacaaatac	aagtgatatt	180
tctgtaacag	ctaccaacga	cagtcgcctc	tatcctggag	cacttctcgt	agtggatgag	240
accttgttag	agaataatcc	cactcttctt	gcggttgata	gtgctccgat	gacttatagt	300
attgattttgc	ctggttttggc	aagtagcgat	agctttctcc	aagtggaaga	ccccagcaat	360
tcaagtgttc	gcggagcggg	aaacgatttg	ttggctaagt	ggcatcaaga	ttatggtcag	420
gtcaataatg	tcccaatgca	gtatgaaaaa	ataacggctc	acagcatgga	acaactcaag	480
gtcaagtttg	gttctgactt	tgaaaagaca	gggaattctc	ttgatattga	ttttaactct	540
gtccattcag	gtgaaaagca	gattcagatt	gttaatttta	agcagattta	ttatacagtc	600
agcgtagacg	ctgttaaaaa	tccaggagat	gtgtttcaag	atactgtaac	ggtagaggat	660
ttaaaacaga	gaggaatttc	tgcagagcgt	cctttgggtct	atatttcgag	tgttgcttat	720
gggcgcccaag	tctatctcaa	gttggaacc	acgagtaaga	gtgatgaagt	agaggctgct	780
tttgaggctt	tgataaaaagg	agtcaaggta	gctcctcaga	cagagtggaa	gcagattttg	840
gacaatacag	aagtgaaggc	ggttatttta	gggggcgacc	caagttcggg	tgcccagagt	900
gtaacaggca	aggtggatat	ggtagaggac	ttgattcaag	aaggcagtcg	ctttacagca	960
gatcatccag	gcttgccgat	ttcctataca	acttcttttt	tacgtgacaa	tgtagttgcg	1020
acctttcaaa	acagtacaga	ctatgttgag	actaaggtta	cagcttacag	aaacggagat	1080

ttactgctgg atcatagtgg tgcctatggt gcccaatatt atattacttg ggatgaatta	1140
tcctatgatc atcaaggtaa ggaagtcttg actcctaagg cttgggacag aaatgggcag	1200
gatttgacgg ctcactttac cactagtatt cctttaaaag ggaatgttcg taatctctct	1260
gtcaaaatta gagagtgtac	1280

<210> 5
 <211> 260
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 5
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 1 5 10 15
 Thr Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys
 20 25 30
 Gly Leu Lys Ser Leu Thr Leu Glu Asp Ser Ile Ser Gln Asn Gly Thr
 35 40 45
 Leu Thr Leu Ser Ala Gln Gly Ala Glu Lys Thr Phe Lys Val Gly Asp
 50 55 60
 Lys Asp Asn Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Ile Ser
 65 70 75 80
 Arg Phe Asp Phe Val Gln Lys Ile Glu Val Asp Gly Gln Thr Ile Thr
 85 90 95
 Leu Ala Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asp His Ser Ala Val
 100 105 110
 Val Ala Leu Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser
 115 120 125
 Leu Ile Asn Gln Arg Ser Phe Leu Val Ser Gly Leu Gly Gly Glu His
 130 135 140
 Thr Ala Phe Asn Gln Leu Pro Ser Gly Lys Ala Glu Tyr His Gly Lys
 145 150 155 160
 Ala Phe Ser Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp
 165 170 175
 Phe Ala Ala Lys Gln Gly His Gly Lys Ile Glu His Leu Lys Thr Pro
 180 185 190
 Glu Gln Asn Val Glu Leu Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys
 195 200 205
 Ser His Ala Val Ile Leu Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys
 210 215 220
 Gly Thr Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala
 225 230 235 240
 Gly Ser Ala Thr Val Lys Ile Arg Glu Lys Val His Glu Ile Gly Ile
 245 250 255
 Ala Gly Lys Gln
 260

<210> 6
 <211> 786
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic sequence

<400> 6

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gaagattcta	tttcacaaaa	tggcaccctt	accttgtecg	cgcaaggcgc	tgaaaaaact	180
tttaaagtcg	gtgacaaaga	taatagctta	aatacaggta	aactcaaaaa	tgataaaaatc	240
tcgcgttttg	atttcgtgca	aaaaatcgaa	gtagatggcc	aaaccattac	attagcaagc	300
ggtgaattcc	aaatatataa	acaagaccat	tcagcagtcg	ttgcattgca	aattgaaaaa	360
atcaacaacc	ccgacaaaat	cgacagcctg	ataaaccaac	gttccttcct	tgtcagcggt	420
ttgggcgggtg	aacatacagc	cttcaaccaa	ttaccaagcg	gcaaagcgga	gtatcacggt	480
aaagcattta	gctcagatga	tgcaggcggt	aaattaactt	atacaattga	ctttgcagca	540
aaacaaggac	atggcaaaaat	tgaacattta	aaaacacccg	aacagaacgt	agagctcgca	600
tccgcagAAC	tcaaagcaga	tgaaaaatca	cacgcagtcA	ttttgggtga	cacgcgctac	660
ggcagcgaag	aaaaaggtac	ttaccactta	gctctttttg	gcgaccgagc	tcaagaaatc	720
gcaggtagcg	caaccgtaaa	gataagggaa	aaggttcacg	aaattgggat	cgcgggcaaa	780
caataa						786

<210> 7

<211> 2199

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence

<400> 7

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gaagattcta	tttcacaaaa	tggcaccctt	accttgtecg	cgcaaggcgc	tgaaaaaact	180
tttaaagtcg	gtgacaaaga	taatagctta	aatacaggta	aactcaaaaa	tgataaaaatc	240
tcgcgttttg	atttcgtgca	aaaaatcgaa	gtagatggcc	aaaccattac	attagcaagc	300
ggtgaattcc	aaatatataa	acaagaccat	tcagcagtcg	ttgcattgca	aattgaaaaa	360
atcaacaacc	ccgacaaaat	cgacagcctg	ataaaccaac	gttccttcct	tgtcagcggt	420
ttgggcgggtg	aacatacagc	cttcaaccaa	ttaccaagcg	gcaaagcgga	gtatcacggt	480
aaagcattta	gctcagatga	tgcaggcggt	aaattaactt	atacaattga	ctttgcagca	540
aaacaaggac	atggcaaaaat	tgaacattta	aaaacacccg	aacagaacgt	agagctcgca	600
tccgcagAAC	tcaaagcaga	tgaaaaatca	cacgcagtcA	ttttgggtga	cacgcgctac	660
ggcagcgaag	aaaaaggtac	ttaccactta	gctctttttg	gcgaccgagc	tcaagaaatc	720
gcaggtagcg	caaccgtaaa	gataagggaa	aaggttcacg	aaattgggat	cgcgggcaaa	780
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cagctacccg	atgagtttgt	tgttatcgaa	agaaagaagc	ggagcttgtc	gacaaataca	960
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gtggatgaga	ccttgttaga	gaataatccc	actcttcttg	cggttgatcg	tgctccgatg	1080
acttatagta	ttgatttgcc	tggtttgcca	agtagcgata	gctttctcca	agtggaagac	1140
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caactcaagg	tcaagttttg	ttctgacttt	gaaaagacag	ggaattctct	tgatattgat	1320
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gttgcttatg	ggcgccaagt	ctatctcaag	ttggaaacca	cgagtaagag	tgatgaagta	1560
gaggctgctt	ttgaggcttt	gataaaaagga	gtcaaggtag	ctcctcagac	agagtggag	1620
cagatttttg	acaatacaga	agtgaaggcg	gttatttttag	ggggcgaccc	aagttcgggt	1680

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gcccagagttg taacaggcaa ggtggatatg gtagaggact tgattcaaga aggcagtcgc 1740
tttacagcag atcatccagg cttgccgatt tcctatacaa cttctttttt acgtgacaat 1800
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aacggagatt tactgctgga tcatagtggg gcctatgttg cccaatatta tattacttgg 1920
gatgaattat cctatgatca tcaaggtaag gaagtcttga ctccctaaggc ttgggacaga 1980
aatgggcagg atttgacggc tcaactttacc actagtattc ctttaaaagg gaatgttcgt 2040
aatctctctg tcaaaattag agagtgtacc gggcttgcct gggaatgggtg gcgtacgggt 2100
tatgaaaaaa ccgatttgcc actagtgcgt aagcggacga tttctatttg gggaacaact 2160
ctctatcttc aggtagagga taaggtagaa aatgactaa 2199

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<210> 8

<211> 731

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence

<400> 8

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Thr Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys
          20          25          30
Gly Leu Lys Ser Leu Thr Leu Glu Asp Ser Ile Ser Gln Asn Gly Thr
          35          40          45
Leu Thr Leu Ser Ala Gln Gly Ala Glu Lys Thr Phe Lys Val Gly Asp
          50          55          60
Lys Asp Asn Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Ile Ser
65          70          75          80
Arg Phe Asp Phe Val Gln Lys Ile Glu Val Asp Gly Gln Thr Ile Thr
          85          90          95
Leu Ala Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asp His Ser Ala Val
          100          105          110
Val Ala Leu Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser
          115          120          125
Leu Ile Asn Gln Arg Ser Phe Leu Val Ser Gly Leu Gly Gly Glu His
          130          135          140
Thr Ala Phe Asn Gln Leu Pro Ser Gly Lys Ala Glu Tyr His Gly Lys
          145          150          155          160
Ala Phe Ser Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp
          165          170          175
Phe Ala Ala Lys Gln Gly His Gly Lys Ile Glu His Leu Lys Thr Pro
          180          185          190
Glu Gln Asn Val Glu Leu Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys
          195          200          205
Ser His Ala Val Ile Leu Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys
          210          215          220
Gly Thr Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala
          225          230          235          240
Gly Ser Ala Thr Val Lys Ile Arg Glu Lys Val His Glu Ile Gly Ile
          245          250          255
Ala Gly Lys Gln Gly Ser Gly Ala Asn Lys Ala Val Asn Asp Phe Ile
          260          265          270
Leu Ala Met Asn Tyr Asp Lys Lys Lys Leu Leu Thr His Gln Gly Glu
          275          280          285

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Ser Ile Glu Asn Arg Phe Ile Lys Glu Gly Asn Gln Leu Pro Asp Glu
 290 295 300
 Phe Val Val Ile Glu Arg Lys Lys Arg Ser Leu Ser Thr Asn Thr Ser
 305 310 315 320
 Asp Ile Ser Val Thr Ala Thr Asn Asp Ser Arg Leu Tyr Pro Gly Ala
 325 330 335
 Leu Leu Val Val Asp Glu Thr Leu Leu Glu Asn Asn Pro Thr Leu Leu
 340 345 350
 Ala Val Asp Arg Ala Pro Met Thr Tyr Ser Ile Asp Leu Pro Gly Leu
 355 360 365
 Ala Ser Ser Asp Ser Phe Leu Gln Val Glu Asp Pro Ser Asn Ser Ser
 370 375 380
 Val Arg Gly Ala Val Asn Asp Leu Leu Ala Lys Trp His Gln Asp Tyr
 385 390 395 400
 Gly Gln Val Asn Asn Val Pro Met Gln Tyr Glu Lys Ile Thr Ala His
 405 410 415
 Ser Met Glu Gln Leu Lys Val Lys Phe Gly Ser Asp Phe Glu Lys Thr
 420 425 430
 Gly Asn Ser Leu Asp Ile Asp Phe Asn Ser Val His Ser Gly Glu Lys
 435 440 445
 Gln Ile Gln Ile Val Asn Phe Lys Gln Ile Tyr Tyr Thr Val Ser Val
 450 455 460
 Asp Ala Val Lys Asn Pro Gly Asp Val Phe Gln Asp Thr Val Thr Val
 465 470 475 480
 Glu Asp Leu Lys Gln Arg Gly Ile Ser Ala Glu Arg Pro Leu Val Tyr
 485 490 495
 Ile Ser Ser Val Ala Tyr Gly Arg Gln Val Tyr Leu Lys Leu Glu Thr
 500 505 510
 Thr Ser Lys Ser Asp Glu Val Glu Ala Ala Phe Glu Ala Leu Ile Lys
 515 520 525
 Gly Val Lys Val Ala Pro Gln Thr Glu Trp Lys Gln Ile Leu Asp Asn
 530 535 540
 Thr Glu Val Lys Ala Val Ile Leu Gly Gly Asp Pro Ser Ser Gly Ala
 545 550 555 560
 Arg Val Val Thr Gly Lys Val Asp Met Val Glu Asp Leu Ile Gln Glu
 565 570 575
 Gly Ser Arg Phe Thr Ala Asp His Pro Gly Leu Pro Ile Ser Tyr Thr
 580 585 590
 Thr Ser Phe Leu Arg Asp Asn Val Val Ala Thr Phe Gln Asn Ser Thr
 595 600 605
 Asp Tyr Val Glu Thr Lys Val Thr Ala Tyr Arg Asn Gly Asp Leu Leu
 610 615 620
 Leu Asp His Ser Gly Ala Tyr Val Ala Gln Tyr Tyr Ile Thr Trp Asp
 625 630 635 640
 Glu Leu Ser Tyr Asp His Gln Gly Lys Glu Val Leu Thr Pro Lys Ala
 645 650 655
 Trp Asp Arg Asn Gly Gln Asp Leu Thr Ala His Phe Thr Thr Ser Ile
 660 665 670
 Pro Leu Lys Gly Asn Val Arg Asn Leu Ser Val Lys Ile Arg Glu Cys
 675 680 685
 Thr Gly Leu Ala Trp Glu Trp Trp Arg Thr Val Tyr Glu Lys Thr Asp
 690 695 700
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 705 710 715 720
 Tyr Pro Gln Val Glu Asp Lys Val Glu Asn Asp
 725 730

<210> 9
 <211> 1608
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 9
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 ggtacacaag gaaattatga cgatgattgg aaagagtttt atagtaccga caataaatac 180
 gacgctgcgg gatactctgt agataatgaa aacctgcctc ctggaaaaagc tggaggcgtg 240
 gtcaaaagtga cgtatccagg actgacgaag gttctcgcac taaaagtggg taatgccgaa 300
 actattaaga aagagttagg tttaagtctc actgaaccgt tgatggagca agtcggaacg 360
 gaagagttta tcaaaagggt cggatgatgg gcttcgcgtg tagtgctcag ccttcccttc 420
 gctgagggga gttctagcgt tgaatatatt aataactggg aacaggcgaa agcgttaagc 480
 gtagaacttg agattaattt tgaaaccctg ggaaaacgtg gccaaagatgc gatgtatgag 540
 tatatggctc aagcctgtgc aggaatcgt gtcaggcgat cagtaggtag ctcatgtca 600
 tgcataaatc ttgattggga tgtcataagg gataaaacta agacaaagat agagtctttg 660
 aaagagcatg gccctatcaa aaataaaatg agcgaaagtc ccaataaaac agtatctgag 720
 gaaaaagcta aacaataact agaagaattt catcaaacgg cattagagca tcttgaattg 780
 tcagaactta aaaccgttac tgggaccaat cctgtattcg ctgggggctaa ctatgcggcg 840
 tgggcagtaa acgttgcgca agttatcgat agcgaaacag ctgataattt ggaaaagaca 900
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 ctggacgtta ataagtccaa gactcatatt tccgtaaatg gtcggaaaat aaggatgcgt 1380
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 aatggtgtgc atgcgaatct tcacgtggca tttcacagaa gcagctcgga gaaaattcat 1500
 tctaataaaa tttcatcgga tccataggc gttcttgggt accagaaaac agtagatcac 1560
 accaagggtta attctaagct atcgtatatt tttgaaatca aaagctga 1608

<210> 10
 <211> 535
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 10
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 20 25 30
 Lys Gly Ile Gln Lys Pro Lys Ser Gly Thr Gln Gly Asn Tyr Asp Asp
 35 40 45
 Asp Trp Lys Glu Phe Tyr Ser Thr Asp Asn Lys Tyr Asp Ala Ala Gly
 50 55 60
 Tyr Ser Val Asp Asn Glu Asn Pro Leu Ser Gly Lys Ala Gly Gly Val
 65 70 75 80

Gly Tyr Gln Lys Thr Val Asp His Thr Lys Val Asn Ser Lys Leu Ser
 515 520 525
 Leu Phe Phe Glu Ile Lys Ser
 530 535

<210> 11
 <211> 579
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 11
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 cacgggacta aacctgggta tgtagattcc attcaaaaag gtatacaaaa gccaaaatct 120
 ggtacacaag gaaattatga cgatgattgg aaagagtttt atagtaccga caataaatac 180
 gacgctgcgg gatactctgt agataatgaa aaccgcgtct ctggaaaagc tggaggcgtg 240
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 actattaaga aagagttagg tttaagtctc actgaaccgt tgatggagca agtcggaacg 360
 gaagagttta tcaaaagggt cggtgatggg gcttcgcgtg tagtgctcag ccttcccttc 420
 gctgagggga gttctagcgt tgaatatatt aataactggg aacaggcgaa agcgtaagc 480
 gtagaacttg agattaattt tgaaaccgct ggaaaacgtg gccaatgatgc gatgtatgag 540
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<210> 12
 <211> 193
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 12
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 Phe Ser Ser Tyr His Gly Thr Lys Pro Gly Tyr Val Asp Ser Ile Gln
 20 25 30
 Lys Gly Ile Gln Lys Pro Lys Ser Gly Thr Gln Gly Asn Tyr Asp Asp
 35 40 45
 Asp Trp Lys Glu Phe Tyr Ser Thr Asp Asn Lys Tyr Asp Ala Ala Gly
 50 55 60
 Tyr Ser Val Asp Asn Glu Asn Pro Leu Ser Gly Lys Ala Gly Gly Val
 65 70 75 80
 Val Lys Val Thr Tyr Pro Gly Leu Thr Lys Val Leu Ala Leu Lys Val
 85 90 95
 Asp Asn Ala Glu Thr Ile Lys Lys Glu Leu Gly Leu Ser Leu Thr Glu
 100 105 110
 Pro Leu Met Glu Gln Val Gly Thr Glu Glu Phe Ile Lys Arg Phe Gly
 115 120 125
 Asp Gly Ala Ser Arg Val Val Leu Ser Leu Pro Phe Ala Glu Gly Ser
 130 135 140
 Ser Ser Val Glu Tyr Ile Asn Asn Trp Glu Gln Ala Lys Ala Leu Ser
 145 150 155 160

Arg

<220>
<223> Synthetic sequence

89

<210> 14
 <211> 795
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 14
 Gly Ala Asp Asp Val Val Asp Ser Ser Lys Ser Phe Val Met Glu Asn
 1 5 10 15
 Phe Ser Ser Tyr His Gly Thr Lys Pro Gly Tyr Val Asp Ser Ile Gln
 20 25 30
 Lys Gly Ile Gln Lys Pro Lys Ser Gly Thr Gln Gly Asn Tyr Asp Asp
 35 40 45
 Asp Trp Lys Glu Phe Tyr Ser Thr Asp Asn Lys Tyr Asp Ala Ala Gly
 50 55 60
 Tyr Ser Val Asp Asn Glu Asn Pro Leu Ser Gly Lys Ala Gly Gly Val
 65 70 75 80
 Val Lys Val Thr Tyr Pro Gly Leu Thr Lys Val Leu Ala Leu Lys Val
 85 90 95
 Asp Asn Ala Glu Thr Ile Lys Lys Glu Leu Gly Leu Ser Leu Thr Glu
 100 105 110
 Pro Leu Met Glu Gln Val Gly Thr Glu Glu Phe Ile Lys Arg Phe Gly
 115 120 125
 Asp Gly Ala Ser Arg Val Val Leu Ser Leu Pro Phe Ala Glu Gly Ser
 130 135 140
 Ser Ser Val Glu Tyr Ile Asn Asn Trp Glu Gln Ala Lys Ala Leu Ser
 145 150 155 160
 Val Glu Leu Glu Ile Asn Phe Glu Thr Arg Gly Lys Arg Gly Gln Asp
 165 170 175
 Ala Met Tyr Glu Tyr Met Ala Gln Ala Cys Ala Gly Asn Arg Val Arg
 180 185 190
 Arg Ser Val Gly Ser Ser Leu Ser Cys Ile Asn Leu Asp Trp Asp Val
 195 200 205
 Ile Arg Asp Lys Thr Lys Thr Lys Ile Glu Ser Leu Lys Glu His Gly
 210 215 220
 Pro Ile Lys Asn Lys Met Ser Glu Ser Pro Asn Lys Thr Val Ser Glu
 225 230 235 240
 Glu Lys Ala Lys Gln Tyr Leu Glu Glu Phe His Gln Thr Ala Leu Glu
 245 250 255
 His Pro Glu Leu Ser Glu Leu Lys Thr Val Thr Gly Thr Asn Pro Val
 260 265 270
 Phe Ala Gly Ala Asn Tyr Ala Ala Trp Ala Val Asn Val Ala Gln Val
 275 280 285
 Ile Asp Ser Glu Thr Ala Asp Asn Leu Glu Lys Thr Ala Ala Ala Leu
 290 295 300
 Ser Ile Leu Pro Gly Ile Gly Ser Val Met Gly Ile Ala Asp Gly Ala
 305 310 315 320
 Val His His Asn Thr Glu Glu Ile Val Ala Gln Ser Ile Ala Leu Ser
 325 330 335
 Ser Leu Met Val Ala Gln Ala Ile Pro Leu Val Gly Glu Leu Val Asp
 340 345 350
 Ile Gly Phe Ala Ala Tyr Asn Phe Val Glu Ser Ile Ile Asn Leu Phe
 355 360 365
 Gln Val Val His Asn Ser Tyr Asn Arg Pro Ala Tyr Ser Pro Gly His
 370 375 380

Lys Thr Gln Pro Phe Leu His Asp Gly Tyr Ala Val Ser Trp Asn Thr
 385 390 395 400
 Val Glu Asp Ser Ile Ile Arg Thr Gly Phe Gln Gly Glu Ser Gly His
 405 410 415
 Asp Ile Lys Ile Thr Ala Glu Asn Thr Pro Leu Pro Ile Ala Gly Val
 420 425 430
 Leu Leu Pro Thr Ile Pro Gly Lys Leu Asp Val Asn Lys Ser Lys Thr
 435 440 445
 His Ile Ser Val Asn Gly Arg Lys Ile Arg Met Arg Cys Arg Ala Ile
 450 455 460
 Asp Gly Asp Val Thr Phe Cys Arg Leu Lys Ser Pro Val Tyr Val Gly
 465 470 475 480
 Asn Gly Val His Ala Asn Leu His Val Ala Phe His Arg Ser Ser Ser
 485 490 495
 Glu Lys Ile His Ser Asn Glu Ile Ser Ser Asp Ser Ile Gly Val Leu
 500 505 510
 Gly Tyr Gln Lys Thr Val Asp His Thr Lys Val Asn Ser Lys Leu Ser
 515 520 525
 Leu Phe Phe Glu Ile Lys Ser Ser Ser Gly Ser Gly Ser Gly Gly Gly
 530 535 540
 Gly Val Ala Ala Asp Ile Gly Thr Gly Leu Ala Asp Ala Leu Thr Ala
 545 550 555 560
 Pro Leu Asp His Lys Asp Lys Gly Leu Lys Ser Leu Thr Leu Glu Asp
 565 570 575
 Ser Ile Ser Gln Asn Gly Thr Leu Thr Leu Ser Ala Gln Gly Ala Glu
 580 585 590
 Lys Thr Phe Lys Val Gly Asp Lys Asp Asn Ser Leu Asn Thr Gly Lys
 595 600 605
 Leu Lys Asn Asp Lys Ile Ser Arg Phe Asp Phe Val Gln Lys Ile Glu
 610 615 620
 Val Asp Gly Gln Thr Ile Thr Leu Ala Ser Gly Glu Phe Gln Ile Tyr
 625 630 635 640
 Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu Lys Ile Asn
 645 650 655
 Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser Phe Leu Val
 660 665 670
 Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu Pro Ser Gly
 675 680 685
 Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp Ala Gly Gly
 690 695 700
 Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly His Gly Lys
 705 710 715 720
 Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu Ala Ser Ala
 725 730 735
 Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu Gly Asp Thr
 740 745 750
 Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu Ala Leu Phe Gly
 755 760 765
 Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys Ile Arg Glu
 770 775 780
 Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 785 790 795

<210> 15

<211> 2400

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence

<400> 15

atgagctctg	gaagcgggaag	cgggggcggt	ggagttgcag	cagacattgg	aacaggatta	60
gcagatgcac	tgacggcacc	gttggatcat	aaagacaaag	gcttgaaatc	gcttacctta	120
gaagattcta	tttcacaaaa	tggcaccctt	accttgtccg	cgcaaggcgc	tgaaaaaact	180
tttaaagtcg	gtgacaaaga	taatagctta	aatacaggta	aactcaaaaa	tgataaaatc	240
tcgcgttttg	atttcgtgca	aaaaatcgaa	gtagatggcc	aaaccattac	attagcaagc	300
ggtgaattcc	aaatatataa	acaagaccat	tcagcagtcg	ttgcattgca	aattgaaaaa	360
atcaacaacc	cgcacaaaat	cgacagcctg	ataaaccaac	gttccttcct	tgtcagcggg	420
ttgggcgggt	aacatacagc	cttcaaccaa	ttaccaagcg	gcaaagcgga	gtatcacggg	480
aaagcattta	gctcagatga	tgcaggcggg	aaattaactt	atacaattga	ctttgcagca	540
aaacaaggac	atggcaaaaat	tgaacattta	aaaacacccg	aacagaacgt	agagctcgca	600
tcgcgagAAC	tcaaagcaga	tgaaaaatca	cacgcagtea	ttttgggtga	cacgcgctac	660
ggcagcgaag	aaaaaggtac	ttaccactta	gctctttttg	gcgaccgagc	tcaagaaatc	720
gcaggtagcg	caaccgtaaa	gataagggaa	aaggttcacg	aaattgggat	cgccgggcaa	780
caaggaagcg	gtggcgctga	tgatgttggt	gattcttcta	aatcttttgt	gatggaaaac	840
ttttcttcgt	accacgggac	taaacctggg	tatgtagatt	ccattcaaaa	aggtatacaa	900
aagccaaaat	ctggtacaca	aggaaattat	gacgatgatt	ggaaagagtt	ttatagtacc	960
gacaataaat	acgacgctgc	gggatactct	gtagataatg	aaaacccgct	ctctggaaaa	1020
gctggaggcg	tgggtcaaagt	gacgtatcca	ggactgacga	aggttctcgc	actaaaagtg	1080
gataatgccg	aaactattaa	gaaagagtta	ggtttaagtc	tcactgaacc	gttgatggag	1140
caagtcggaa	cggaagagtt	tatcaaaaag	ttcggtgatg	gtgcttcgcg	tgtagtgctc	1200
agccttcctc	tcgctgaggg	gagttctagc	gttgaatata	ttaataactg	ggaacaggcg	1260
aaagcgttaa	gcgtagaact	tgagattaat	tttgaaaccc	gtggaaaacg	tgGCCaagat	1320
gcgatgtatg	agtatatggc	tcaagcctgt	gcaggaaatc	gtgtcaggcg	atcagtaggt	1380
agctcattgt	calgcataaa	tcttgattgg	galgtcataa	gggataaaaac	taagacaaaag	1440
atagagtctt	tgaagagagc	tggccctatc	aaaaataaaa	tgagcgaag	tcccaataaa	1500
acagtatctg	aggaaaaagc	taaacaatac	ctagaagaat	ttcatcaaac	ggcattagag	1560
catcctgaat	tgtcagaact	taaaaccggt	actgggacca	atcctgtatt	cgctggggct	1620
aactatgcgg	cgtgggcagt	aaacgttgcg	caagttatcg	atagcgaaac	agctgataat	1680
ttggaaaaga	caactgctgc	tctttcgata	cttcctggta	tcggtagcgt	aatgggcatt	1740
gcagacgggt	ccgttcacca	caatacagaa	gagatagtgg	cacaatcaat	agctttatcg	1800
tctttaatgg	ttgctcaage	tattccattg	gtaggagagc	tagttgatat	tggtttcgcg	1860
gcatataatt	ttgtagagag	tattatcaat	ttatttcaag	tagttcataa	ttcgtataat	1920
cgccccgcgt	attctccggg	gcataaaaacg	caaccatttc	ttcatgacgg	gtatgctgtc	1980
agttggaaca	ctggtgaaga	ttcgataatc	cgaactgggt	ttcaagggga	gagtgggcac	2040
gacataaaaa	ttactgctga	aaataccccg	cttccaatcg	cgggtgtcct	actaccgact	2100
attcctggaa	agctggacgt	taataagtcg	aagactcata	tttccgtaaa	tggtcggaaa	2160
ataaggatgc	gttgcagagc	tatagacggg	gatgtaactt	tttgctgccc	taaatctcct	2220
gtttatgttg	gtaatgggtg	gcatgcgaat	cttcacgtgg	catttcacag	aagcagctcg	2280
gagaaaattc	attctaataa	aatttcgctg	gattccatag	gcgttcttgg	gtaccagaaa	2340
acagtagatc	acaccaaggt	taattctaag	ctatcgctat	tttttgaaat	caaaagctaa	2400

<210> 16

<211> 798

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence

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<400> 16
Ser Ser Gly Ser Gly Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly
1      5      10      15
Thr Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys
20      25      30
Gly Leu Lys Ser Leu Thr Leu Glu Asp Ser Ile Ser Gln Asn Gly Thr
35      40      45
Leu Thr Leu Ser Ala Gln Gly Ala Glu Lys Thr Phe Lys Val Gly Asp
50      55      60
Lys Asp Asn Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Ile Ser
65      70      75      80
Arg Phe Asp Phe Val Gln Lys Ile Glu Val Asp Gly Gln Thr Ile Thr
85      90      95
Leu Ala Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asp His Ser Ala Val
100     105     110
Val Ala Leu Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser
115     120     125
Leu Ile Asn Gln Arg Ser Phe Leu Val Ser Gly Leu Gly Gly Glu His
130     135     140
Thr Ala Phe Asn Gln Leu Pro Ser Gly Lys Ala Glu Tyr His Gly Lys
145     150     155     160
Ala Phe Ser Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp
165     170     175
Phe Ala Ala Lys Gln Gly His Gly Lys Ile Glu His Leu Lys Thr Pro
180     185     190
Glu Gln Asn Val Glu Leu Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys
195     200     205
Ser His Ala Val Ile Leu Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys
210     215     220
Gly Thr Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala
225     230     235     240
Gly Ser Ala Thr Val Lys Ile Arg Glu Lys Val His Glu Ile Gly Ile
245     250     255
Ala Gly Lys Gln Gly Ser Gly Gly Ala Asp Asp Val Val Asp Ser Ser
260     265     270
Lys Ser Phe Val Met Glu Asn Phe Ser Ser Tyr His Gly Thr Lys Pro
275     280     285
Gly Tyr Val Asp Ser Ile Gln Lys Gly Ile Gln Lys Pro Lys Ser Gly
290     295     300
Thr Gln Gly Asn Tyr Asp Asp Asp Trp Lys Glu Phe Tyr Ser Thr Asp
305     310     315     320
Asn Lys Tyr Asp Ala Ala Gly Tyr Ser Val Asp Asn Glu Asn Pro Leu
325     330     335
Ser Gly Lys Ala Gly Gly Val Val Lys Val Thr Tyr Pro Gly Leu Thr
340     345     350
Lys Val Leu Ala Leu Lys Val Asp Asn Ala Glu Thr Ile Lys Lys Glu
355     360     365
Leu Gly Leu Ser Leu Thr Glu Pro Leu Met Glu Gln Val Gly Thr Glu
370     375     380
Glu Phe Ile Lys Arg Phe Gly Asp Gly Ala Ser Arg Val Val Leu Ser
385     390     395     400
Leu Pro Phe Ala Glu Gly Ser Ser Ser Val Glu Tyr Ile Asn Asn Trp
405     410     415
Glu Gln Ala Lys Ala Leu Ser Val Glu Leu Glu Ile Asn Phe Glu Thr
420     425     430
Arg Gly Lys Arg Gly Gln Asp Ala Met Tyr Glu Tyr Met Ala Gln Ala
435     440     445

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Cys Ala Gly Asn Arg Val Arg Arg Ser Val Gly Ser Ser Leu Ser Cys
 450 455 460
 Ile Asn Leu Asp Trp Asp Val Ile Arg Asp Lys Thr Lys Thr Lys Ile
 465 470 475 480
 Glu Ser Leu Lys Glu His Gly Pro Ile Lys Asn Lys Met Ser Glu Ser
 485 490 495
 Pro Asn Lys Thr Val Ser Glu Glu Lys Ala Lys Gln Tyr Leu Glu Glu
 500 505 510
 Phe His Gln Thr Ala Leu Glu His Pro Glu Leu Ser Glu Leu Lys Thr
 515 520 525
 Val Thr Gly Thr Asn Pro Val Phe Ala Gly Ala Asn Tyr Ala Ala Trp
 530 535 540
 Ala Val Asn Val Ala Gln Val Ile Asp Ser Glu Thr Ala Asp Asn Leu
 545 550 555 560
 Glu Lys Thr Thr Ala Ala Leu Ser Ile Leu Pro Gly Ile Gly Ser Val
 565 570 575
 Met Gly Ile Ala Asp Gly Ala Val His His Asn Thr Glu Glu Ile Val
 580 585 590
 Ala Gln Ser Ile Ala Leu Ser Ser Leu Met Val Ala Gln Ala Ile Pro
 595 600 605
 Leu Val Gly Glu Leu Val Asp Ile Gly Phe Ala Ala Tyr Asn Phe Val
 610 615 620
 Glu Ser Ile Ile Asn Leu Phe Gln Val Val His Asn Ser Tyr Asn Arg
 625 630 635 640
 Pro Ala Tyr Ser Pro Gly His Lys Thr Gln Pro Phe Leu His Asp Gly
 645 650 655
 Tyr Ala Val Ser Trp Asn Thr Val Glu Asp Ser Ile Ile Arg Thr Gly
 660 665 670
 Phe Gln Gly Glu Ser Gly His Asp Ile Lys Ile Thr Ala Glu Asn Thr
 675 680 685
 Pro Leu Pro Ile Ala Gly Val Leu Leu Pro Thr Ile Pro Gly Lys Leu
 690 695 700
 Asp Val Asn Lys Ser Lys Thr His Ile Ser Val Asn Gly Arg Lys Ile
 705 710 715 720
 Arg Met Arg Cys Arg Ala Ile Asp Gly Asp Val Thr Phe Cys Arg Pro
 725 730 735
 Lys Ser Pro Val Tyr Val Gly Asn Gly Val His Ala Asn Leu His Val
 740 745 750
 Ala Phe His Arg Ser Ser Ser Glu Lys Ile His Ser Asn Glu Ile Ser
 755 760 765
 Ser Asp Ser Ile Gly Val Leu Gly Tyr Gln Lys Thr Val Asp His Thr
 770 775 780
 Lys Val Asn Ser Lys Leu Ser Leu Phe Phe Glu Ile Lys Ser
 785 790 795

<210> 17

<211> 1365

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence

<400> 17

atgggcgctg atgatgttgt tgattcttct aaatcttttg tgatggaaaa cttttcttcg
 taccacggga ctaaacctgg ttatgtagat tccattcaaa aaggtataca aaagccaaaa

60

120

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tctggtacac aaggaaatta tgacgatgat tggaaagagt tttatagtac cgacaataaa 180
tacgacgctg cgggatactc tgtagataat gaaaacccgc tctctggaaa agctggaggc 240
gtggtcaaag tgacgtatcc aggactgacg aaggttctcg cactaaaagt ggataatgcc 300
gaaactatta agaaagagtt aggtttaagt ctcaactgaac cgttgatgga gcaagtcgga 360
acggaagagt ttatcaaaag gttegggtgat ggtgcttcgc gtgtagtgct cagccttccc 420
ttcgctgagg ggagttctag cgttgaatat attaataact gggaacaggc gaaagcgta 480
agcgtagaac ttgagattaa ttttgaaacc cgtggaaaac gtggccaaga tgcgatgtat 540
gagtatatgg ctcaagcctg tgcaggaaat cgtgtcaggc gaagctctgg aagcggaagc 600
gggggcggtg gagttgcagc agacattgga acaggattag cagatgcact gacggcaccg 660
ttggatcata aagacaaagg cttgaaatcg cttaccttag aagattctat ttcacaaaat 720
ggcaccctta ccttgtcgcg gcaaggcgct gaaaaaactt ttaaagtcgg tgacagagat 780
aatagcttaa atacaggtaa actcaaaaat gataaaatct cgcgttttga tttcgtgcaa 840
aaaatcgaag tagatggcca aaccattaca ttagcaagcg gtgaattcca aatatataaa 900
caagaccatt cagcagtcgt tgcattgcaa attgaaaaaa tcaacaaccc cgacaaaatc 960
gacagcctga taaaccaacg ttccttcctt gtcagcgggt tgggcggtga acatacagcc 1020
ttcaaccaat taccaagcgg caaagcggag tatcacggta aagcatttag ctcagatgat 1080
gcaggcggta aattaactta tacaattgac tttgcagcaa aacaaggaca tggcaaaatt 1140
gaacatttaa aaacacccga acagaacgta gagctcgcaa ccgcagaact caaagcagat 1200
gaaaaatcac acgcagtcac tttgggtgac acgcgctacg gcagcgaaga aaaaggtact 1260
taccacttag ctcttttttg cgaccgagct caagaaatcg caggtagcgc aaccgtaaag 1320
ataagggaaa aggttcacga aattgggatc gcgggcaaac aataa 1365

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<210> 18

<211> 453

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence

<400> 18

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

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Arg Ser Ser Gly Ser Gly Ser Gly Gly Gly Gly Val Ala Ala Asp Ile
 195 200 205
 Gly Thr Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp
 210 215 220
 Lys Gly Leu Lys Ser Leu Thr Leu Glu Asp Ser Ile Ser Gln Asn Gly
 225 230 235 240
 Thr Leu Thr Leu Ser Ala Gln Gly Ala Glu Lys Thr Phe Lys Val Gly
 245 250 255
 Asp Arg Asp Asn Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Ile
 260 265 270
 Ser Arg Phe Asp Phe Val Gln Lys Ile Glu Val Asp Gly Gln Thr Ile
 275 280 285
 Thr Leu Ala Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asp His Ser Ala
 290 295 300
 Val Val Ala Leu Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp
 305 310 315 320
 Ser Leu Ile Asn Gln Arg Ser Phe Leu Val Ser Gly Leu Gly Gly Glu
 325 330 335
 His Thr Ala Phe Asn Gln Leu Pro Ser Gly Lys Ala Glu Tyr His Gly
 340 345 350
 Lys Ala Phe Ser Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile
 355 360 365
 Asp Phe Ala Ala Lys Gln Gly His Gly Lys Ile Glu His Leu Lys Thr
 370 375 380
 Pro Glu Gln Asn Val Glu Leu Ala Thr Ala Glu Leu Lys Ala Asp Glu
 385 390 395 400
 Lys Ser His Ala Val Ile Leu Gly Asp Thr Arg Tyr Gly Ser Glu Glu
 405 410 415
 Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile
 420 425 430
 Ala Gly Ser Ala Thr Val Lys Ile Arg Glu Lys Val His Glu Ile Gly
 435 440 445
 Ile Ala Gly Lys Gln
 450

<210> 19
 <211> 258
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 19
 Cys Gly Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Thr Gly
 1 5 10 15
 Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Gly Leu
 20 25 30
 Lys Ser Leu Thr Leu Glu Asp Ser Ile Ser Gln Asn Gly Thr Leu Thr
 35 40 45
 Leu Ser Ala Gln Gly Ala Glu Lys Thr Phe Lys Val Gly Asp Lys Asp
 50 55 60
 Asn Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Ile Ser Arg Phe
 65 70 75 80
 Asp Phe Val Gln Lys Ile Glu Val Asp Gly Gln Thr Ile Thr Leu Ala
 85 90 95

Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala
 100 105 110
 Leu Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile
 115 120 125
 Asn Gln Arg Ser Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala
 130 135 140
 Phe Asn Gln Leu Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe
 145 150 155 160
 Ser Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala
 165 170 175
 Ala Lys Gln Gly His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln
 180 185 190
 Asn Val Glu Leu Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His
 195 200 205
 Ala Val Ile Leu Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr
 210 215 220
 Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser
 225 230 235 240
 Ala Thr Val Lys Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly
 245 250 255
 Lys Gln

<210> 20
 <211> 260
 <212> PRT
 <213> Neisseria meningitidis (group B)

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

Gly Ser Tyr Ser Leu Gly Ile Phe Gly Glu Lys Ala Gln Glu Val Ala
 225 230 235 240
 Gly Ser Ala Glu Val Glu Thr Ala Asn Gly Ile His His Ile Gly Leu
 245 250 255
 Ala Ala Lys Gln
 260

<210> 21
 <211> 471
 <212> PRT
 <213> Streptococcus pneumoniae

<400> 21
 Met Ala Asn Lys Ala Val Asn Asp Phe Ile Leu Ala Met Asn Tyr Asp
 1 5 10 15
 Lys Lys Lys Leu Leu Thr His Gln Gly Glu Ser Ile Glu Asn Arg Phe
 20 25 30
 Ile Lys Glu Gly Asn Gln Leu Pro Asp Glu Phe Val Val Ile Glu Arg
 35 40 45
 Lys Lys Arg Ser Leu Ser Thr Asn Thr Ser Asp Ile Ser Val Thr Ala
 50 55 60
 Thr Asn Asp Ser Arg Leu Tyr Pro Gly Ala Leu Leu Val Val Asp Glu
 65 70 75 80
 Thr Leu Leu Glu Asn Asn Pro Thr Leu Leu Ala Val Asp Arg Ala Pro
 85 90 95
 Met Thr Tyr Ser Ile Asp Leu Pro Gly Leu Ala Ser Ser Asp Ser Phe
 100 105 110
 Leu Gln Val Glu Asp Pro Ser Asn Ser Ser Val Arg Gly Ala Val Asn
 115 120 125
 Asp Leu Leu Ala Lys Trp His Gln Asp Tyr Gly Gln Val Asn Asn Val
 130 135 140
 Pro Ala Arg Met Gln Tyr Glu Lys Ile Thr Ala His Ser Met Glu Gln
 145 150 155 160
 Leu Lys Val Lys Phe Gly Ser Asp Phe Glu Lys Thr Gly Asn Ser Leu
 165 170 175
 Asp Ile Asp Phe Asn Ser Val His Ser Gly Glu Lys Gln Ile Gln Ile
 180 185 190
 Val Asn Phe Lys Gln Ile Tyr Tyr Thr Val Ser Val Asp Ala Val Lys
 195 200 205
 Asn Pro Gly Asp Val Phe Gln Asp Thr Val Thr Val Glu Asp Leu Lys
 210 215 220
 Gln Arg Gly Ile Ser Ala Glu Arg Pro Leu Val Tyr Ile Ser Ser Val
 225 230 235 240
 Ala Tyr Gly Arg Gln Val Tyr Leu Lys Leu Glu Thr Thr Ser Lys Ser
 245 250 255
 Asp Glu Val Glu Ala Ala Phe Glu Ala Leu Ile Lys Gly Val Lys Val
 260 265 270
 Ala Pro Gln Thr Glu Trp Lys Gln Ile Leu Asp Asn Thr Glu Val Lys
 275 280 285
 Ala Val Ile Leu Gly Gly Asp Pro Ser Ser Gly Ala Arg Val Val Thr
 290 295 300
 Gly Lys Val Asp Met Val Glu Asp Leu Ile Gln Glu Gly Ser Arg Phe
 305 310 315 320
 Thr Ala Asp His Pro Gly Leu Pro Ile Ser Tyr Thr Thr Ser Phe Leu
 325 330 335

Arg Asp Asn Val Val Ala Thr Phe Gln Asn Ser Thr Asp Tyr Val Glu
 340 345 350
 Thr Lys Val Thr Ala Tyr Arg Asn Gly Asp Leu Leu Leu Asp His Ser
 355 360 365
 Gly Ala Tyr Val Ala Gln Tyr Tyr Ile Thr Trp Asp Glu Leu Ser Tyr
 370 375 380
 Asp His Gln Gly Lys Glu Val Leu Thr Pro Lys Ala Trp Asp Arg Asn
 385 390 395 400
 Gly Gln Asp Leu Thr Ala His Phe Thr Thr Ser Ile Pro Leu Lys Gly
 405 410 415
 Asn Val Arg Asn Leu Ser Val Lys Ile Arg Glu Cys Thr Gly Leu Ala
 420 425 430
 Trp Glu Trp Trp Arg Thr Val Tyr Glu Lys Thr Asp Leu Pro Leu Val
 435 440 445
 Arg Lys Arg Thr Ile Ser Ile Trp Gly Thr Thr Leu Tyr Pro Gln Val
 450 455 460
 Glu Asp Lys Val Glu Asn Asp
 465 470

<210> 22

<211> 254

<212> PRT

<213> Neisseria meningitidis (group B)

<400> 22

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

Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240
 Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 23
 <211> 261
 <212> PRT
 <213> Neisseria meningitidis (group B)

<400> 23
 Cys Ser Ser Gly Ser Gly Ser Gly Gly Gly Gly Val Ala Ala Asp Ile
 1 5 10 15
 Gly Thr Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp
 20 25 30
 Lys Gly Leu Lys Ser Leu Thr Leu Glu Asp Ser Ile Ser Gln Asn Gly
 35 40 45
 Thr Leu Thr Leu Ser Ala Gln Gly Ala Glu Lys Thr Phe Lys Val Gly
 50 55 60
 Asp Lys Asp Asn Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Ile
 65 70 75 80
 Ser Arg Phe Asp Phe Val Gln Lys Ile Glu Val Asp Gly Gln Thr Ile
 85 90 95
 Thr Leu Ala Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asp His Ser Ala
 100 105 110
 Val Val Ala Leu Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp
 115 120 125
 Ser Leu Ile Asn Gln Arg Ser Phe Leu Val Ser Gly Leu Gly Gly Glu
 130 135 140
 His Thr Ala Phe Asn Gln Leu Pro Ser Gly Lys Ala Glu Tyr His Gly
 145 150 155 160
 Lys Ala Phe Ser Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile
 165 170 175
 Asp Phe Ala Ala Lys Gln Gly His Gly Lys Ile Glu His Leu Lys Thr
 180 185 190
 Pro Glu Gln Asn Val Glu Leu Ala Ser Ala Glu Leu Lys Ala Asp Glu
 195 200 205
 Lys Ser His Ala Val Ile Leu Gly Asp Thr Arg Tyr Gly Ser Glu Glu
 210 215 220
 Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile
 225 230 235 240
 Ala Gly Ser Ala Thr Val Lys Ile Arg Glu Lys Val His Glu Ile Gly
 245 250 255
 Ile Ala Gly Lys Gln
 260

<210> 24
 <211> 259
 <212> PRT
 <213> Neisseria meningitidis (group B)

<400> 24
 Cys Ser Ser Gly Gly Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Thr
 1 5 10 15

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

<210> 25
 <211> 260
 <212> PRT
 <213> Neisseria meningitidis (group B)

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

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

<210> 26
 <211> 257
 <212> PRT
 <213> Neisseria meningitidis (group B)

<400> 26
 Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15
 Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Gly Leu Lys
 20 25 30
 Ser Leu Thr Leu Glu Asp Ser Ile Ser Gln Asn Gly Thr Leu Thr Leu
 35 40 45
 Ser Ala Gln Gly Ala Glu Lys Thr Phe Lys Val Gly Asp Lys Asp Asn
 50 55 60
 Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Ile Ser Arg Phe Asp
 65 70 75 80
 Phe Val Gln Lys Ile Glu Val Asp Gly Gln Thr Ile Thr Leu Ala Ser
 85 90 95
 Gly Glu Phe Gln Ile Tyr Lys Gln Asn His Ser Ala Val Val Ala Leu
 100 105 110
 Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn
 115 120 125
 Gln Arg Ser Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe
 130 135 140
 Asn Gln Leu Pro Gly Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser
 145 150 155 160
 Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala
 165 170 175
 Lys Gln Gly His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn
 180 185 190
 Val Glu Leu Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala
 195 200 205
 Val Ile Leu Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr
 210 215 220
 His Leu Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala
 225 230 235 240
 Thr Val Lys Ile Gly Glu Lys Val His Glu Ile Ser Ile Ala Gly Lys
 245 250 255
 Gln

<210> 27
 <211> 254
 <212> PRT
 <213> Neisseria meningitidis (group B)

<400> 27
 Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15
 Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
 20 25 30
 Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45
 Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60
 Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80
 Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95
 Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu
 100 105 110
 Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
 115 120 125
 Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
 130 135 140
 Pro Gly Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160
 Pro Asn Gly Arg Leu His Tyr Ser Ile Asp Phe Thr Lys Lys Gln Gly
 165 170 175
 Tyr Gly Arg Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190
 Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205
 Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220
 Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240
 Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 28
 <211> 254
 <212> PRT
 <213> Neisseria meningitidis (group B)

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

Gln Ile Glu Val Asp Gly Gln Thr Ile Thr Leu Ala Ser Gly Glu Phe
 85 90 95
 Gln Ile Tyr Lys Gln Asn His Ser Ala Val Val Ala Leu Gln Ile Glu
 100 105 110
 Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
 115 120 125
 Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
 130 135 140
 Pro Asp Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160
 Pro Asn Gly Arg Leu His Tyr Ser Ile Asp Phe Thr Lys Lys Gln Gly
 165 170 175
 Tyr Gly Arg Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190
 Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205
 Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220
 Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240
 Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 29
 <211> 254
 <212> PRT
 <213> Neisseria meningitidis (group B)

<400> 29
 Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15
 Ala Asp Ala Leu Thr Thr Pro Leu Asp His Lys Asp Lys Ser Leu Gln
 20 25 30
 Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45
 Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60
 Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80
 Gln Ile Glu Val Asp Gly Gln Thr Ile Thr Leu Ala Ser Gly Glu Phe
 85 90 95
 Gln Ile Tyr Lys Gln Asn His Ser Ala Val Val Ala Leu Gln Ile Glu
 100 105 110
 Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
 115 120 125
 Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
 130 135 140
 Pro Asp Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160
 Pro Asn Gly Arg Leu His Tyr Ser Ile Asp Phe Thr Lys Lys Gln Gly
 165 170 175
 Tyr Gly Arg Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190
 Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205

Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220
 Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240
 Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 30
 <211> 254
 <212> PRT
 <213> Neisseria meningitidis (group B)

<400> 30
 Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15
 Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
 20 25 30
 Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45
 Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60
 Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80
 Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95
 Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu
 100 105 110
 Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
 115 120 125
 Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
 130 135 140
 Pro Asp Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
 145 150 155 160
 Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly
 165 170 175
 His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190
 Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205
 Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220
 Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240
 Ile Gly Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 31
 <211> 254
 <212> PRT
 <213> Neisseria meningitidis (group B)

<400> 31
 Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15

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

<210> 33
 <211> 255
 <212> PRT
 <213> Neisseria meningitidis (group B)

<400> 33
 Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15
 Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
 20 25 30
 Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45
 Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60
 Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80
 Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95
 Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Leu Gln Thr Glu
 100 105 110
 Gln Glu Gln Asp Pro Glu His Ser Gly Lys Met Val Ala Lys Arg Arg
 115 120 125
 Phe Lys Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys Leu
 130 135 140
 Pro Lys Asp Val Met Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp
 145 150 155 160
 Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln
 165 170 175
 Gly His Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val Glu
 180 185 190
 Leu Ala Thr Ala Tyr Ile Lys Pro Asp Glu Lys His His Ala Val Ile
 195 200 205
 Ser Gly Ser Val Leu Tyr Asn Gln Asp Glu Lys Gly Ser Tyr Ser Leu
 210 215 220
 Gly Ile Phe Gly Gly Gln Ala Gln Glu Val Ala Gly Ser Ala Glu Val
 225 230 235 240
 Glu Thr Ala Asn Gly Ile His His Ile Gly Leu Ala Ala Lys Gln
 245 250 255

<210> 34
 <211> 263
 <212> PRT
 <213> Neisseria meningitidis (group B)

<400> 34
 Cys Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Val Ala Ala Asp
 1 5 10 15
 Ile Gly Ala Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys
 20 25 30
 Asp Lys Gly Leu Lys Ser Leu Thr Leu Glu Asp Ser Ile Ser Gln Asn
 35 40 45
 Gly Thr Leu Thr Leu Ser Ala Gln Gly Ala Glu Arg Thr Phe Lys Ala
 50 55 60
 Gly Asp Lys Asp Asn Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys
 65 70 75 80
 Ile Ser Arg Phe Asp Phe Ile Arg Gln Ile Glu Val Asp Gly Gln Leu
 85 90 95
 Ile Thr Leu Glu Ser Gly Glu Phe Gln Val Tyr Lys Gln Ser His Ser
 100 105 110
 Ala Leu Thr Ala Leu Gln Thr Glu Gln Val Gln Asp Ser Glu His Ser
 115 120 125
 Gly Lys Met Val Ala Lys Arg Gln Phe Arg Ile Gly Asp Ile Val Gly
 130 135 140
 Glu His Thr Ser Phe Asp Lys Leu Pro Lys Asp Val Met Ala Thr Tyr
 145 150 155 160
 Arg Gly Thr Ala Phe Gly Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr
 165 170 175
 Thr Ile Asp Phe Ala Ala Lys Gln Gly His Gly Lys Ile Glu His Leu
 180 185 190
 Lys Ser Pro Glu Leu Asn Val Asp Leu Ala Ala Ala Asp Ile Lys Pro
 195 200 205
 Asp Glu Lys His His Ala Val Ile Ser Gly Ser Val Leu Tyr Asn Gln
 210 215 220
 Ala Glu Lys Gly Ser Tyr Ser Leu Gly Ile Phe Gly Gly Gln Ala Gln
 225 230 235 240
 Glu Val Ala Gly Ser Ala Glu Val Glu Thr Ala Asn Gly Ile Arg His
 245 250 255
 Ile Gly Leu Ala Ala Lys Gln
 260

<210> 35
 <211> 255
 <212> PRT
 <213> Neisseria meningitidis (group B)

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

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Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
65      70      75      80
Gln Ile Glu Val Asp Gly Lys Leu Ile Thr Leu Glu Ser Gly Glu Phe
      85      90      95
Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Leu Gln Thr Glu
      100     105     110
Gln Val Gln Asp Ser Glu Asp Ser Gly Lys Met Val Ala Lys Arg Gln
      115     120     125
Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys Leu
      130     135     140
Pro Lys Gly Gly Ser Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp
145     150     155     160
Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln
      165     170     175
Gly His Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val Glu
      180     185     190
Leu Ala Thr Ala Tyr Ile Lys Pro Asp Glu Lys Arg His Ala Val Ile
      195     200     205
Ser Gly Ser Val Leu Tyr Asn Gln Asp Glu Lys Gly Ser Tyr Ser Leu
      210     215     220
Gly Ile Phe Gly Gly Gln Ala Gln Glu Val Ala Gly Ser Ala Glu Val
225     230     235     240
Glu Thr Ala Asn Gly Ile His His Ile Gly Leu Ala Ala Lys Gln
      245     250     255

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<210> 36
<211> 255
<212> PRT
<213> Neisseria meningitidis (group B)

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

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Leu Ala Ala Ala Asp Ile Lys Pro Asp Glu Lys His His Ala Val Ile
 195 200 205
 Ser Gly Ser Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser Tyr Ser Leu
 210 215 220
 Gly Ile Phe Gly Gly Lys Ala Gln Glu Val Ala Gly Ser Ala Glu Val
 225 230 235 240
 Lys Thr Val Asn Gly Ile Arg His Ile Gly Leu Ala Ala Lys Gln
 245 250 255

<210> 37
 <211> 255
 <212> PRT
 <213> Neisseria meningitidis (group B)

<400> 37
 Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15
 Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
 20 25 30
 Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45
 Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60
 Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80
 Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95
 Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Leu Gln Thr Glu
 100 105 110
 Gln Val Gln Asp Ser Glu His Ser Gly Lys Met Val Ala Lys Arg Gln
 115 120 125
 Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys Leu
 130 135 140
 Pro Glu Gly Gly Arg Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp
 145 150 155 160
 Asp Ala Ser Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln
 165 170 175
 Gly His Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val Asp
 180 185 190
 Leu Ala Ala Ser Asp Ile Lys Pro Asp Lys Lys Arg His Ala Val Ile
 195 200 205
 Ser Gly Ser Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser Tyr Ser Leu
 210 215 220
 Gly Ile Phe Gly Gly Gln Ala Gln Glu Val Ala Gly Ser Ala Glu Val
 225 230 235 240
 Glu Thr Ala Asn Gly Ile Arg His Ile Gly Leu Ala Ala Lys Gln
 245 250 255

<210> 38
 <211> 255
 <212> PRT
 <213> Neisseria meningitidis (group B)

<400> 38

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

<210> 39

<211> 255

<212> PRT

<213> Neisseria meningitidis (group B)

<400> 39

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

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

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<210> 40
<211> 263
<212> PRT
<213> Neisseria meningitidis (group B)

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

```

Glu Val Ala Gly Ser Ala Glu Val Glu Thr Ala Asn Gly Ile Arg His
 245 250 255
 Ile Gly Leu Ala Ala Lys Gln
 260

<210> 41
 <211> 255
 <212> PRT
 <213> Neisseria meningitidis (group B)

<400> 41
 Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15
 Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Gly Leu Gln
 20 25 30
 Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45
 Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60
 Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80
 Gln Ile Glu Val Asp Gly Lys Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95
 Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Leu Gln Thr Glu
 100 105 110
 Gln Val Gln Asp Ser Glu Asp Ser Gly Lys Met Val Ala Lys Arg Gln
 115 120 125
 Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys Leu
 130 135 140
 Pro Lys Gly Gly Ser Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp
 145 150 155 160
 Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln
 165 170 175
 Gly His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu
 180 185 190
 Leu Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile
 195 200 205
 Leu Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu
 210 215 220
 Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val
 225 230 235 240
 Lys Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250 255

<210> 42
 <211> 259
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 42
 Ser Ser Gly Gly Gly Gly Ser Gly Gly Ile Ala Ala Asp Ile Gly Thr
 1 5 10 15

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

<210> 43
 <211> 258
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 43
 Ser Ser Gly Gly Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Thr Gly
 1 5 10 15
 Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Gly Leu
 20 25 30
 Lys Ser Leu Thr Leu Glu Asp Ser Ile Pro Gln Asn Gly Thr Leu Thr
 35 40 45
 Leu Ser Ala Gln Gly Ala Glu Lys Thr Phe Lys Ala Gly Asp Lys Asp
 50 55 60
 Asn Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Ile Ser Arg Phe
 65 70 75 80
 Asp Phe Val Gln Lys Ile Glu Val Asp Gly Gln Thr Ile Thr Leu Ala
 85 90 95
 Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala
 100 105 110

```

Leu Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile
      115              120              125
Asn Gln Arg Ser Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala
      130              135              140
Phe Asn Gln Leu Pro Gly Asp Lys Ala Glu Tyr His Gly Lys Ala Phe
145              150              155              160
Ser Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala
      165              170              175
Ala Lys Gln Gly His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln
      180              185              190
Asn Val Glu Leu Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His
      195              200              205
Ala Val Ile Leu Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr
      210              215              220
Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser
225              230              235              240
Ala Thr Val Lys Ile Gly Glu Lys Val His Glu Ile Gly Ile Ala Gly
      245              250              255
Lys Gln

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<210> 44
<211> 260
<212> PRT
<213> Artificial Sequence

```

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<220>
<223> Synthetic sequence

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```

<400> 44
Ser Ser Gly Ser Gly Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly
1      5      10      15
Thr Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys
      20      25      30
Gly Leu Lys Ser Leu Thr Leu Glu Asp Ser Ile Ser Gln Asn Gly Thr
      35      40      45
Leu Thr Leu Ser Ala Gln Gly Ala Glu Lys Thr Phe Lys Val Gly Asp
      50      55      60
Lys Asp Asn Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Ile Ser
65      70      75      80
Arg Phe Asp Phe Val Gln Lys Ile Glu Val Asp Gly Gln Thr Ile Thr
      85      90      95
Leu Ala Ser Gly Clu Phe Gln Ile Tyr Lys Gln Asp His Ser Ala Val
      100     105     110
Val Ala Leu Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser
      115     120     125
Leu Ile Asn Gln Arg Ser Phe Leu Val Ser Gly Leu Gly Gly Glu His
130     135     140
Thr Ala Phe Asn Gln Leu Pro Ser Gly Lys Ala Glu Tyr His Gly Lys
145     150     155     160
Ala Phe Ser Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp
      165     170     175
Phe Ala Ala Lys Gln Gly His Gly Lys Ile Clu His Leu Lys Thr Pro
      180     185     190
Glu Gln Asn Val Glu Leu Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys
195     200     205

```

Ser His Ala Val Ile Leu Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys
 210 215 220
 Gly Thr Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala
 225 230 235 240
 Gly Ser Ala Thr Val Lys Ile Arg Glu Lys Val His Glu Ile Gly Ile
 245 250 255
 Ala Gly Lys Gln
 260

<210> 45
 <211> 256
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 45
 Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu Ala
 1 5 10 15
 Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Gly Leu Lys Ser
 20 25 30
 Leu Thr Leu Glu Asp Ser Ile Ser Gln Asn Gly Thr Leu Thr Leu Ser
 35 40 45
 Ala Gln Gly Ala Glu Lys Thr Phe Lys Val Gly Asp Lys Asp Asn Scr
 50 55 60
 Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Ile Ser Arg Phe Asp Phe
 65 70 75 80
 Val Gln Lys Ile Glu Val Asp Gly Gln Thr Ile Thr Leu Ala Ser Gly
 85 90 95
 Glu Phe Gln Ile Tyr Lys Gln Asn His Ser Ala Val Val Ala Leu Gln
 100 105 110
 Ile Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln
 115 120 125
 Arg Ser Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn
 130 135 140
 Gln Leu Pro Gly Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser
 145 150 155 160
 Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys
 165 170 175
 Gln Gly His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val
 180 185 190
 Glu Leu Ala Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val
 195 200 205
 Ile Leu Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His
 210 215 220
 Leu Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr
 225 230 235 240
 Val Lys Ile Gly Glu Lys Val His Glu Ile Ser Ile Ala Gly Lys Gln
 245 250 255

<210> 46
 <211> 253
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic sequence

<400> 46

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

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<210> 47

<211> 258

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence

<400> 47

```

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

```

Asp Phe Ile Arg Gln Ile Glu Val Asp Gly Gln Thr Ile Thr Leu Ala
 85 90 95
 Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asn His Ser Ala Val Val Ala
 100 105 110
 Leu Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile
 115 120 125
 Asn Gln Arg Ser Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala
 130 135 140
 Phe Asn Gln Leu Pro Asp Gly Lys Ala Glu Tyr His Gly Lys Ala Phe
 145 150 155 160
 Ser Ser Asp Asp Pro Asn Gly Arg Leu His Tyr Ser Ile Asp Phe Thr
 165 170 175
 Lys Lys Gln Gly Tyr Gly Arg Ile Glu His Leu Lys Thr Pro Glu Gln
 180 185 190
 Asn Val Glu Leu Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His
 195 200 205
 Ala Val Ile Leu Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr
 210 215 220
 Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser
 225 230 235 240
 Ala Thr Val Lys Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly
 245 250 255
 Lys Gln

<210> 48
 <211> 253
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

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

Gly Arg Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu Ala
 180 185 190
 Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu Gly
 195 200 205
 Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu Ala Leu
 210 215 220
 Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys Ile
 225 230 235 240
 Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 49
 <211> 253
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 49
 Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu Ala
 1 5 10 15
 Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln Ser
 20 25 30
 Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu Ala
 35 40 45
 Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn Thr
 50 55 60
 Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg Gln
 65 70 75 80
 Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe Gln
 85 90 95
 Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu Lys
 100 105 110
 Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser Phe
 115 120 125
 Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu Pro
 130 135 140
 Asp Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp Ala
 145 150 155 160
 Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly His
 165 170 175
 Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu Ala
 180 185 190
 Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu Gly
 195 200 205
 Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu Ala Leu
 210 215 220
 Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys Ile
 225 230 235 240
 Gly Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 50
 <211> 253

<212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 50
 Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu Ala
 1 5 10 15
 Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln Ser
 20 25 30
 Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu Ala
 35 40 45
 Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn Thr
 50 55 60
 Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg Gln
 65 70 75 80
 Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe Gln
 85 90 95
 Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu Lys
 100 105 110
 Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser Phe
 115 120 125
 Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu Pro
 130 135 140
 Asp Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp Ala
 145 150 155 160
 Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly His
 165 170 175
 Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu Ala
 180 185 190
 Ala Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu Gly
 195 200 205
 Asp Thr Arg Tyr Gly Ser Glu Glu Lys Gly Thr Tyr His Leu Ala Leu
 210 215 220
 Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys Ile
 225 230 235 240
 Gly Glu Lys Val His Glu Ile Ser Ile Ala Gly Lys Gln
 245 250

<210> 51
 <211> 253
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 51
 Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu Ala
 1 5 10 15
 Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln Ser
 20 25 30
 Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu Ala
 35 40 45

Ala	Gln	Gly	Ala	Glu	Lys	Thr	Tyr	Gly	Asn	Gly	Asp	Ser	Leu	Asn	Thr
50						55					60				
Gly	Lys	Leu	Lys	Asn	Asp	Lys	Val	Ser	Arg	Phe	Asp	Phe	Ile	Arg	Gln
65				70						75					80
Ile	Glu	Val	Asp	Gly	Gln	Leu	Ile	Thr	Leu	Glu	Ser	Gly	Glu	Phe	Gln
			85						90					95	
Ile	Tyr	Lys	Gln	Asp	His	Ser	Ala	Val	Val	Ala	Leu	Gln	Ile	Glu	Lys
			100					105					110		
Ile	Asn	Asn	Pro	Asp	Lys	Ile	Asp	Ser	Leu	Ile	Asn	Gln	Arg	Ser	Phe
		115					120					125			
Leu	Val	Ser	Gly	Leu	Gly	Gly	Glu	His	Thr	Ala	Phe	Asn	Gln	Leu	Pro
130						135					140				
Ser	Gly	Lys	Ala	Glu	Tyr	His	Gly	Lys	Ala	Phe	Ser	Ser	Asp	Asp	Ala
145					150					155					160
Gly	Gly	Lys	Leu	Thr	Tyr	Thr	Ile	Asp	Phe	Ala	Ala	Lys	Gln	Gly	His
				165					170					175	
Gly	Lys	Ile	Glu	His	Leu	Lys	Thr	Pro	Glu	Gln	Asn	Val	Glu	Leu	Ala
			180					185					190		
Ser	Ala	Glu	Leu	Lys	Ala	Asp	Glu	Lys	Ser	His	Ala	Val	Ile	Leu	Gly
		195					200					205			
Asp	Thr	Arg	Tyr	Gly	Gly	Glu	Glu	Lys	Gly	Thr	Tyr	His	Leu	Ala	Leu
210						215					220				
Phe	Gly	Asp	Arg	Ala	Gln	Glu	Ile	Ala	Gly	Ser	Ala	Thr	Val	Lys	Ile
225					230					235					240
Arg	Glu	Lys	Val	His	Glu	Ile	Gly	Ile	Ala	Gly	Lys	Gln			
				245						250					

<210> 52
 <211> 261
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 52
 Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Val Ala Ala Asp Ile
 1 5 10 15
 Gly Thr Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp
 20 25 30
 Lys Gly Leu Lys Ser Leu Thr Leu Glu Asp Ser Ile Pro Gln Asn Gly
 35 40 45
 Thr Leu Thr Leu Ser Ala Gln Gly Ala Glu Lys Thr Phe Lys Ala Gly
 50 55 60
 Asp Lys Asp Asn Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Ile
 65 70 75 80
 Ser Arg Phe Asp Phe Val Gln Lys Ile Glu Val Asp Gly Gln Thr Ile
 85 90 95
 Thr Leu Ala Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asn His Ser Ala
 100 105 110
 Val Val Ala Leu Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp
 115 120 125
 Ser Leu Ile Asn Gln Arg Ser Phe Leu Val Ser Gly Leu Gly Gly Glu
 130 135 140
 His Thr Ala Phe Asn Gln Leu Pro Gly Asp Lys Ala Glu Tyr His Gly
 145 150 155 160

Lys Ala Phe Ser Ser Asp Asp Pro Asn Gly Arg Leu His Tyr Thr Ile
 165 170 175
 Asp Phe Thr Asn Lys Gln Gly Tyr Gly Arg Ile Glu His Leu Lys Thr
 180 185 190
 Pro Glu Leu Asn Val Asp Leu Ala Ser Ala Glu Leu Lys Ala Asp Glu
 195 200 205
 Lys Ser His Ala Val Ile Leu Gly Asp Thr Arg Tyr Gly Ser Glu Glu
 210 215 220
 Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile
 225 230 235 240
 Ala Gly Ser Ala Thr Val Lys Ile Gly Glu Lys Val His Glu Ile Gly
 245 250 255
 Ile Ala Gly Lys Gln
 260

<210> 53
 <211> 259
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 53
 Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Val Thr Ala Asp Ile
 1 5 10 15
 Gly Thr Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp
 20 25 30
 Lys Gly Leu Lys Ser Leu Thr Leu Glu Asp Ser Ile Ser Gln Asn Gly
 35 40 45
 Thr Leu Thr Leu Ser Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly
 50 55 60
 Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe
 65 70 75 80
 Asp Phe Ile Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu
 85 90 95
 Ser Gly Glu Phe Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala
 100 105 110
 Leu Gln Thr Glu Gln Glu Gln Asp Pro Glu His Ser Glu Lys Met Val
 115 120 125
 Ala Lys Arg Arg Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser
 130 135 140
 Phe Asp Lys Leu Pro Lys Asp Val Met Ala Thr Tyr Arg Gly Thr Ala
 145 150 155 160
 Phe Gly Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe
 165 170 175
 Ala Ala Lys Gln Gly His Gly Lys Ile Glu His Leu Lys Ser Pro Glu
 180 185 190
 Leu Asn Val Asp Leu Ala Val Ala Tyr Ile Lys Pro Asp Glu Lys His
 195 200 205
 His Ala Val Ile Ser Gly Ser Val Leu Tyr Asn Gln Asp Glu Lys Gly
 210 215 220
 Ser Tyr Ser Leu Gly Ile Phe Gly Glu Lys Ala Gln Glu Val Ala Gly
 225 230 235 240

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

<210> 54
 <211> 262
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 54
 Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Val Ala Ala Asp Ile
 1 5 10 15
 Gly Ala Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp
 20 25 30
 Lys Gly Leu Lys Ser Leu Thr Leu Glu Asp Ser Ile Ser Gln Asn Gly
 35 40 45
 Thr Leu Thr Leu Ser Ala Gln Gly Ala Glu Arg Thr Phe Lys Ala Gly
 50 55 60
 Asp Lys Asp Asn Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Ile
 65 70 75 80
 Ser Arg Phe Asp Phe Ile Arg Gln Ile Glu Val Asp Gly Gln Leu Ile
 85 90 95
 Thr Leu Glu Ser Gly Glu Phe Gln Val Tyr Lys Gln Ser His Ser Ala
 100 105 110
 Leu Thr Ala Leu Gln Thr Glu Gln Val Gln Asp Ser Glu His Ser Gly
 115 120 125
 Lys Met Val Ala Lys Arg Gln Phe Arg Ile Gly Asp Ile Val Gly Glu
 130 135 140
 His Thr Ser Phe Asp Lys Leu Pro Lys Asp Val Met Ala Thr Tyr Arg
 145 150 155 160
 Gly Thr Ala Phe Gly Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr
 165 170 175
 Ile Asp Phe Ala Ala Lys Gln Gly His Gly Lys Ile Glu His Leu Lys
 180 185 190
 Ser Pro Glu Leu Asn Val Asp Leu Ala Ala Ala Asp Ile Lys Pro Asp
 195 200 205
 Glu Lys His His Ala Val Ile Ser Gly Ser Val Leu Tyr Asn Gln Ala
 210 215 220
 Glu Lys Gly Ser Tyr Ser Leu Gly Ile Phe Gly Gly Gln Ala Gln Glu
 225 230 235 240
 Val Ala Gly Ser Ala Glu Val Glu Thr Ala Asn Gly Ile Arg His Ile
 245 250 255
 Gly Leu Ala Ala Lys Gln
 260

<210> 55
 <211> 254
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 55

```

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

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<210> 56

<211> 254

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence

<400> 56

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

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Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Leu Gln Thr Glu Gln
      100                      105                      110
Val Gln Asp Ser Glu His Ser Gly Lys Met Val Ala Lys Arg Gln Phe
      115                      120                      125
Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys Leu Pro
      130                      135                      140
Glu Gly Gly Arg Ala Thr Tyr Arg Gly Thr Ala Phe Ser Ser Asp Asp
      145                      150                      155                      160
Ala Gly Gly Lys Leu Ile Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly
      165                      170                      175
His Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val Asp Leu
      180                      185                      190
Ala Ala Ala Asp Ile Lys Pro Asp Glu Lys His His Ala Val Ile Ser
      195                      200                      205
Gly Ser Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser Tyr Ser Leu Gly
      210                      215                      220
Ile Phe Gly Gly Lys Ala Gln Glu Val Ala Gly Ser Ala Glu Val Lys
      225                      230                      235                      240
Thr Val Asn Gly Ile Arg His Ile Gly Leu Ala Ala Lys Gln
      245                      250

```

```

<210> 57
<211> 254
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Synthetic sequence

```

```

<400> 57
Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu Ala
1      5      10      15
Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln Ser
      20      25      30
Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu Ala
      35      40      45
Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn Thr
      50      55      60
Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg Gln
      65      70      75      80
Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe Gln
      85      90      95
Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Leu Gln Thr Glu Gln
      100     105     110
Val Gln Asp Ser Glu His Ser Gly Lys Met Val Ala Lys Arg Gln Phe
      115     120     125
Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys Leu Pro
      130     135     140
Glu Gly Gly Arg Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp Asp
      145     150     155     160
Ala Ser Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly
      165     170     175
His Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val Asp Leu
      180     185     190
Ala Ala Ser Asp Ile Lys Pro Asp Lys Lys Arg His Ala Val Ile Ser
      195     200     205

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Gly Ser Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser Tyr Ser Leu Gly
 210 215 220
 Ile Phe Gly Gly Gln Ala Gln Glu Val Ala Gly Ser Ala Glu Val Glu
 225 230 235 240
 Thr Ala Asn Gly Ile Arg His Ile Gly Leu Ala Ala Lys Gln
 245 250

<210> 58
 <211> 254
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 58
 Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Val Leu Ala
 1 5 10 15
 Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln Ser
 20 25 30
 Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu Ala
 35 40 45
 Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn Thr
 50 55 60
 Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg Gln
 65 70 75 80
 Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe Gln
 85 90 95
 Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Leu Gln Thr Glu Gln
 100 105 110
 Val Gln Asp Ser Glu His Ser Gly Lys Met Val Ala Lys Arg Gln Phe
 115 120 125
 Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys Leu Pro
 130 135 140
 Glu Gly Gly Arg Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp Asp
 145 150 155 160
 Ala Ser Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly
 165 170 175
 His Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val Asp Leu
 180 185 190
 Ala Ala Ser Asp Ile Lys Pro Asp Lys Lys Arg His Ala Val Ile Ser
 195 200 205
 Gly Ser Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser Tyr Ser Leu Gly
 210 215 220
 Ile Phe Gly Gly Gln Ala Gln Glu Val Ala Gly Ser Ala Glu Val Glu
 225 230 235 240
 Thr Ala Asn Gly Ile Arg His Ile Gly Leu Ala Ala Lys Gln
 245 250

<210> 59
 <211> 254
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic sequence

<400> 59

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

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<210> 60

<211> 262

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence

<400> 60

```

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

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Ser Arg Phe Asp Phe Ile Arg Gln Ile Glu Val Asp Gly Gln Leu Ile
 85 90 95
 Thr Leu Glu Ser Gly Glu Phe Gln Val Tyr Lys Gln Ser His Ser Ala
 100 105 110
 Leu Thr Ala Leu Gln Thr Glu Gln Val Gln Asp Ser Glu His Ser Gly
 115 120 125
 Lys Met Val Ala Lys Arg Gln Phe Arg Ile Gly Asp Ile Val Gly Glu
 130 135 140
 His Thr Ser Phe Gly Lys Leu Pro Lys Asp Val Met Ala Thr Tyr Arg
 145 150 155 160
 Gly Thr Ala Phe Gly Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr
 165 170 175
 Ile Asp Phe Ala Ala Lys Gln Gly His Gly Lys Ile Glu His Leu Lys
 180 185 190
 Ser Pro Glu Leu Asn Val Asp Leu Ala Ala Ala Asp Ile Lys Pro Asp
 195 200 205
 Glu Lys His His Ala Val Ile Ser Gly Ser Val Leu Tyr Asn Gln Ala
 210 215 220
 Glu Lys Gly Ser Tyr Ser Leu Gly Ile Phe Gly Gly Gln Ala Gln Glu
 225 230 235 240
 Val Ala Gly Ser Ala Glu Val Glu Thr Ala Asn Gly Ile Arg His Ile
 245 250 255
 Gly Leu Ala Ala Lys Gln
 260

<210> 61

<211> 254

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence

<400> 61

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

His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
 180 185 190
 Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
 195 200 205
 Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu Ala
 210 215 220
 Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
 225 230 235 240
 Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
 245 250

<210> 62

<211> 259

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence

<400> 62

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

<210> 63
 <211> 255
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 63
 Gly Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Val Leu
 1 5 10 15
 Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
 20 25 30
 Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45
 Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60
 Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80
 Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95
 Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Leu Gln Thr Glu
 100 105 110
 Gln Val Gln Asp Ser Glu His Ser Gly Lys Met Val Ala Lys Arg Gln
 115 120 125
 Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe Asp Lys Leu
 130 135 140
 Pro Glu Gly Gly Arg Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp
 145 150 155 160
 Asp Ala Ser Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln
 165 170 175
 Gly His Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val Asp
 180 185 190
 Leu Ala Ala Ser Asp Ile Lys Pro Asp Lys Lys Arg His Ala Val Ile
 195 200 205
 Ser Gly Ser Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser Tyr Ser Leu
 210 215 220
 Gly Ile Phe Gly Gly Gln Ala Gln Glu Val Ala Gly Ser Ala Glu Val
 225 230 235 240
 Glu Thr Ala Asn Gly Ile Arg His Ile Gly Leu Ala Ala Lys Gln
 245 250 255

<210> 64
 <211> 254
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 64
 Gly Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15
 Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
 20 25 30

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

<210> 65
 <211> 768
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 65
 ggcagcagcg gaggcggcgg tgctgcgcgc gacatcggcg cgggtgcttgc cgatgcacta 60
 accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtcgcgc 120
 aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc 180
 gacagcctca atacgggcaa attgaagaac gacaaggtoa gcogettcga ctttatccgt 240
 caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca agtgtacaaa 300
 caaagccatt ccgccttaac cgccttcag accgagcaag tacaagattc ggagcattca 360
 gggaagatgg ttgcgaaacg ccagttcaga atcggcgata tagcgggtga acatacatct 420
 tttgacaagc ttcccgaagg cggcaggcg acatatcgcg ggacggcatt cggttcagac 480
 gatgccagtg gaaaactgac ctacaccata gatttcgcgc ccaagcaggg acacggcaaa 540
 atcgaacatt tgaaatcgcc agaactcaat gttgacctgg ccgcctccga tatcaagccg 600
 gataaaaaac gccatgccgt catcagcggg tccgtccttt acaaccaagc cgagaaaggc 660
 agttactctc taggcattct tggcgggcaa gccaggaag ttgccggcag cgcagaagtg 720
 gaaaccgcaa acggcatacg ccatatcggt cttgccgcca agcagtaa 768

<210> 66
 <211> 783

<212> DNA

<213> *Neisseria meningitidis* (group B)

<400> 66

tgcagcagcg	gaggcggcgg	aagcggcggt	atcgccgcgc	acatcggcac	ggggcttgcc	60
gatgcactaa	ctgcgcgcgt	cgaccataaa	gacaaagggt	tgaaatccct	gacattggaa	120
gactccattc	cccaaaacgg	aacactgacc	ctgtcggcac	aaggtgcgga	aaaaactttc	180
aaagccggcg	acaaagacaa	cagcctcaac	acgggcaaac	tgaagaacga	caaaatcage	240
cgcttcgact	tcgtgcaaaa	aatcgaagt	gacggacaaa	ccatcacact	ggcaagcggc	300
gaatttcaaa	tatacaaa	ggaccactcc	gccgtcgttg	ccctacagat	tgaaaaaatc	360
aacaaccccg	acaaaatcga	cagcctgata	aaccaacgct	ccttccttgt	cagcgggttg	420
ggcggagaa	ataccgcctt	caaccaactg	cccgccggca	aagccgagta	tcacggcaaa	480
gcattcagct	ccgacgaccc	gaacggcagg	ctgcactact	ccattgattt	tacaaaaaaa	540
cagggttacg	gcagaatcga	acacctgaaa	acgcccagag	agaatgtcga	gcttgccctc	600
gccgaactca	aagcagatga	aaaatcacac	gccgtcattt	tgggcgacac	gcgctacggc	660
agcgaagaaa	aaggcactta	ccacctcgct	cttttcggcg	accgagccca	agaaatcgcc	720
ggctcggcaa	ccgtgaagat	aagggaagaa	gttcacgaaa	tcggcatcgc	cggcaaacag	780
tag						783

<210> 67

<211> 789

<212> DNA

<213> *Neisseria meningitidis* (group B)

<400> 67

tgcagcagcg	gaggaggcgg	aagcggaggc	ggcgggtgtc	ccgcgcgacat	cggcacgggg	60
cttgccgatg	cactaaccgc	accgctcgac	cataaagaca	aaggtttgaa	atccctgaca	120
ttggaagact	ccattcccca	aaacgggaaca	ctgaccctgt	cggcacaagg	tgcggaaaaa	180
actttcaaa	ccggcgacaa	agacaacagc	ctcaacacgg	gcaaactgaa	gaacgacaaa	240
atcagccgct	tcgacttcgt	gcaaaaaatc	gaagtggacg	gacaaacct	cacgctggca	300
agcggcgaa	ttcaaatata	caaacagaac	cactccgccc	tcgttgccct	acagattgaa	360
aaaatcaaca	accccgacaa	aatcgacagc	ctgataaacc	aacgcctcct	ccttgctcgc	420
ggtttgggcg	gagaacatac	cgccttcaac	caactgccc	gcgacaaagc	cgagtatcac	480
ggcaaagcat	tcagctccga	cgacccgaac	ggcaggctgc	actacacct	cgattttacc	540
aacaaacagg	gttacggcag	aatcgaacac	ctgaaaacgc	ccgaactcaa	tgtcgatctg	600
gcctccgccc	aactcaaagc	agatgaaaaa	tcacacgcgc	tcattttggg	cgacaogcgc	660
tacggcagcg	aagaaaaagg	cacttaccac	ctcgcccttt	tcggcgaccc	cgcccaagaa	720
atcgccggct	cggcaaccgt	gaagataggg	gaaaagggtc	acgaaatcgg	catcgccggc	780
aaacagtag						789

<210> 68

<211> 780

<212> DNA

<213> *Neisseria meningitidis* (group B)

<400> 68

tgcagcagcg	gaggcggagg	cggcgggtgc	gccgccgaca	tcggcacggg	gcttgccgat	60
gcactaactg	cgcgcgtcga	ccataaagac	aaaggtttga	aatccctgac	attggaagac	120
tccattcccc	aaaacggaac	actgaccctg	tcggcacaag	gtgcggaaaa	aactttcaaa	180
gccggcgaca	aagacaacag	cctcaacacg	ggcaaaactga	agaacgacaa	aatcagccgc	240
ttcgacttcg	tgcaaaaaat	cgaagtggac	ggacaaaacca	tcacactggc	aagcggcgaa	300
tttcaaatat	acaaacagga	ccactccgcc	gtcgttgccc	tacagattga	aaaaatcaac	360
aaccccgaca	aaatcgacag	cctgataaac	caacgctcct	tccttgctcag	cggtttgggc	420
ggagaacata	cgccttcaa	ccaactgccc	ggcgacaaag	ccgagtatca	cggcaaagca	480
ttcagctccg	acgatgcggg	cggaaaactg	acctatacca	tagattttgc	cgccaaacag	540

ggacacggca	aaatcgaaca	cctgaaaaca	cccgagcaaa	atgtcgagct	tgccgcgcgc	600
gaactcaaag	cagatgaaaa	atcacacgcc	gtcatttttg	gcgacacgcg	ctacggcagc	660
gaagaaaaag	gcacttacca	cctcgccctt	ttcggcgcgc	gcgcccaaga	aatcgccggc	720
tcggcaaccg	tgaagatagg	ggaaaagggt	cacgaaatcg	gcacgcgcgc	caaacagtag	780

<210> 69
 <211> 786
 <212> DNA
 <213> *Neisseria meningitidis* (group B)

<400> 69	
tgcagcagcg	gaagcgggaag
gccgatgcac	taactgcgcc
gaagactcca	tttcccaaaa
ttcaaagtcg	gcgacaaaga
agccgcttcg	actttgtgca
ggcgaatttc	aaatatacaa
atcaacaacc	ccgacaaaat
ttgggcggag	aacataccgc
aaagcattca	gctccgacga
aaacagggac	acggcaaaaat
tccgcgcgaac	tcaaagcaga
ggcagcgaag	aaaaaggcac
gccggctcgg	caaccgtgaa
cagtag	

<210> 70
 <211> 774
 <212> DNA
 <213> *Neisseria meningitidis* (group B)

<400> 70	
tgcagcagcg	gagggcggcgg
accgcaccgc	tcgaccataa
tcccaaaaacg	gaacactgac
gacaaagaca	acagtctcaa
tttgtgcaaa	aaatcgaagt
atatacaaac	agaaccactc
gacaaaatcg	acagcctgat
cataccgcct	tcaaccaact
tccgacgatg	ccggcggaaa
ggcaaaaatcg	aacacctgaa
aaagcagatg	aaaaatcaca
aaaggcactt	accacctcgc
accgtgaaga	taggagaaaa

<210> 71
 <211> 765
 <212> DNA
 <213> *Neisseria meningitidis* (group B)

<400> 71	
tgcagcagcg	gagggcggcgg
accgcaccgc	tcgaccataa

aggaaaaacg	agaaactgaa	gctggcggca	caaggtgcgg	aaaaaactta	tggaaacggc	180
gacagcctca	atacgggcaa	attgaagaac	gacaaggtca	gccgcttcga	ctttatccgt	240
caaategaag	tggacgggca	gctcattacc	ttggagagcg	gagagttcca	aatatacaaaa	300
caggaccact	ccgccgtcgt	tgccctacag	attgaaaaaa	tcaacaaccc	cgacaaaatc	360
gacagcctga	taaaccaacg	ctccttcctt	gtcagcgggt	tgggtggaga	acataccgcc	420
ttcaaccaac	tgcccggcgg	caaagccgag	tatcacggca	aagcattcag	ctccgacgac	480
ccgaacggca	ggctgcacta	ctccattgat	tttaccaaaa	aacaggggta	cggcagaatc	540
gaacacctga	aaacgcccga	gcagaatgtc	gagcttgcc	ccgccgaact	caaagcagat	600
gaaaaatcac	acgccgtcat	tttgggcgac	acgcgctacg	gcgcgaaga	aaaaggcact	660
taccacctcg	ctcttttcgg	cgaccgagcc	caagaaatcg	ccggctcggc	aaccgtgaag	720
ataagggaaa	aggttcacga	aatcggcctc	gccggcaaac	agtag		765

<210> 72

<211> 765

<212> DNA

<213> Neisseria meningitidis (group B)

<400> 72

tgcagcagcg	gaggcggcgg	tgtegcgcgc	gacatcggcg	cggggccttgc	cgatgcacta	60
accgcaccgc	tcgaccataa	agacaaaagt	ttgcagtctt	tgacgctgga	tcagtccgtc	120
aggaaaaacg	agaaactgaa	gctggcggca	caaggtgcgg	aaaaaactta	tggaaacggc	180
gacagcctca	atacgggcaa	attgaagaac	gacaaggtca	gccgcttcga	ctttatccgt	240
caaategaag	tggacggaca	aaccatcacg	ctggcaagcg	gcgaatttca	aatatacaaaa	300
cagaaccact	ccgccgtcgt	tgccctacag	attgaaaaaa	tcaacaaccc	cgacaaaatc	360
gacagcctga	taaaccaacg	ctccttcctt	gtcagcgggt	tgggcggaga	acataccgcc	420
ttcaaccaac	tgctgacgg	caaagccgag	tatcacggca	aagcattcag	ctccgacgac	480
ccgaacggca	ggctgcacta	ctccattgat	tttaccaaaa	aacaggggta	cggcagaatc	540
gaacacctga	aaacgcccga	gcagaatgtc	gagcttgcc	ccgccgaact	caaagcagat	600
gaaaaatcac	acgccgtcat	tttgggcgac	acgcgctacg	gcggcgaaga	aaaaggcact	660
taccacctcg	cccttttcgg	cgaccgcgc	caagaaatcg	ccggctcggc	aaccgtgaag	720
ataagggaaa	aggttcacga	aatcggcctc	gccggcaaac	agtag		765

<210> 73

<211> 765

<212> DNA

<213> Neisseria meningitidis (group B)

<400> 73

tgcagcagcg	gaggcggcgg	tgtegcgcgc	gacatcggcg	cggggccttgc	cgatgcacta	60
accacaccgc	tcgaccataa	agacaaaagt	ttgcagtctt	tgacgctgga	tcagtccgtc	120
aggaaaaacg	agaaactgaa	gctggcggca	caaggtgcgg	aaaaaactta	tggaaacggc	180
gacagcctca	atacgggcaa	attgaagaac	gacaaggtca	gccgcttcga	ctttatccgt	240
caaategaag	tggacggaca	aaccatcacg	ctggcaagcg	gcgaatttca	aatatacaaaa	300
cagaaccact	ccgccgtcgt	tgccctacag	attgaaaaaa	tcaacaaccc	cgacaaaatc	360
gacagcctga	taaaccaacg	ctccttcctt	gtcagcgggt	tgggcggaga	acataccgcc	420
ttcaaccaac	tgctgacgg	caaagccgag	tatcacggca	aagcattcag	ctccgacgac	480
ccgaacggca	ggctgcacta	ctccattgat	tttaccaaaa	aacaggggta	cggcagaatc	540
gaacacctga	aaacgcccga	gcagaatgtc	gagcttgcc	ccgccgaact	caaagcagat	600
gaaaaatcac	acgccgtcat	tttgggcgac	acgcgctacg	gcggcgaaga	aaaaggcact	660
taccacctcg	cccttttcgg	cgaccgcgc	caagaaatcg	ccggctcggc	aaccgtgaag	720
ataagggaaa	aggttcacga	aatcggcctc	gccggcaaac	agtag		765

<210> 74

<211> 765

<212> DNA

<213> *Neisseria meningitidis* (group B)

<400> 74

tgcagcagcg	gagggcggcg	tgtegcgcgc	gacatcggcg	cggggcttgc	cgatgcacta	60
accgcaccgc	tcgaccataa	agacaaaagt	ttgcagtctt	tgacgctgga	tcagtccgtc	120
aggaaaaacg	agaaactgaa	gctggcgggca	caaggtgcgg	aaaaaactta	tggaaacggc	180
gacagcctca	atacgggcaa	attgaagaac	gacaaggtea	gccgcttcga	ctttatccgt	240
caaategaag	tggacgggca	gctcattacc	ttggagagcg	gagagttcca	aatatacaaa	300
caggaccact	ccgccgtcgt	tgccctacag	attgaaaaaa	tcaacaaccc	cgacaaaatc	360
gacagcctga	taaaccaaac	ctccttcctt	gtcagcgggt	tgggcggaga	acataccgcc	420
ttcaaccaac	tgctgacgg	caaagccgag	tatcacggca	aagcattcag	ctccgacgat	480
gctggcgga	aactgaccta	taccatagat	ttcgccgcca	aacagggaca	cggcaaaatc	540
gaacacctga	aaacacccga	gcaaaatgtc	gagcttgccg	ccgccgaact	caaagcagat	600
gaaaaatcac	acgccgtcat	tttgggcgac	acgcgctacg	gcagcgaaga	aaaaggcact	660
taccacctcg	cccttttcgg	cgaccgcgcc	caagaaatcg	ccggctcggc	aaccgtgaag	720
ataggggaaa	aggttcacga	aatcggcata	gccggcaaac	agtag		765

<210> 75

<211> 765

<212> DNA

<213> *Neisseria meningitidis* (group B)

<400> 75

tgcagcagcg	gagggcggcg	tgtegcgcgc	gacatcggcg	cggggcttgc	cgatgcacta	60
accgcaccgc	tcgaccataa	agacaaaagt	ttgcagtctt	tgacgctgga	tcagtccgtc	120
aggaaaaacg	agaaactgaa	gctggcgggca	caaggtgcgg	aaaaaactta	tggaaacggc	180
gacagcctca	atacgggcaa	attgaagaac	gacaaggtea	gccgcttcga	ctttatccgt	240
caaategaag	tggacgggca	gctcattacc	ttggagagcg	gagagttcca	aatatacaaa	300
caggaccact	ccgccgtcgt	tgccctacag	attgaaaaaa	tcaacaaccc	cgacaaaatc	360
gacagcctga	taaaccaaac	ctccttcctt	gtcagcgggt	tgggcggaga	acataccgcc	420
ttcaaccaac	tgctgacgg	caaagccgag	tatcacggca	aagcattcag	ctccgacgat	480
gctggcgga	aactgaccta	taccatagat	ttcgccgcca	aacagggaca	cggcaaaatc	540
gaacacctga	aaacacccga	gcaaaatgtc	gagcttgccg	ccgccgaact	caaagcagat	600
gaaaaatcac	acgccgtcat	tttgggcgac	acgcgctacg	gcagcgaaga	aaaaggcact	660
taccacctcg	cccttttcgg	cgaccgcgcc	caagaaatcg	ccggctcggc	aaccgtgaag	720
ataggagaaa	aggttcacga	aatcagcata	gccggcaaac	agtag		765

<210> 76

<211> 765

<212> DNA

<213> *Neisseria meningitidis* (group B)

<400> 76

tgcagcagcg	gagggcggcg	tgtegcgcgc	gacatcggcg	cggggcttgc	cgatgcacta	60
accgcaccgc	tcgaccataa	agacaaaagt	ttgcagtctt	tgacgctgga	tcagtccgtc	120
aggaaaaacg	agaaactgaa	gctggcgggca	caaggtgcgg	aaaaaactta	tggaaacggc	180
gacagcctca	atacgggcaa	attgaagaac	gacaaggtea	gccgcttcga	ctttatccgt	240
caaategaag	tggacgggca	gctcattacc	ttggagagcg	gagagttcca	aatatacaaa	300
caggaccact	ccgccgtcgt	tgccctacag	attgaaaaaa	tcaacaaccc	cgacaaaatc	360
gacagcctga	taaaccaaac	ctccttcctt	gtcagcgggt	tgggtggaga	acataccgcc	420
ttcaaccaac	tgccagcgg	caaagccgag	tatcacggca	aagcattcag	ctccgacgat	480
gctggcgga	aactgaccta	taccatagat	ttcgccgcca	aacagggaca	cggcaaaatc	540
gaacacttga	aaacacccga	gcaaaatgtc	gagcttgccg	ccgccgaact	caaagcagat	600
gaaaaatcac	acgccgtcat	tttgggcgac	acgcgctacg	gcggcgaaga	aaaaggcact	660

taccacctcg cccttttcgg cgaccgcgcc caagaaatcg ccggtccggc aaccgtgaag 720
ataagggaag aggttcacga aatcggcata gccggcaaac agtag 765

<210> 77
<211> 783
<212> DNA
<213> *Neisseria meningitidis* (group B)

<400> 77
tgcagcagcg gaggcggcgg aagcggaggg ggcggtgtca ccgccgacat cggcacgggg 60
cttgccgatg cactaactgc gccgctcgac cataaagaca aaggtttgaa atccctgaca 120
ttggaagact ccatttccca aaacggaaca ctgaccctgt cggcacaagg tgcggaaaaa 180
acttatggaa acggcgacag ccttaatacg ggcaaatga agaacgacaa ggtcagccgt 240
ttcgacttta tccgtcaaata cgaagtggac gggcagctca ttaccttga gagcggagag 300
ttccaagtgt acaaacaaag ccattccgcc ttaaccgccc ttcagaccga gcaagaacaa 360
gatccagagc attccgagaa gatgggttgc aaacgcgggt tcagaatcgg cgacatagcg 420
ggcgaacata catcttttga caagcttccc aaagacgtca tggcgacata tcgcgggacg 480
gcgttcgggt cagacgatgc cggcggaaaa ctgacctata ctatagattt tgctgccaaa 540
cagggacacg gcaaaatcga acatttgaaa tcgccggaac tcaatgtcga tctggccgtc 600
gcctatatca agccgatga aaaacaccat gccgtcatca gcggttcctg tctttacaac 660
caagacgaga aaggcagtta ctccctcggg atctttggcg aaaaagccca ggaagttgcc 720
ggcagcgcgg aagtggaaac cgcaaacggc atacaccata tcggtcttgc cgccaagcag 780
taa 783

<210> 78
<211> 792
<212> DNA
<213> *Neisseria meningitidis* (group B)

<400> 78
tgcagcagcg gaggcggcgg aagcggaggg ggcggtgtcg ccgccgacat cggcgcgggg 60
cttgccgatg cactaaccgc accgctcgac cataaagaca aaggtttgaa atccctgaca 120
ttggaagact ccatttccca aaacggaaca ctgaccctgt cggcacaagg tgcggaaaga 180
actttcaaag ccggcgacaa agacaacagt ctcaacacag gcaaactgaa gaacgacaaa 240
atcagccgct tcgactttat ccgtcaaata gaagtggacg ggcagctcat taccttggag 300
agcggagagt tccaagtgtt caaacaaagg cattccgctt taaccgccc ttcagaccgag 360
caagtacaag actcggagca ttccgggaag atggttgcga aacgccagtt cagaatcggc 420
gacatagtgg gcgaacatac atcttttgac aagcttccca aagacgtcat ggcgacatat 480
cgccgggacg cgttcgggtt agacgatgcc ggccgaaaac tgacctacac catagatttc 540
gccgccaaag agggacacgg caaaatcgaa catttgaaat cgcctgaact caatgttgac 600
ctggccgccc ccgatatcaa gccggatgaa aaacaccatg ccgtcatcag cggttccgtc 660
ctttacaacc aagccgagaa aggcagttac tctctaggca tctttggcgg gcaagcccag 720
gaagttgccg gcagcgcgga agtggaaacc gcaaacggca tacgccatat cggctcttgc 780
gccaaagcaat aa 792

<210> 79
<211> 792
<212> DNA
<213> *Neisseria meningitidis* (group B)

<400> 79
tgcagcagcg gaggcggcgg aagcggaggg ggcggtgtcg ccgccgacat cggcgcgggg 60
cttgccgatg cactaaccgc accgctcgac cataaagaca aaggtttgaa atccctgaca 120
ttggaagact ccatttccca aaacggaaca ctgaccctgt cggcacaagg tgcggaaaga 180

actttcaaag	cogggcgacaa	agacaacagt	ctcaacacag	gcaaactgaa	gaacgacaaa	240
atcagccgct	tcgactttat	ccgtcaaate	gaagtggacg	ggcagctcat	taccttggag	300
agcggagagt	lccaagtgtg	caaacaaagc	cattccgcct	taaccgccct	tcagaccgag	360
caagtacaag	actcggagca	ttccgggaag	atggttgcca	aacgccagtt	cagaatcggc	420
gacatagtgg	gcgaacatac	atcttttggc	aagcttccca	aagacgtcat	ggcgacatat	480
cgcgggacgg	cgttcgggtc	agacgatgcc	ggcggaaaac	tgacctacac	catagatttc	540
gccgccaaagc	agggacacgg	caaaatcgaa	catttgaaat	cgccagaact	caatgttgac	600
ctggccgccc	ccgatataca	gccggatgaa	aaacaccatg	ccgtcatcag	cggttccgtc	660
ctttacaacc	aagccgagaa	aggcagttac	tctctaggca	tctttggcgg	gcaagcccag	720
gaagttgccg	gcagcgcgga	agtggaaacc	gcaaacggca	tacgccatat	cggttcttgcc	780
gccaagcaat	aa					792

<210> 80

<211> 768

<212> DNA

<213> Neisseria meningitidis (group B)

<400> 80

tgcagcagcg	gagggcgcg	tgctgccgcc	gacatcggcg	cggggccttgc	cgatgcacta	60
accgcaccgc	tcgaccataa	agacaaaagt	ttgcagtctt	tgacgctgga	tcagtccgtc	120
aggaaaaacg	agaaactgaa	gctggcgcca	caaggtgcgg	aaaaaactta	tggaaacggc	180
gacagcctta	atacgggcaa	attgaagaac	gacaaggcca	gccgtttcga	ctttatccgt	240
caaatcgaag	tggacgggca	gctcattacc	ttggagagcg	gagagttcca	agtgtacaaa	300
caaagccatt	ccgccttaac	cgccttccag	accgagcaag	aacaagatcc	agagcattcc	360
gggaagatgg	ttgcgaaacg	ccggttcaaa	atcggcgaca	tagcgggcga	acatacatct	420
tttgacaagc	ttcccaaaga	cgtcatggcg	acatatcgcg	ggacggcggt	cggttcagac	480
gatgccggcg	gaaaactgac	ctatactata	gattttgctg	ccaaacaggg	acacggcaaa	540
atcgaacatt	tgaaatcgcc	cgaactcaat	gtcgagcttg	ccaccgccta	tatcaagccg	600
gatgaaaaac	accatgccgt	catcagcggt	tccgtccttt	acaatcaaga	cgagaaaggc	660
agttactccc	tcggtatctt	tggcgggcaa	gccaggaag	ttgccggcag	cgcggaagtg	720
gaaaccgcaa	acggcataca	ccatatcggt	cttgccgcca	agcaataa		768

<210> 81

<211> 768

<212> DNA

<213> Neisseria meningitidis (group B)

<400> 81

tgcagcagcg	gagggggcg	tgctgccgcc	gacatcggtg	cggggccttgc	cgatgcacta	60
accgcaccgc	tcgaccataa	agacaaaagt	ttgcagtctt	taacgctgga	tcagtccgtc	120
aggaaaaacg	agaaactgaa	gctggcgcca	caaggtgcgg	aaaaaactta	tggaaacggc	180
gacagcctta	atacgggcaa	attgaagaac	gacaaggcca	gccgtttcga	ctttatccgl	240
caaatcgaag	tggacgggaa	gctcattacc	ttggagagcg	gagagttcca	agtgtacaaa	300
caaagccatt	ccgccttaac	cgccttccag	accgagcaag	tacaagactc	ggaggattcc	360
gggaagatgg	ttgcgaaacg	ccagttcaga	atcggcgaca	tagcgggcga	acatacatct	420
tttgacaagc	ttcccaaagg	cggcagtgcg	acatatcgcg	ggacggcggt	cggttcagac	480
gatgctggcg	gaaaactgac	ctatactata	gattttcgccg	ccaagcaggg	acacggcaaa	540
atcgaacatt	tgaaatcgcc	cgaactcaat	gtcgagcttg	ccaccgccta	tatcaagccg	600
gatgaaaaac	gccatgccgt	tatcagcggt	tccgtccttt	acaaccaaga	cgagaaaggc	660
agttactccc	tcggtatctt	tggcgggcaa	gccaggaag	ttgccggcag	cgcggaagtg	720
gaaaccgcaa	acggcataca	ccatatcggt	cttgccgcca	agcagtaa		768

<210> 82

<211> 768

<212> DNA

<213> Neisseria meningitidis (group B)

<400> 82

tgcagcagcg	gagggggcg	tgtegccgcc	gacatcggtg	cggggcttgc	cgatgcacta	60
accgcaccgc	tcgaccataa	agacaaaggt	ttgcagtctt	tgatactgga	tcagtccgtc	120
aggaaaaacg	aaaaactgaa	gctggcgcca	caaggtgcgg	aaaaaactta	tggaaacggc	180
gacagcctca	atacgggcaa	attgaagaac	gacaaggcca	gccgcttcga	ctttatccgt	240
caaatcgaag	tggacgggca	gtcattacc	ttggagagcg	gagagttcca	agtgtacaaa	300
caaagccatt	ccgccttaac	cgcccttcag	accgagcaag	tacaagactc	ggagcattcc	360
gggaagatgg	ttgcgaaacg	ccagttcaga	atcggcgaca	tagcgggcca	acatacatct	420
tttgacaagc	ttcccgaagg	cggcaggggc	acatatcgcg	ggacggcggt	cagttcagac	480
gatgccggtg	gaaaactgat	ttacaccata	gatttcgccg	ccaagcaggg	acacggcaaa	540
atcgaacatt	tgaaatcgcc	agaactcaat	gtcgacctag	ccgcgcgcca	tatcaagccg	600
gatgaaaaac	accatgccgt	catcagcggt	tccgtccttt	acaaccaagc	cgagaaaggc	660
agttactccc	tcggtatctt	tggcggaaaa	gcccggaag	ttgccggcag	cgcggaagtg	720
aaaaccgtaa	acggcatacg	ccatatcggc	cttgccgccca	agcaataa		768

<210> 83

<211> 768

<212> DNA

<213> Neisseria meningitidis (group B)

<400> 83

tgcagcagcg	gagggcgcg	tgtegccgcc	gacatcggcg	cggggcttgc	cgatgcacta	60
accgcaccgc	tcgaccataa	agacaaaagt	ttgcagtctt	tgacgctgga	tcagtccgtc	120
aggaaaaacg	agaaactgaa	gctggcgcca	caaggtgcgg	aaaaaactta	tggaaacggc	180
gacagcctca	atacgggcaa	attgaagaac	gacaaggcca	gccgcttcga	ctttatccgt	240
caaatcgaag	tggacgggca	gtcattacc	ttggagagcg	gagagttcca	agtgtacaaa	300
caaagccatt	ccgccttaac	cgcccttcag	accgagcaag	tacaagattc	ggagcattca	360
gggaagatgg	ttgcgaaacg	ccagttcaga	atcggcgata	tagcgggtga	acatacatct	420
tttgacaaac	ttcccgaagg	cggcaggggc	acatatcgcg	ggacggcatt	cggttcagac	480
gatgccagtg	gaaaactgac	ctacaccata	gatttcgccg	ccaagcaggg	acacggcaaa	540
atcgaacatt	tgaaatcgcc	agaactcaat	gttgacctgg	ccgcctccga	tatcaagccg	600
gataaaaaac	gccatgccgt	catcagcggt	tccgtccttt	acaaccaagc	cgagaaaggc	660
agttactctc	taggcattct	tggcgggcaa	gcccggaag	ttgccggcag	cgcagaagtg	720
gaaaccgcaa	acggcatacg	ccatatcggt	cttgccgccca	agcagtaa		768

<210> 84

<211> 768

<212> DNA

<213> Neisseria meningitidis (group B)

<400> 84

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accgcaccgc	tcgaccataa	agacaaaagt	ttgcagtctt	tgacgctgga	tcagtccgtc	120
aggaaaaacg	agaaactgaa	gctggcgcca	caaggtgcgg	aaaaaactta	tggaaacggc	180
gacagcctca	atacgggcaa	attgaagaac	gacaaggcca	gccgcttcga	ctttatccgt	240
caaatcgaag	tggacgggca	gtcattacc	ttggagagcg	gagagttcca	agtgtacaaa	300
caaagccatt	ccgccttaac	cgcccttcag	accgagcaag	tacaagattc	ggagcattca	360
gggaagatgg	ttgcgaaacg	ccagttcaga	atcggcgata	tagcgggtga	acatacatct	420
tttgacaagc	ttcccgaagg	cggcaggggc	acatatcgcg	ggacggcatt	cggttcagac	480
gatgccagtg	gaaaactgac	ctacaccata	gatttcgccg	ccaagcaggg	acacggcaaa	540
atcgaacatt	tgaaatcgcc	agaactcaat	gttgacctgg	ccgcctccga	tatcaagccg	600
gataaaaaac	gccatgccgt	catcagcggt	tccgtccttt	acaaccaagc	cgagaaaggc	660

agttactctc taggcatctt tggcgggcaa gcccaggaag ttgccggcag cgcagaagtg 720
gaaaccgcaa acggcatacg ccatactggt cttgccgcca agcagtaa 768

<210> 85
<211> 768
<212> DNA
<213> *Neisseria meningitidis* (group B)

<400> 85
tgcagcagcg gagggggtgg tgtegccgcc gacatcggtg cggggcttgc cgatgcacta 60
accgcaccgc tcgaccataa agacaaagggt ttgcagtctt tgacgctgga tcagtccgtc 120
aggaaaaacg agaaactgaa gctggcggca caagggtcgg aaaaaactta tggaaacggt 180
gacagcctca atacgggcaa attgaagaac gacaagggtca gccgtttcga ctttatccgc 240
caaatcgaag tggacgggca gctcattacc ttggagagtg gagagttcca agtatacaaa 300
caaagccatt ccgccttaac cgcctttcag accgagcaaa tacaagattc ggagcattcc 360
gggaagatgg ttgcgaaacg ccagttcaga atcggcgaca tagcgggcga acatacatct 420
tttgacaagc ttcccgaagg cggcagggcg acatatecgc ggacggcggt cggttcagac 480
gatgccggcg gaaaactgac ctacaccata gatttcgccg ccaagcaggg aaacggcaaa 540
atcgaacatt tgaaatcgcc agaactcaat gtcgacctgg ccgccgccga tatcaagccg 600
gatggaaaac gccatgccgt catcagcgggt tccgtccttt acaaccaagc cgagaaaggc 660
agttactccc tcggtatctt tggcggaaaa gcccaggaag ttgccggcag cgcggaagtg 720
aaaaccgtaa acggcatacg ccatactggc cttgccgcca agcaataa 768

<210> 86
<211> 783
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence

<400> 86
agcagcggaa gcggaagcgg aggcggcggt gtgcgccgcc acatcggcac agggcttggc 60
gatgcactaa ctgogccgct cgaccataaa gacaaagggt tgaaatccct gacattggaa 120
gactccattt cccaaaacgg aacaclgacc ctgtcggcac aagggtcgga aaaaactttc 180
aaagtcggcg acaaagacaa cagtctcaat acaggcaaat tgaagaacga caaaatcagc 240
cgcttcgact ttgtgcaaaa aatcgaagtg gacggacaaa ccatacgcgt ggcaagcggc 300
gaattttcaa tatacaaaac ggaccactcc gccgtcggtt ccctacagat tgaaaaaatc 360
aacaaccccc acaaaatcga cagcctgata aaccaacgct ccttccttgt cagcggtttg 420
ggcggagaa acatccgcct caaccaactg cccagcggca aagccgagta tcacggcaaa 480
gcattcagct ccgacgatgc cggcggaaaa ctgacctata ccatagattt tgccgcaaaa 540
cagggacacg gcaaaatcga acacctgaaa acaccgagc agaatgtcga gcttgccctc 600
gccgaactca aagcagatga aaaatcacac gccgtcattt tgggcgacac gcgctacggc 660
agcgaagaaa aaggcactta ccacctcgt cttttcggcg accgagccca agaaatcgcc 720
ggctcggcaa ccglgaagat aagggaagaa gtacacgaaa tcggcatcgc cggcaaacag 780
tag 783

<210> 87
<211> 765
<212> DNA
<213> *Neisseria meningitidis* (group B)

<400> 87
tgcagcagcg gagggggcgg tgtegccgcc gacattgggt cggggcttgc cgatgcacta 60

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accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtccgtc 120
aggaaaaacg agaaactgaa gctggcggca caaggtgcgg aaaaaactta tggaaacggc 180
gacagcctca atacgggcaa attgaagaac gacaaggta gccgcttcga ctttatccgt 240
caaatcgaag tggacggaca aaccatcacg ctggcaagcg gcgaatttca aatatacaaa 300
cagaaccact ccgccgtcgt tgccctacag attgaaaaaa tcaacaaccc cgacaaaatc 360
gacagcctga taaaccaacg ctcttctctt gtcagcgggt tgggcggaga acataccgcc 420
ttcaaccaac tgccctgacg caaagccgag tatcacggca aagcattcag ctccgacgac 480
ccgaacggca ggctgcacta ctccattgat ttaccacaaa aacaggggta cggcagaatc 540
gaacacctga aaacgcccga gcagaatgtc gagcttgctt ccgccgaact caaagcagat 600
gaaaaatcac acgccgtcat tttgggcgac acgcgctacg gcggcgaaga aaaaggcact 660
taccacctcg cccttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag 720
ataagggaag aggttcacga aatcggcac gccggcaaac agtag 765

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<210> 88
<211> 471
<212> PRT
<213> Streptococcus pneumoniae

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<400> 88
Met Ala Asn Lys Ala Val Asn Asp Phe Ile Leu Ala Met Asn Tyr Asp
1          5          10          15
Lys Lys Lys Leu Leu Thr His Gln Gly Glu Ser Ile Glu Asn Arg Phe
20          25          30
Ile Lys Glu Gly Asn Gln Leu Pro Asp Glu Phe Val Val Ile Glu Arg
35          40          45
Lys Lys Arg Ser Leu Ser Thr Asn Thr Ser Asp Ile Ser Val Thr Ala
50          55          60
Thr Asn Asp Ser Arg Leu Tyr Pro Gly Ala Leu Leu Val Val Asp Glu
65          70          75          80
Thr Leu Leu Glu Asn Asn Pro Thr Leu Leu Ala Val Asp Arg Ala Pro
85          90          95
Met Thr Tyr Ser Ile Asp Leu Pro Gly Leu Ala Ser Ser Asp Ser Phe
100         105         110
Leu Gln Val Glu Asp Pro Ser Asn Ser Ser Val Arg Gly Ala Val Asn
115         120         125
Asp Leu Leu Ala Lys Trp His Gln Asp Tyr Gly Gln Val Asn Asn Val
130         135         140
Pro Ala Arg Met Gln Tyr Glu Lys Ile Thr Ala His Ser Met Glu Gln
145         150         155         160
Leu Lys Val Lys Phe Gly Ser Asp Phe Glu Lys Thr Gly Asn Ser Leu
165         170         175
Asp Ile Asp Phe Asn Ser Val His Ser Gly Glu Lys Gln Ile Gln Ile
180         185         190
Val Asn Phe Lys Gln Ile Tyr Tyr Thr Val Ser Val Asp Ala Val Lys
195         200         205
Asn Pro Gly Asp Val Phe Gln Asp Thr Val Thr Val Glu Asp Leu Lys
210         215         220
Gln Arg Gly Ile Ser Ala Glu Arg Pro Leu Val Tyr Ile Ser Ser Val
225         230         235         240
Ala Tyr Gly Arg Gln Val Tyr Leu Lys Leu Glu Thr Thr Ser Lys Ser
245         250         255
Asp Glu Val Glu Ala Ala Phe Glu Ala Leu Ile Lys Gly Val Lys Val
260         265         270
Ala Pro Gln Thr Glu Trp Lys Gln Ile Leu Asp Asn Thr Glu Val Lys
275         280         285

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Ala Val Ile Leu Gly Gly Asp Pro Ser Ser Gly Ala Arg Val Val Thr
 290 295 300
 Gly Lys Val Asp Met Val Glu Asp Leu Ile Gln Glu Gly Ser Arg Phe
 305 310 315 320
 Thr Ala Asp His Pro Gly Leu Pro Ile Ser Tyr Thr Thr Ser Phe Leu
 325 330 335
 Arg Asp Asn Val Val Ala Thr Phe Gln Asn Ser Thr Asp Tyr Val Glu
 340 345 350
 Thr Lys Val Thr Ala Tyr Arg Asn Gly Asp Leu Leu Leu Asp His Ser
 355 360 365
 Gly Ala Tyr Val Ala Gln Tyr Tyr Ile Thr Trp Asn Glu Leu Ser Tyr
 370 375 380
 Asp His Gln Gly Lys Glu Val Leu Thr Pro Lys Ala Trp Asp Arg Asn
 385 390 395 400
 Gly Gln Asp Leu Thr Ala His Phe Thr Thr Ser Ile Pro Leu Lys Gly
 405 410 415
 Asn Val Arg Asn Leu Ser Val Lys Ile Arg Glu Cys Thr Gly Leu Ala
 420 425 430
 Trp Glu Trp Trp Arg Thr Val Tyr Glu Lys Thr Asp Leu Pro Leu Val
 435 440 445
 Arg Lys Arg Thr Ile Ser Ile Trp Gly Thr Thr Leu Tyr Pro Gln Val
 450 455 460
 Glu Asp Lys Val Glu Asn Asp
 465 470

<210> 89
 <211> 499
 <212> PRT
 <213> Clostridium perfringens

<400> 89
 Met Ile Arg Phe Lys Lys Thr Lys Leu Ile Ala Ser Ile Ala Met Ala
 1 5 10 15
 Leu Cys Leu Phe Ser Gln Pro Val Ile Ser Phe Ser Lys Asp Ile Thr
 20 25 30
 Asp Lys Asn Gln Ser Ile Asp Ser Gly Ile Ser Ser Leu Ser Tyr Asn
 35 40 45
 Arg Asn Glu Val Leu Ala Ser Asn Gly Asp Lys Ile Glu Ser Phe Val
 50 55 60
 Pro Lys Glu Gly Lys Lys Ala Gly Asn Lys Phe Ile Val Val Glu Arg
 65 70 75 80
 Gln Lys Arg Ser Leu Thr Thr Ser Pro Val Asp Ile Ser Ile Ile Asp
 85 90 95
 Ser Val Asn Asp Arg Thr Tyr Pro Gly Ala Leu Gln Leu Ala Asp Lys
 100 105 110
 Ala Phe Val Glu Asn Arg Pro Thr Ile Leu Met Val Lys Glu Ala Ile
 115 120 125
 Asn Ile Asn Ile Asp Leu Pro Gly Leu Lys Gly Glu Asn Ser Ile Lys
 130 135 140
 Val Asp Asp Pro Thr Tyr Gly Lys Val Ser Gly Ala Ile Asp Glu Leu
 145 150 155 160
 Val Ser Lys Trp Asn Glu Lys Tyr Ser Ser Thr His Thr Leu Pro Ala
 165 170 175
 Arg Thr Gln Tyr Ser Glu Ser Met Val Tyr Ser Lys Ser Gln Ile Ser
 180 185 190

Ser Ala Leu Asn Val Asn Ala Lys Val Leu Glu Asn Ser Leu Gly Val
 195 200 205
 Asp Phe Asn Ala Val Ala Asn Asn Glu Lys Lys Val Met Ile Leu Ala
 210 215 220
 Tyr Lys Gln Ile Phe Tyr Thr Val Ser Ala Asp Leu Pro Lys Asn Pro
 225 230 235 240
 Ser Asp Leu Phe Asp Asp Ser Val Thr Phe Asn Asp Leu Lys Gln Lys
 245 250 255
 Gly Val Ser Asn Glu Ala Pro Pro Leu Met Val Ser Asn Val Ala Tyr
 260 265 270
 Gly Arg Thr Ile Tyr Val Lys Leu Glu Thr Thr Ser Ser Ser Lys Asp
 275 280 285
 Val Gln Ala Ala Phe Lys Ala Leu Ile Lys Asn Thr Asp Ile Lys Asn
 290 295 300
 Ser Gln Gln Tyr Lys Asp Ile Tyr Glu Asn Ser Ser Phe Thr Ala Val
 305 310 315 320
 Val Leu Gly Gly Asp Ala Gln Glu His Asn Lys Val Val Thr Lys Asp
 325 330 335
 Phe Asp Glu Ile Arg Lys Val Ile Lys Asp Asn Ala Thr Phe Ser Thr
 340 345 350
 Lys Asn Pro Ala Tyr Pro Ile Ser Tyr Thr Ser Val Phe Leu Lys Asp
 355 360 365
 Asn Ser Val Ala Ala Val His Asn Lys Thr Asp Tyr Ile Glu Thr Thr
 370 375 380
 Ser Thr Glu Tyr Ser Lys Gly Lys Ile Asn Leu Asp His Ser Gly Ala
 385 390 395 400
 Tyr Val Ala Gln Phe Glu Val Ala Trp Asp Glu Val Ser Tyr Asp Lys
 405 410 415
 Glu Gly Asn Glu Val Leu Thr His Lys Thr Trp Asp Gly Asn Tyr Gln
 420 425 430
 Asp Lys Thr Ala His Tyr Ser Thr Val Ile Pro Leu Glu Ala Asn Ala
 435 440 445
 Arg Asn Ile Arg Ile Lys Ala Arg Glu Cys Thr Gly Leu Ala Trp Glu
 450 455 460
 Trp Trp Arg Asp Val Ile Ser Glu Tyr Asp Val Pro Leu Thr Asn Asn
 465 470 475 480
 Ile Asn Val Ser Ile Trp Gly Thr Thr Leu Tyr Pro Gly Ser Ser Ile
 485 490 495
 Thr Tyr Asn

<210> 90
 <211> 532
 <212> PRT
 <213> Streptococcus intermedius

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

His	Gln	Gly	Glu	Lys	Leu	Lys	Asn	His	Ser	Ser	Arg	Glu	Ala	Phe	His	
				85					90					95		
Arg	Pro	Gly	Glu	Tyr	Val	Val	Ile	Glu	Lys	Lys	Lys	Gln	Ser	Ile	Ser	
			100					105					110			
Asn	Ala	Thr	Ser	Lys	Leu	Ser	Val	Ser	Ser	Ala	Asn	Asp	Asp	Arg	Ile	
			115				120					125				
Phe	Pro	Gly	Ala	Leu	Leu	Lys	Ala	Asp	Gln	Ser	Leu	Leu	Glu	Asn	Leu	
			130				135					140				
Pro	Thr	Leu	Ile	Pro	Val	Asn	Arg	Gly	Lys	Thr	Thr	Ile	Ser	Val	Asn	
145					150					155					160	
Leu	Pro	Gly	Leu	Lys	Asn	Gly	Glu	Ser	Asn	Leu	Thr	Val	Glu	Asn	Pro	
				165					170					175		
Ser	Asn	Ser	Thr	Val	Arg	Thr	Ala	Val	Asn	Asn	Leu	Val	Glu	Lys	Trp	
			180					185					190			
Ile	Gln	Asn	Tyr	Ser	Lys	Thr	His	Ala	Val	Pro	Ala	Arg	Met	Gln	Tyr	
		195					200					205				
Glu	Ser	Ile	Ser	Ala	Gln	Ser	Met	Ser	Gln	Leu	Gln	Ala	Lys	Phe	Gly	
		210				215					220					
Ala	Asp	Phe	Ser	Lys	Val	Gly	Ala	Pro	Leu	Asn	Val	Asp	Phe	Ser	Ser	
225					230					235					240	
Val	His	Lys	Gly	Glu	Lys	Gln	Val	Phe	Ile	Ala	Asn	Phe	Arg	Gln	Val	
				245					250					255		
Tyr	Tyr	Thr	Ala	Ser	Val	Asp	Ser	Pro	Asn	Ser	Pro	Ser	Ala	Leu	Phe	
			260					265					270			
Gly	Ser	Gly	Ile	Thr	Pro	Thr	Asp	Leu	Ile	Asn	Arg	Gly	Val	Asn	Ser	
		275					280					285				
Lys	Thr	Pro	Pro	Val	Tyr	Val	Ser	Asn	Val	Ser	Tyr	Gly	Arg	Ala	Met	
		290				295					300					
Tyr	Val	Lys	Phe	Glu	Thr	Thr	Ser	Lys	Ser	Thr	Lys	Val	Gln	Ala	Ala	
305					310					315					320	
Ile	Asp	Ala	Val	Val	Lys	Gly	Ala	Lys	Leu	Lys	Ala	Gly	Thr	Glu	Tyr	
				325					330					335		
Glu	Asn	Ile	Leu	Lys	Asn	Thr	Lys	Ile	Thr	Ala	Val	Val	Leu	Gly	Gly	
			340					345					350			
Asn	Pro	Gly	Glu	Ala	Ser	Lys	Val	Ile	Thr	Gly	Asn	Ile	Asp	Thr	Leu	
		355					360					365				
Lys	Asp	Leu	Ile	Gln	Lys	Gly	Ser	Asn	Phe	Ser	Ala	Gln	Ser	Pro	Ala	
		370				375					380					
Val	Pro	Ile	Ser	Tyr	Thr	Thr	Ser	Phe	Val	Lys	Asp	Asn	Ser	Ile	Ala	
385					390					395					400	
Thr	Ile	Gln	Asn	Asn	Thr	Asp	Tyr	Ile	Glu	Thr	Lys	Val	Thr	Ser	Tyr	
			405						410					415		
Lys	Asp	Gly	Ala	Leu	Thr	Leu	Asn	His	Asp	Gly	Ala	Phe	Val	Ala	Arg	
			420					425					430			
Phe	Tyr	Val	Tyr	Trp	Glu	Glu	Leu	Gly	His	Asp	Ala	Asp	Gly	Tyr	Glu	
		435					440					445				
Thr	Ile	Arg	Ser	Arg	Ser	Trp	Ser	Gly	Asn	Gly	Tyr	Asn	Arg	Gly	Ala	
		450				455					460					
His	Tyr	Ser	Thr	Thr	Leu	Arg	Phe	Lys	Gly	Asn	Val	Arg	Asn	Ile	Arg	
465					470					475					480	
Val	Lys	Val	Leu	Gly	Ala	Thr	Gly	Leu	Ala	Trp	Glu	Pro	Trp	Arg	Leu	
				485					490					495		
Ile	Tyr	Ser	Lys	Asn	Asp	Leu	Pro	Leu	Val	Pro	Gln	Arg	Asn	Ile	Ser	
			500					505					510			

Thr Trp Gly Thr Thr Leu His Pro Gln Phe Glu Asp Lys Val Val Lys
 515 520 525
 Asp Asn Thr Asp
 530

<210> 91
 <211> 501
 <212> PRT
 <213> Paenibacillus alvei

<400> 91
 Met Lys Lys Lys Ser Asn His Leu Lys Gly Arg Lys Val Leu Val Ser
 1 5 10 15
 Leu Leu Val Ser Leu Gln Val Phe Ala Phe Ala Ser Ile Ser Ser Ala
 20 25 30
 Ala Pro Thr Glu Pro Asn Asp Ile Asp Met Gly Ile Ala Gly Leu Asn
 35 40 45
 Tyr Asn Arg Asn Glu Val Leu Ala Ile Gln Gly Asp Gln Ile Ser Ser
 50 55 60
 Phe Val Pro Lys Glu Gly Ile Gln Ser Asn Gly Lys Phe Ile Val Val
 65 70 75 80
 Glu Arg Asp Lys Lys Ser Leu Thr Thr Ser Pro Val Asp Ile Ser Ile
 85 90 95
 Val Asp Ser Ile Thr Asn Arg Thr Tyr Pro Gly Ala Ile Gln Leu Ala
 100 105 110
 Asn Lys Asp Phe Ala Asp Asn Gln Pro Ser Leu Val Met Ala Ala Arg
 115 120 125
 Lys Pro Leu Asp Ile Ser Ile Asp Leu Pro Gly Leu Lys Asn Glu Asn
 130 135 140
 Thr Ile Ser Val Gln Asn Pro Asn Tyr Gly Thr Val Ser Ser Ala Ile
 145 150 155 160
 Asp Gln Leu Val Ser Thr Trp Gly Glu Lys Tyr Ser Ser Thr His Thr
 165 170 175
 Leu Pro Ala Arg Leu Gln Tyr Ala Glu Ser Met Val Tyr Ser Gln Asn
 180 185 190
 Gln Ile Ser Ser Ala Leu Asn Val Asn Ala Lys Val Leu Asn Gly Thr
 195 200 205
 Leu Gly Ile Asp Phe Asn Ala Val Ala Asn Gly Glu Lys Lys Val Met
 210 215 220
 Val Ala Ala Tyr Lys Gln Ile Phe Tyr Thr Val Ser Ala Gly Leu Pro
 225 230 235 240
 Asn Asn Pro Ser Asp Leu Phe Asp Asp Ser Val Thr Phe Ala Glu Leu
 245 250 255
 Ala Arg Lys Gly Val Ser Asn Glu Ala Pro Pro Leu Met Val Ser Asn
 260 265 270
 Val Ala Tyr Gly Arg Thr Ile Tyr Val Lys Leu Glu Thr Thr Ser Lys
 275 280 285
 Ser Asn Asp Val Gln Thr Ala Phe Lys Leu Leu Leu Asn Asn Pro Ser
 290 295 300
 Ile Gln Ala Ser Gly Gln Tyr Lys Asp Ile Tyr Glu Asn Ser Ser Phe
 305 310 315 320
 Thr Ala Val Val Leu Gly Gly Asp Ala Gln Thr His Asn Gln Val Val
 325 330 335
 Thr Lys Asp Phe Asn Val Ile Gln Ser Val Ile Lys Asp Asn Ala Gln
 340 345 350

Phe Ser Ser Lys Asn Pro Ala Tyr Pro Ile Ser Tyr Thr Ser Val Phe
 355 360 365
 Leu Lys Asp Asn Ser Ile Ala Ala Val His Asn Asn Thr Glu Tyr Ile
 370 375 380
 Glu Thr Lys Thr Thr Glu Tyr Ser Lys Gly Lys Ile Lys Leu Asp His
 385 390 395 400
 Ser Gly Ala Tyr Val Ala Gln Phe Glu Val Tyr Trp Asp Glu Phe Ser
 405 410 415
 Tyr Asp Ala Asp Gly Gln Glu Ile Val Thr Arg Lys Ser Trp Asp Gly
 420 425 430
 Asn Trp Arg Asp Arg Ser Ala His Phe Ser Thr Glu Ile Pro Leu Pro
 435 440 445
 Pro Asn Ala Lys Asn Ile Arg Ile Phe Ala Arg Glu Cys Thr Gly Leu
 450 455 460
 Ala Trp Glu Trp Trp Arg Thr Val Val Asp Glu Tyr Asn Val Pro Leu
 465 470 475 480
 Ala Ser Asp Ile Asn Val Ser Ile Trp Gly Thr Thr Leu Tyr Pro Lys
 485 490 495
 Ser Ser Ile Thr His
 500

<210> 92
 <211> 512
 <212> PRT
 <213> Bacillus anthracis

<400> 92
 Met Ile Phe Leu Asn Ile Lys Lys Asn Thr Lys Arg Arg Lys Phe Leu
 1 5 10 15
 Ala Cys Leu Leu Val Ser Leu Cys Thr Ile His Tyr Ser Ser Ile Ser
 20 25 30
 Phe Ala Glu Thr Gln Ala Gly Asn Ala Thr Gly Ala Ile Lys Asn Ala
 35 40 45
 Ser Asp Ile Asn Thr Gly Ile Ala Asn Leu Lys Tyr Asp Ser Arg Asp
 50 55 60
 Ile Leu Ala Val Asn Gly Asp Lys Val Glu Ser Phe Ile Pro Lys Glu
 65 70 75 80
 Ser Ile Asn Ser Asn Gly Lys Phe Val Val Val Glu Arg Glu Lys Lys
 85 90 95
 Ser Leu Thr Thr Ser Pro Val Asp Ile Leu Ile Ile Asp Ser Val Val
 100 105 110
 Asn Arg Thr Tyr Pro Gly Ala Val Gln Leu Ala Asn Lys Ala Phe Ala
 115 120 125
 Asp Asn Gln Pro Ser Leu Leu Val Ala Lys Arg Lys Pro Leu Asn Ile
 130 135 140
 Ser Ile Asp Leu Pro Gly Met Arg Lys Glu Asn Thr Ile Thr Val Gln
 145 150 155 160
 Asn Pro Thr Tyr Gly Asn Val Ala Gly Ala Val Asp Asp Leu Val Ser
 165 170 175
 Thr Trp Asn Glu Lys Tyr Ser Thr Thr His Thr Leu Pro Ala Arg Met
 180 185 190
 Gln Tyr Thr Glu Ser Met Val Tyr Ser Lys Ser Gln Ile Ala Ser Ala
 195 200 205
 Leu Asn Val Asn Ala Lys Tyr Leu Asp Asn Ser Leu Asn Ile Asp Phe
 210 215 220

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Asn Ala Val Ala Asn Gly Glu Lys Lys Val Met Val Ala Ala Tyr Lys
225                230                235                240
Gln Ile Phe Tyr Thr Val Ser Ala Glu Leu Pro Asn Asn Pro Ser Asp
                245                250                255
Leu Phe Asp Asn Ser Val Thr Phe Asp Glu Leu Thr Arg Lys Gly Val
                260                265                270
Ser Asn Ser Ala Pro Pro Val Met Val Ser Asn Val Ala Tyr Gly Arg
                275                280                285
Thr Val Tyr Val Lys Leu Glu Thr Thr Ser Lys Ser Lys Asp Val Gln
                290                295                300
Ala Ala Phe Lys Ala Leu Leu Lys Asn Asn Ser Val Glu Thr Ser Gly
305                310                315                320
Gln Tyr Lys Asp Ile Phe Glu Glu Ser Thr Phe Thr Ala Val Val Leu
                325                330                335
Gly Gly Asp Ala Lys Glu His Asn Lys Val Val Thr Lys Asp Phe Asn
                340                345                350
Glu Ile Arg Asn Ile Ile Lys Asp Asn Ala Glu Leu Ser Phe Lys Asn
                355                360                365
Pro Ala Tyr Pro Ile Ser Tyr Thr Ser Thr Phe Leu Lys Asp Asn Ala
                370                375                380
Thr Ala Ala Val His Asn Asn Thr Asp Tyr Ile Glu Thr Thr Thr Thr
385                390                395                400
Glu Tyr Ser Ser Ala Lys Met Thr Leu Asp His Tyr Gly Ala Tyr Val
                405                410                415
Ala Gln Phe Asp Val Phe Trp Asp Glu Phe Thr Phe Asp Gln Asn Gly
                420                425                430
Lys Glu Val Leu Thr His Lys Thr Trp Glu Gly Ser Gly Lys Asp Lys
                435                440                445
Thr Ala His Tyr Ser Thr Val Ile Pro Leu Pro Pro Asn Ser Lys Asn
                450                455                460
Ile Lys Ile Val Ala Arg Glu Cys Thr Gly Leu Ala Trp Glu Trp Trp
465                470                475                480
Arg Thr Ile Ile Asn Glu Gln Asn Val Pro Leu Thr Asn Glu Ile Lys
                485                490                495
Val Ser Ile Gly Gly Thr Thr Leu Tyr Pro Thr Ala Thr Ile Ser His
                500                505                510

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<210> 93
<211> 485
<212> PRT
<213> Bacillus cereus

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```

<400> 93
Met Lys Asn Phe Lys Gly Arg Lys Phe Leu Thr Cys Val Leu Val Ser
1                5                10                15
Leu Cys Thr Leu Asn Tyr Ser Ser Ile Ser Phe Ala Glu Thr Gln Ala
                20                25                30
Gly His Ala Asn Asp Ile Thr Lys Asn Ala Ser Ser Ile Asp Thr Gly
                35                40                45
Ile Gly Asn Leu Thr Tyr Asn Asn Gln Glu Val Leu Ala Val Asn Gly
                50                55                60
Asp Lys Val Glu Ser Phe Val Pro Lys Glu Ser Ile Asn Ser Asn Gly
65                70                75                80
Lys Phe Val Val Val Asp Val Arg Lys Asn His Leu Gln Arg His Gln
                85                90                95

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Ser	Ile	Phe	Arg	Leu	Leu	Asp	Ser	Val	Ala	Asn	Arg	Thr	Tyr	Pro	Gly
			100					105					110		
Ala	Val	Gln	Leu	Ala	Asn	Lys	Ala	Phe	Ala	Asp	Asn	Gln	Pro	Ser	Leu
		115					120					125			
Leu	Val	Ala	Lys	Arg	Lys	Pro	Leu	Asn	Ile	Ser	Ile	Asp	Leu	Pro	Gly
		130				135						140			
Met	Arg	Lys	Glu	Asn	Thr	Ile	Thr	Val	Gln	Asn	Pro	Thr	Tyr	Gly	Asn
145					150					155					160
Val	Ala	Gly	Ala	Val	Asp	Asp	Leu	Val	Ser	Thr	Trp	Asn	Glu	Lys	Tyr
				165					170					175	
Ser	Ala	Thr	His	Thr	Leu	Pro	Ala	Arg	Met	Gln	Tyr	Thr	Glu	Ser	Met
			180					185					190		
Val	Tyr	Ser	Lys	Ala	Gln	Ile	Ala	Ser	Ala	Leu	Asn	Val	Asn	Ala	Lys
		195					200					205			
Tyr	Leu	Asp	Asn	Ser	Leu	Asn	Ile	Asp	Phe	Asn	Ala	Val	Ala	Asn	Gly
		210				215					220				
Glu	Lys	Lys	Val	Met	Val	Ala	Ala	Tyr	Lys	Gln	Ile	Phe	Tyr	Thr	Val
225					230					235					240
Ser	Ala	Glu	Leu	Pro	Asn	Asn	Pro	Ser	Asp	Leu	Phe	Asp	Asn	Ser	Val
				245					250					255	
Thr	Phe	Gly	Glu	Leu	Thr	Arg	Lys	Gly	Val	Ser	Asn	Ser	Ala	Pro	Pro
			260					265					270		
Val	Met	Val	Ser	Asn	Val	Ala	Tyr	Gly	Arg	Thr	Val	Tyr	Val	Lys	Leu
		275					280					285			
Glu	Thr	Thr	Ser	Lys	Ser	Lys	Asp	Val	Gln	Ala	Ala	Phe	Lys	Ala	Leu
		290				295					300				
Leu	Lys	Asn	Asn	Ser	Val	Glu	Thr	Ser	Gly	Gln	Tyr	Lys	Asp	Ile	Phe
305					310					315					320
Glu	Glu	Ser	Thr	Phe	Thr	Ala	Val	Val	Leu	Gly	Gly	Asp	Ala	Lys	Glu
				325					330					335	
His	Asn	Lys	Val	Val	Thr	Lys	Asp	Phe	Asn	Glu	Ile	Arg	Asn	Ile	Ile
			340					345					350		
Lys	Asp	Asn	Ala	Glu	Leu	Ser	Phe	Lys	Asn	Pro	Ala	Tyr	Pro	Ile	Ser
		355					360					365			
Tyr	Thr	Ser	Thr	Phe	Leu	Lys	Asp	Asn	Ala	Thr	Ala	Ala	Val	His	Asn
		370				375					380				
Asn	Thr	Asp	Tyr	Ile	Glu	Thr	Thr	Thr	Thr	Glu	Tyr	Ser	Ser	Ala	Lys
385					390					395					400
Met	Thr	Leu	Asp	His	Tyr	Gly	Ala	Tyr	Val	Ala	Gln	Phe	Asp	Val	Ser
				405					410					415	
Trp	Asp	Gly	Phe	Thr	Phe	Asp	Gln	Asn	Gly	Lys	Glu	Ile	Leu	Thr	His
			420					425					430		
Lys	Thr	Trp	Glu	Gly	Ser	Gly	Lys	Asp	Lys	Thr	Ala	His	Tyr	Ser	Thr
		435				440						445			
Val	Ile	Pro	Leu	Pro	Pro	Asn	Ser	Lys	Asn	Ile	Lys	Ile	Val	Ala	Arg
		450				455					460				
Glu	Cys	Thr	Gly	Leu	Ala	Trp	Glu	Trp	Trp	Arg	Thr	Ile	Ile	Lys	Met
465					470					475					480
Asn	Lys	Met	Phe	His											
				485											

<210> 94
 <211> 528
 <212> PRT
 <213> *Listeria ivanovii*

<400> 94

Met	Lys	Lys	Ile	Met	Leu	Leu	Leu	Met	Thr	Leu	Leu	Leu	Val	Ser	Leu
1				5					10					15	
Pro	Leu	Ala	Gln	Glu	Ala	Gln	Ala	Asp	Ala	Ser	Val	Tyr	Ser	Tyr	Gln
			20					25						30	
Gly	Ile	Ile	Ser	His	Met	Ala	Pro	Pro	Ala	Ser	Pro	Pro	Ala	Lys	Pro
		35					40					45			
Lys	Thr	Pro	Val	Glu	Lys	Lys	Asn	Ala	Ala	Gln	Ile	Asp	Gln	Tyr	Ile
	50					55					60				
Gln	Gly	Leu	Asp	Tyr	Asp	Lys	Asn	Asn	Ile	Leu	Val	Tyr	Asp	Gly	Glu
65					70					75					80
Ala	Val	Lys	Asn	Val	Pro	Pro	Lys	Ala	Gly	Tyr	Lys	Glu	Gly	Asn	Gln
			85						90					95	
Tyr	Ile	Val	Val	Glu	Lys	Lys	Lys	Lys	Ser	Ile	Asn	Gln	Asn	Asn	Ala
			100					105						110	
Asp	Ile	Gln	Val	Ile	Asn	Ser	Leu	Ala	Ser	Leu	Thr	Tyr	Pro	Gly	Ala
		115					120					125			
Leu	Val	Lys	Ala	Asn	Ser	Glu	Leu	Val	Glu	Asn	Gln	Pro	Asp	Val	Leu
	130					135					140				
Pro	Val	Lys	Arg	Asp	Ser	Val	Thr	Leu	Ser	Ile	Asp	Leu	Pro	Gly	Met
145					150					155					160
Val	Asn	His	Asp	Asn	Glu	Ile	Val	Val	Gln	Asn	Ala	Thr	Lys	Ser	Asn
				165					170					175	
Ile	Asn	Asp	Gly	Val	Asn	Thr	Leu	Val	Asp	Arg	Trp	Asn	Asn	Lys	Tyr
			180					185						190	
Ser	Glu	Glu	Tyr	Pro	Asn	Ile	Ser	Ala	Lys	Ile	Asp	Tyr	Asp	Gln	Glu
		195					200				205				
Met	Ala	Tyr	Ser	Glu	Ser	Gln	Leu	Val	Ala	Lys	Phe	Gly	Ala	Ala	Phe
	210					215					220				
Lys	Ala	Val	Asn	Asn	Ser	Leu	Asn	Val	Asn	Phe	Gly	Ala	Ile	Ser	Glu
225					230					235					240
Gly	Lys	Val	Gln	Glu	Glu	Val	Ile	Asn	Phe	Lys	Gln	Ile	Tyr	Tyr	Thr
			245					250						255	
Val	Asn	Val	Asn	Glu	Pro	Thr	Ser	Pro	Ser	Arg	Phe	Phe	Gly	Lys	Ser
			260					265					270		
Val	Thr	Lys	Glu	Asn	Leu	Gln	Ala	Leu	Gly	Val	Asn	Ala	Glu	Asn	Pro
		275					280					285			
Pro	Ala	Tyr	Ile	Ser	Ser	Val	Ala	Tyr	Gly	Arg	Asp	Ile	Phe	Val	Lys
	290					295					300				
Leu	Ser	Thr	Ser	Ser	His	Ser	Thr	Arg	Val	Lys	Ala	Ala	Phe	Asp	Thr
305					310					315					320
Ala	Phe	Lys	Gly	Lys	Ser	Val	Lys	Gly	Asp	Thr	Glu	Leu	Glu	Asn	Ile
			325					330						335	
Ile	Gln	Asn	Ala	Ser	Phe	Lys	Ala	Val	Ile	Tyr	Gly	Gly	Ser	Ala	Lys
			340					345					350		
Asp	Glu	Val	Glu	Ile	Ile	Asp	Gly	Asp	Leu	Ser	Lys	Leu	Arg	Asp	Ile
		355					360					365			
Leu	Lys	Gln	Gly	Ala	Asn	Phe	Asp	Lys	Lys	Asn	Pro	Gly	Val	Pro	Ile
	370					375					380				
Ala	Tyr	Thr	Thr	Asn	Phe	Leu	Lys	Asp	Asn	Gln	Leu	Ala	Val	Val	Lys
385					390					395					400
Asn	Asn	Ser	Glu	Tyr	Ile	Glu	Thr	Thr	Ser	Lys	Ala	Tyr	Ser	Asp	Gly
			405					410						415	
Lys	Ile	Asn	Leu	Asp	His	Ser	Gly	Ala	Tyr	Val	Ala	Arg	Phe	Asn	Val
			420					425					430		
Thr	Trp	Asp	Glu	Val	Ser	Tyr	Asp	Ala	Asn	Gly	Asn	Glu	Val	Val	Glu
		435					440					445			

His Lys Lys Trp Ser Glu Asn Asp Lys Asp Lys Leu Ala His Phe Thr
 450 455 460
 Thr Ser Ile Tyr Leu Pro Gly Asn Ala Arg Asn Ile Asn Ile His Ala
 465 470 475 480
 Lys Glu Cys Thr Gly Leu Ala Trp Glu Trp Trp Arg Thr Val Val Asp
 485 490 495
 Asp Arg Asn Leu Pro Leu Val Lys Asn Arg Asn Val Cys Ile Trp Gly
 500 505 510
 Thr Thr Leu Tyr Pro Ala Tyr Ser Asp Thr Val Asp Asn Pro Ile Lys
 515 520 525

<210> 95

<211> 534

<212> PRT

<213> Arcanobacterium pyogenes

<400> 95

Met Lys Arg Lys Ala Phe Ala Ser Leu Val Ala Ser Val Val Ala Ala
 1 5 10 15
 Ala Thr Val Thr Met Pro Thr Ala Ser Phe Ala Ala Gly Leu Gly Asn
 20 25 30
 Ser Ser Gly Leu Thr Asp Gly Leu Ser Ala Pro Arg Ala Ser Ile Ser
 35 40 45
 Pro Thr Asp Lys Val Asp Leu Lys Ser Ala Gln Glu Thr Asp Glu Thr
 50 55 60
 Gly Val Asp Lys Tyr Ile Arg Gly Leu Lys Tyr Asp Pro Ser Gly Val
 65 70 75 80
 Leu Ala Val Lys Gly Glu Ser Ile Glu Asn Val Pro Val Thr Lys Asp
 85 90 95
 Gln Leu Lys Asp Gly Thr Tyr Thr Val Phe Lys His Glu Arg Lys Ser
 100 105 110
 Phe Asn Asn Leu Arg Ser Asp Ile Ser Ala Phe Asp Ala Asn Asn Ala
 115 120 125
 His Val Tyr Pro Gly Ala Leu Val Leu Ala Asn Lys Asp Leu Ala Lys
 130 135 140
 Gly Ser Pro Thr Ser Ile Gly Ile Ala Arg Ala Pro Gln Thr Val Ser
 145 150 155 160
 Val Asp Leu Pro Gly Leu Val Asp Gly Lys Asn Lys Val Val Ile Asn
 165 170 175
 Asn Pro Thr Lys Ser Ser Val Thr Gln Gly Leu Asn Gly Leu Leu Asp
 180 185 190
 Gly Trp Ile Gln Arg Asn Ser Lys Tyr Pro Asp His Ala Ala Lys Ile
 195 200 205
 Ser Tyr Asp Glu Thr Met Val Thr Ser Lys Arg Gln Leu Glu Ala Lys
 210 215 220
 Leu Gly Leu Gly Phe Glu Lys Val Ser Ala Lys Leu Asn Val Asp Phe
 225 230 235 240
 Asp Ala Ile His Lys Arg Glu Arg Gln Val Ala Ile Ala Ser Phe Lys
 245 250 255
 Gln Ile Tyr Tyr Thr Ala Ser Val Asp Thr Pro Thr Ser Pro His Ser
 260 265 270
 Val Phe Gly Pro Asn Val Thr Ala Gln Asp Leu Lys Asp Arg Gly Val
 275 280 285
 Asn Asn Lys Asn Pro Leu Gly Tyr Ile Ser Ser Val Ser Tyr Gly Arg
 290 295 300

Gln Ile Phe Val Lys Leu Glu Thr Thr Ser Thr Ser Asn Asp Val Gln
 305 310 315 320
 Ala Ala Phe Ser Gly Leu Phe Lys Ala Lys Phe Gly Asn Leu Ser Thr
 325 330 335
 Glu Phe Lys Ala Lys Tyr Ala Asp Ile Leu Asn Lys Thr Arg Ala Thr
 340 345 350
 Val Tyr Ala Val Gly Gly Ser Ala Arg Gly Gly Val Glu Val Ala Thr
 355 360 365
 Gly Asn Ile Asp Ala Leu Lys Lys Ile Ile Lys Glu Glu Ser Thr Tyr
 370 375 380
 Ser Thr Lys Val Pro Ala Val Pro Val Ser Tyr Ala Val Asn Phe Leu
 385 390 395 400
 Lys Asp Asn Gln Leu Ala Ala Val Arg Ser Ser Gly Asp Tyr Ile Glu
 405 410 415
 Thr Thr Ala Thr Thr Tyr Lys Ser Gly Glu Ile Thr Phe Arg His Gly
 420 425 430
 Gly Gly Tyr Val Ala Lys Phe Arg Leu Lys Trp Asp Glu Ile Ser Tyr
 435 440 445
 Asp Pro Gln Gly Lys Glu Ile Arg Thr Pro Lys Thr Trp Ser Gly Asn
 450 455 460
 Trp Ala Ala Arg Thr Leu Gly Phe Arg Glu Thr Ile Gln Leu Pro Ala
 465 470 475 480
 Asn Ala Arg Asn Ile His Val Glu Ala Gly Glu Ala Thr Gly Leu Ala
 485 490 495
 Trp Asp Pro Trp Trp Thr Val Ile Asn Lys Lys Asn Leu Pro Leu Val
 500 505 510
 Pro His Arg Glu Ile Val Leu Lys Gly Thr Thr Leu Asn Pro Trp Val
 515 520 525
 Glu Asp Asn Val Lys Ser
 530

<210> 96
 <211> 530
 <212> PRT
 <213> *Listeria seeligeri*

<400> 96
 Met Lys Ile Phe Gly Leu Val Ile Met Ser Leu Leu Phe Val Ser Leu
 1 5 10 15
 Pro Ile Thr Gln Gln Pro Glu Ala Arg Asp Val Pro Ala Tyr Asp Arg
 20 25 30
 Ser Glu Val Thr Ile Ser Pro Ala Glu Thr Pro Glu Ser Pro Pro Ala
 35 40 45
 Thr Pro Lys Thr Pro Val Glu Lys Lys His Ala Glu Glu Ile Asn Lys
 50 55 60
 Tyr Ile Trp Gly Leu Asn Tyr Asp Lys Asn Ser Ile Leu Val Tyr Gln
 65 70 75 80
 Gly Glu Ala Val Thr Asn Val Pro Pro Lys Lys Gly Tyr Lys Asp Gly
 85 90 95
 Ser Glu Tyr Ile Val Val Glu Lys Lys Lys Lys Gly Ile Asn Gln Asn
 100 105 110
 Asn Ala Asp Ile Ser Val Ile Asn Ala Ile Ser Ser Leu Thr Tyr Pro
 115 120 125
 Gly Ala Leu Val Lys Ala Asn Arg Glu Leu Val Glu Asn Gln Pro Asn
 130 135 140

Val	Leu	Pro	Val	Lys	Arg	Asp	Ser	Leu	Thr	Leu	Ser	Val	Asp	Leu	Pro
145					150					155					160
Gly	Met	Thr	Lys	Lys	Asp	Asn	Lys	Ile	Phe	Val	Lys	Asn	Pro	Thr	Lys
				165					170						175
Ser	Asn	Val	Asn	Asn	Ala	Val	Asn	Thr	Leu	Val	Glu	Arg	Trp	Asn	Asp
			180					185					190		
Lys	Tyr	Ser	Lys	Ala	Tyr	Pro	Asn	Ile	Asn	Ala	Lys	Ile	Asp	Tyr	Ser
		195					200					205			
Asp	Glu	Met	Ala	Tyr	Ser	Glu	Ser	Gln	Leu	Ile	Ala	Lys	Phe	Gly	Thr
	210					215					220				
Ala	Phe	Lys	Ala	Val	Asn	Asn	Ser	Leu	Asn	Val	Asn	Phe	Glu	Ala	Ile
225					230					235					240
Ser	Asp	Gly	Lys	Val	Gln	Glu	Glu	Val	Ile	Ser	Phe	Lys	Gln	Ile	Tyr
			245						250						255
Tyr	Asn	Ile	Asn	Val	Asn	Glu	Pro	Thr	Ser	Pro	Ser	Lys	Phe	Phe	Gly
			260					265					270		
Gly	Ser	Val	Thr	Lys	Glu	Gln	Leu	Asp	Ala	Leu	Gly	Val	Asn	Ala	Glu
		275					280					285			
Asn	Pro	Pro	Ala	Tyr	Ile	Ser	Ser	Val	Ala	Tyr	Gly	Arg	Gln	Val	Tyr
	290					295					300				
Val	Lys	Leu	Ser	Ser	Ser	Ser	His	Ser	Asn	Lys	Val	Lys	Thr	Ala	Phe
305					310					315					320
Glu	Ala	Ala	Met	Ser	Gly	Lys	Ser	Val	Lys	Gly	Asp	Val	Glu	Leu	Thr
			325						330						335
Asn	Ile	Ile	Lys	Asn	Ser	Ser	Phe	Lys	Ala	Val	Ile	Tyr	Gly	Gly	Ser
			340					345					350		
Ala	Lys	Glu	Glu	Val	Glu	Ile	Ile	Asp	Gly	Asn	Leu	Gly	Glu	Leu	Arg
		355					360					365			
Asp	Ile	Leu	Lys	Lys	Gly	Ser	Thr	Tyr	Asp	Arg	Glu	Asn	Pro	Gly	Val
	370					375					380				
Pro	Ile	Ser	Tyr	Thr	Thr	Asn	Phe	Leu	Lys	Asp	Asn	Asp	Leu	Ala	Val
385					390					395					400
Val	Lys	Asn	Asn	Ser	Glu	Tyr	Ile	Glu	Thr	Thr	Ser	Lys	Ser	Tyr	Thr
			405						410						415
Asp	Gly	Lys	Ile	Asn	Ile	Asp	His	Ser	Gly	Gly	Tyr	Val	Ala	Gln	Phe
			420					425					430		
Asn	Ile	Ser	Trp	Asp	Glu	Val	Ser	Tyr	Asp	Glu	Asn	Gly	Asn	Glu	Ile
		435					440					445			
Lys	Val	His	Lys	Lys	Trp	Gly	Glu	Asn	Tyr	Lys	Ser	Lys	Leu	Ala	His
	450					455					460				
Phe	Thr	Ser	Ser	Ile	Tyr	Leu	Pro	Gly	Asn	Ala	Arg	Asn	Ile	Asn	Ile
465					470					475					480
Tyr	Ala	Arg	Glu	Cys	Thr	Gly	Leu	Phe	Trp	Glu	Trp	Trp	Arg	Thr	Val
			485						490						495
Ile	Asp	Asp	Arg	Asn	Leu	Pro	Leu	Val	Lys	Asn	Arg	Asn	Val	Ser	Ile
			500					505					510		
Trp	Gly	Thr	Thr	Leu	Tyr	Pro	Arg	His	Ser	Asn	Asn	Val	Asp	Asn	Pro
		515					520					525			
Ile	Gln														
	530														

<210> 97

<211> 574

<212> PRT

<213> Streptococcus pyogenes

<400> 97

Met	Lys	Asp	Met	Ser	Asn	Lys	Lys	Thr	Phe	Lys	Lys	Tyr	Ser	Arg	Val
1				5					10					15	
Ala	Gly	Leu	Leu	Thr	Ala	Ala	Leu	Ile	Ile	Gly	Asn	Leu	Val	Thr	Ala
			20					25					30		
Asn	Ala	Glu	Ser	Asn	Lys	Gln	Asn	Thr	Ala	Ser	Thr	Glu	Thr	Thr	Thr
		35					40					45			
Thr	Asn	Glu	Gln	Pro	Lys	Pro	Glu	Ser	Ser	Glu	Leu	Thr	Thr	Glu	Lys
	50					55					60				
Ala	Gly	Gln	Lys	Thr	Asp	Asp	Met	Leu	Asn	Ser	Asn	Asp	Met	Ile	Lys
65					70					75					80
Leu	Ala	Pro	Lys	Glu	Met	Pro	Leu	Glu	Ser	Ala	Glu	Lys	Glu	Glu	Lys
				85					90					95	
Lys	Ser	Glu	Asp	Lys	Lys	Lys	Ser	Glu	Glu	Asp	His	Thr	Glu	Glu	Ile
			100					105					110		
Asn	Asp	Lys	Ile	Tyr	Ser	Leu	Asn	Tyr	Asn	Glu	Leu	Glu	Val	Leu	Ala
		115					120					125			
Lys	Asn	Gly	Glu	Thr	Ile	Glu	Asn	Phe	Val	Pro	Lys	Glu	Gly	Val	Lys
	130					135						140			
Lys	Ala	Asp	Lys	Phe	Ile	Val	Ile	Glu	Arg	Lys	Lys	Lys	Asn	Ile	Asn
145					150					155					160
Thr	Thr	Pro	Val	Asp	Ile	Ser	Ile	Ile	Asp	Ser	Val	Thr	Asp	Arg	Thr
				165					170					175	
Tyr	Pro	Ala	Ala	Leu	Gln	Leu	Ala	Asn	Lys	Gly	Phe	Thr	Glu	Asn	Lys
			180					185					190		
Pro	Asp	Ala	Val	Val	Thr	Lys	Arg	Asn	Pro	Gln	Lys	Ile	His	Ile	Asp
		195					200					205			
Leu	Pro	Gly	Met	Gly	Asp	Lys	Ala	Thr	Val	Glu	Val	Asn	Asp	Pro	Thr
	210					215					220				
Tyr	Ala	Asn	Val	Ser	Thr	Ala	Ile	Asp	Asn	Leu	Val	Asn	Gln	Trp	His
225					230					235					240
Asp	Asn	Tyr	Ser	Gly	Gly	Asn	Thr	Leu	Pro	Ala	Arg	Thr	Gln	Tyr	Thr
				245					250					255	
Glu	Ser	Met	Val	Tyr	Ser	Lys	Ser	Gln	Ile	Glu	Ala	Ala	Leu	Asn	Val
		260						265					270		
Asn	Ser	Lys	Ile	Leu	Asp	Gly	Thr	Leu	Gly	Ile	Asp	Phe	Lys	Ser	Ile
		275					280					285			
Ser	Lys	Gly	Glu	Lys	Lys	Val	Met	Ile	Ala	Ala	Tyr	Lys	Gln	Ile	Phe
	290					295					300				
Tyr	Thr	Val	Ser	Ala	Asn	Leu	Pro	Asn	Asn	Pro	Ala	Asp	Val	Phe	Asp
305					310					315					320
Lys	Ser	Val	Thr	Phe	Lys	Glu	Leu	Gln	Arg	Lys	Gly	Val	Ser	Asn	Glu
				325					330					335	
Ala	Pro	Pro	Leu	Phe	Val	Ser	Asn	Val	Ala	Tyr	Gly	Arg	Thr	Val	Phe
			340					345					350		
Val	Lys	Leu	Glu	Thr	Ser	Ser	Lys	Ser	Asn	Asp	Val	Glu	Ala	Ala	Phe
		355					360					365			
Ser	Ala	Ala	Leu	Lys	Gly	Thr	Asp	Val	Lys	Thr	Asn	Gly	Lys	Tyr	Ser
		370				375					380				
Asp	Ile	Leu	Glu	Asn	Ser	Ser	Phe	Thr	Ala	Val	Val	Leu	Gly	Gly	Asp
385					390					395					400
Ala	Ala	Glu	His	Asn	Lys	Val	Val	Thr	Lys	Asp	Phe	Asp	Val	Ile	Arg
				405					410					415	
Asn	Val	Ile	Lys	Asp	Asn	Ala	Thr	Phe	Ser	Arg	Lys	Asn	Pro	Ala	Tyr
			420					425					430		
Pro	Ile	Ser	Tyr	Thr	Ser	Val	Phe	Leu	Lys	Asn	Asn	Lys	Ile	Ala	Gly
			435				440					445			

Val	Asn	Asn	Arg	Thr	Glu	Tyr	Val	Glu	Thr	Thr	Ser	Thr	Glu	Tyr	Thr
450						455					460				
Ser	Gly	Lys	Ile	Asn	Leu	Ser	His	Arg	Gly	Ala	Tyr	Val	Ala	Gln	Tyr
465					470					475					480
Glu	Ile	Leu	Trp	Asp	Glu	Ile	Asn	Tyr	Asp	Asp	Lys	Gly	Lys	Glu	Val
				485					490					495	
Ile	Thr	Lys	Arg	Arg	Trp	Asp	Asn	Asn	Trp	Tyr	Ser	Lys	Thr	Ser	Pro
			500					505					510		
Phe	Ser	Thr	Val	Ile	Pro	Leu	Gly	Ala	Asn	Ser	Arg	Asn	Ile	Arg	Ile
		515					520					525			
Met	Ala	Arg	Glu	Cys	Thr	Gly	Leu	Ala	Trp	Glu	Trp	Trp	Arg	Lys	Val
	530					535					540				
Ile	Asp	Glu	Arg	Asp	Val	Lys	Leu	Ser	Lys	Glu	Ile	Asn	Val	Asn	Ile
545					550					555					560
Ser	Gly	Ser	Thr	Leu	Ser	Pro	Tyr	Gly	Ser	Ile	Thr	Tyr	Lys		
				565					570						

<210> 98
 <211> 497
 <212> PRT
 <213> Streptococcus suis

<400> 98

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

Thr Asp Glu Val Pro Pro Val Tyr Val Ser Ser Val Ser Tyr Gly Arg
 260 265 270
 Ser Met Phe Ile Lys Leu Glu Thr Ser Ser Arg Ser Thr Gln Val Gln
 275 280 285
 Ala Ala Phe Lys Ala Ala Ile Lys Gly Val Asp Ile Ser Gly Asn Ala
 290 295 300
 Glu Tyr Gln Asp Ile Leu Lys Asn Thr Ser Phe Ser Ala Tyr Ile Phe
 305 310 315 320
 Gly Gly Asp Ala Gly Ser Ala Ala Thr Val Val Ser Gly Asn Ile Glu
 325 330 335
 Thr Leu Lys Lys Ile Ile Glu Glu Gly Ala Arg Tyr Gly Lys Leu Asn
 340 345 350
 Pro Gly Val Pro Ile Ser Tyr Ser Thr Asn Phe Val Lys Asp Asn Arg
 355 360 365
 Pro Ala Gln Ile Leu Ser Asn Ser Glu Tyr Ile Glu Thr Thr Ser Thr
 370 375 380
 Val His Asn Ser Ser Ala Leu Thr Leu Asp His Ser Gly Ala Tyr Val
 385 390 395 400
 Ala Lys Tyr Asn Ile Thr Trp Glu Glu Val Ser Tyr Asn Glu Ala Gly
 405 410 415
 Glu Glu Val Trp Glu Pro Lys Ala Trp Asp Lys Asn Gly Val Asn Leu
 420 425 430
 Thr Ser His Trp Ser Glu Thr Ile Gln Ile Pro Gly Asn Ala Arg Asn
 435 440 445
 Leu His Val Asn Ile Gln Glu Cys Thr Gly Leu Ala Trp Glu Trp Trp
 450 455 460
 Arg Thr Val Tyr Asp Lys Asp Leu Pro Leu Val Gly Gln Arg Lys Ile
 465 470 475 480
 Thr Ile Trp Gly Thr Thr Leu Tyr Pro Gln Tyr Ala Asp Glu Val Ile
 485 490 495
 Glu

<210> 99
 <211> 527
 <212> PRT
 <213> Clostridium tetani

<400> 99
 Met Asn Lys Asn Val Leu Lys Phe Val Ser Arg Ser Leu Leu Ile Phe
 1 5 10 15
 Ser Met Thr Gly Leu Ile Ser Asn Tyr Asn Ser Ser Asn Val Leu Ala
 20 25 30
 Lys Gly Asn Val Glu Glu His Ser Leu Ile Asn Asn Gly Gln Val Val
 35 40 45
 Thr Ser Asn Thr Lys Cys Asn Leu Ala Lys Asp Asn Ser Ser Asp Ile
 50 55 60
 Asp Lys Asn Ile Tyr Gly Leu Ser Tyr Asp Pro Arg Lys Ile Leu Ser
 65 70 75 80
 Tyr Asn Gly Glu Gln Val Glu Asn Phe Val Pro Ala Glu Gly Phe Glu
 85 90 95
 Asn Pro Asp Lys Phe Ile Val Val Lys Arg Glu Lys Lys Ser Ile Ser
 100 105 110
 Asp Ser Thr Ala Asp Ile Ser Ile Ile Asp Ser Ile Asn Asp Arg Thr
 115 120 125
 Tyr Pro Gly Ala Ile Gln Leu Ala Asn Arg Asn Leu Met Glu Asn Lys
 130 135 140

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Pro Asp Ile Ile Ser Cys Glu Arg Lys Pro Ile Thr Ile Ser Val Asp
145          150          155          160
Leu Pro Gly Met Ala Glu Asp Gly Lys Lys Val Val Asn Ser Pro Thr
          165          170          175
Tyr Ser Ser Val Asn Ser Ala Ile Asn Ser Ile Leu Asp Thr Trp Asn
          180          185          190
Ser Lys Tyr Ser Ser Lys Tyr Thr Ile Pro Thr Arg Met Ser Tyr Ser
          195          200          205
Asp Thr Met Val Tyr Ser Gln Ser Gln Leu Ser Ala Ala Val Gly Cys
210          215          220
Asn Phe Lys Ala Leu Asn Lys Ala Leu Asn Ile Asp Phe Asp Ser Ile
225          230          235          240
Phe Lys Gly Glu Lys Lys Val Met Leu Leu Ala Tyr Lys Gln Ile Phe
          245          250          255
Tyr Thr Val Ser Val Asp Pro Pro Asn Arg Pro Ser Asp Leu Phe Gly
          260          265          270
Asp Ser Val Thr Phe Asp Glu Leu Ala Leu Lys Gly Ile Asn Asn Asn
          275          280          285
Asn Pro Pro Ala Tyr Val Ser Asn Val Ala Tyr Gly Arg Thr Ile Tyr
          290          295          300
Val Lys Leu Glu Thr Thr Ser Lys Ser Ser His Val Lys Ala Ala Phe
305          310          315          320
Lys Ala Leu Ile Asn Asn Gln Asp Ile Ser Ser Asn Ala Glu Tyr Lys
          325          330          335
Asp Ile Leu Asn Gln Ser Ser Phe Thr Ala Thr Val Leu Gly Gly Gly
          340          345          350
Ala Gln Glu His Asn Lys Ile Ile Thr Lys Asp Phe Asp Glu Ile Arg
          355          360          365
Asn Ile Ile Lys Asn Asn Ser Val Tyr Ser Pro Gln Asn Pro Gly Tyr
          370          375          380
Pro Ile Ser Tyr Thr Thr Thr Phe Leu Lys Asp Asn Ser Ile Ala Ser
385          390          395          400
Val Asn Asn Lys Thr Glu Tyr Ile Glu Thr Thr Ala Thr Glu Tyr Thr
          405          410          415
Asn Gly Lys Ile Val Leu Asp His Ser Gly Ala Tyr Val Ala Gln Phe
          420          425          430
Gln Val Thr Trp Asp Glu Val Ser Tyr Asp Glu Lys Gly Asn Glu Ile
          435          440          445
Val Glu His Lys Ala Trp Glu Gly Asn Asn Arg Asp Arg Thr Ala His
          450          455          460
Phe Asn Thr Glu Ile Tyr Leu Lys Gly Asn Ala Arg Asn Ile Ser Val
465          470          475          480
Lys Ile Arg Glu Cys Thr Gly Leu Ala Trp Glu Trp Trp Arg Thr Ile
          485          490          495
Val Asp Val Lys Asn Ile Pro Leu Ala Lys Glu Arg Thr Phe Tyr Ile
          500          505          510
Trp Gly Thr Thr Leu Tyr Pro Lys Thr Ser Ile Glu Thr Lys Met
          515          520          525

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<210> 100
<211> 529
<212> PRT
<213> Listeria monocytogenes

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<400> 100
Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Ile Ser Leu
1      5      10      15
Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe His Lys
      20      25      30
Glu Asp Leu Ile Ser Ser Met Ala Pro Pro Thr Ser Pro Pro Ala Ser
      35      40      45
Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Glu Ile Asp Lys Tyr
      50      55      60
Ile Gln Gly Leu Asp Tyr Asn Lys Asn Asn Val Leu Val Tyr His Gly
65      70      75      80
Asp Ala Val Thr Asn Val Pro Pro Arg Lys Gly Tyr Lys Asp Gly Asn
      85      90      95
Glu Tyr Ile Val Val Glu Lys Lys Lys Lys Ser Ile Asn Gln Asn Asn
      100      105      110
Ala Asp Ile Gln Val Val Asn Ala Ile Ser Ser Leu Thr Tyr Pro Gly
      115      120      125
Ala Leu Val Lys Ala Asn Ser Glu Leu Val Glu Asn Gln Pro Asp Val
      130      135      140
Leu Pro Val Lys Arg Asp Ser Leu Thr Leu Ser Ile Asp Leu Pro Gly
145      150      155      160
Met Thr Asn Gln Asp Asn Lys Ile Val Val Lys Asn Ala Thr Lys Ser
      165      170      175
Asn Val Asn Asn Ala Val Asn Thr Leu Val Glu Arg Trp Asn Glu Lys
      180      185      190
Tyr Ala Gln Ala Tyr Pro Asn Val Ser Ala Lys Ile Asp Tyr Asp Asp
      195      200      205
Glu Met Ala Tyr Ser Glu Ser Gln Leu Ile Ala Lys Phe Gly Thr Ala
      210      215      220
Phe Lys Ala Val Asn Asn Ser Leu Asn Val Asn Phe Gly Ala Ile Ser
225      230      235      240
Glu Gly Lys Met Gln Glu Glu Val Ile Ser Phe Lys Gln Ile Tyr Tyr
      245      250      255
Asn Val Asn Val Asn Glu Pro Thr Arg Pro Ser Arg Phe Phe Gly Lys
      260      265      270
Ala Val Thr Lys Glu Gln Leu Gln Ala Leu Gly Val Asn Ala Glu Asn
      275      280      285
Pro Pro Ala Tyr Ile Ser Ser Val Ala Tyr Gly Arg Gln Val Tyr Leu
      290      295      300
Lys Leu Ser Thr Asn Ser His Ser Thr Lys Val Lys Ala Ala Phe Asp
305      310      315      320
Ala Ala Val Ser Gly Lys Ser Val Ser Gly Asp Val Glu Leu Thr Asn
      325      330      335
Ile Ile Lys Asn Ser Ser Phe Lys Ala Val Ile Tyr Gly Gly Ser Ala
      340      345      350
Lys Asp Glu Val Gln Ile Ile Asp Gly Asn Leu Gly Asp Leu Arg Asp
      355      360      365
Ile Leu Lys Lys Gly Ala Thr Phe Asn Arg Glu Thr Pro Gly Val Pro
      370      375      380
Ile Ala Tyr Thr Thr Asn Phe Leu Lys Asp Asn Glu Leu Ala Val Ile
385      390      395      400
Lys Asn Asn Ser Glu Tyr Ile Glu Thr Thr Ser Lys Ala Tyr Thr Asp
      405      410      415
Gly Lys Ile Asn Ile Asp His Ser Gly Gly Tyr Val Ala Gln Phe Asn
      420      425      430
Ile Ser Trp Asp Glu Ile Asn Tyr Asp Pro Glu Gly Asn Glu Ile Val
435      440      445

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Gln His Lys Asn Trp Ser Glu Asn Asn Lys Ser Lys Leu Ala His Phe
 450 455 460
 Thr Ser Ser Ile Tyr Leu Pro Gly Asn Ala Arg Asn Ile Asn Val Tyr
 465 470 475 480
 Ala Lys Glu Cys Thr Gly Leu Ala Trp Glu Trp Trp Arg Thr Val Ile
 485 490 495
 Asp Asp Arg Asn Leu Pro Leu Val Lys Asn Arg Asn Ile Ser Ile Trp
 500 505 510
 Gly Thr Thr Leu Tyr Pro Lys Tyr Ser Asn Ser Val Asp Asn Pro Ile
 515 520 525
 Glu

<210> 101
 <211> 512
 <212> PRT
 <213> Bacillus thuringiensis

<400> 101
 Met Ile Phe Leu Asn Ile Lys Lys Asn Gly Lys Arg Arg Lys Phe Leu
 1 5 10 15
 Thr Cys Val Leu Val Ser Leu Cys Thr Leu Asn Tyr Ser Ser Thr Ser
 20 25 30
 Phe Ala Glu Thr Gln Ala Gly His Ala Thr Asp Ile Thr Lys Asn Ala
 35 40 45
 Ser Ser Ile Asp Thr Gly Ile Gly Asn Leu Thr Tyr Asn Asn Gln Glu
 50 55 60
 Val Leu Ala Val Asn Gly Asp Lys Val Glu Ser Phe Val Pro Lys Glu
 65 70 75 80
 Ser Ile Asn Ser Asn Gly Lys Phe Val Val Val Glu Arg Glu Lys Lys
 85 90 95
 Ser Leu Thr Thr Ser Pro Val Asp Ile Ser Ile Ile Asp Ser Val Ala
 100 105 110
 Asn Arg Thr Tyr Pro Gly Ala Val Gln Leu Ala Asn Lys Ala Phe Ala
 115 120 125
 Asp Asn Gln Pro Ser Leu Leu Val Ala Lys Arg Lys Pro Leu Asn Ile
 130 135 140
 Ser Ile Asp Leu Pro Gly Met Arg Lys Glu Asn Thr Ile Thr Val Gln
 145 150 155 160
 Asn Pro Thr Tyr Gly Asn Val Ala Gly Ala Val Asp Asp Leu Val Ser
 165 170 175
 Thr Trp Asn Glu Lys Tyr Ser Glu Thr His Thr Leu Pro Ala Arg Met
 180 185 190
 Gln Tyr Thr Glu Ser Met Val Tyr Ser Lys Ser Gln Ile Ala Ser Ala
 195 200 205
 Leu Asn Val Asn Ala Lys Tyr Leu Asp Asn Ser Leu Asn Ile Asp Phe
 210 215 220
 Asn Ala Val Ala Asn Gly Glu Lys Lys Val Met Val Ala Ala Tyr Lys
 225 230 235 240
 Gln Ile Phe Tyr Thr Val Ser Ala Glu Leu Pro Asn Asn Pro Ser Asp
 245 250 255
 Leu Phe Asp Asn Ser Val Thr Phe Asp Glu Leu Thr Arg Lys Gly Val
 260 265 270
 Ser Asn Ser Ala Pro Pro Val Met Val Ser Asn Val Ala Tyr Gly Arg
 275 280 285
 Thr Val Tyr Val Lys Leu Glu Thr Thr Ser Lys Ser Lys Asp Val Gln
 290 295 300

Ala Ala Phe Lys Ala Leu Leu Lys Asn Asn Ser Val Glu Thr Ser Gly
 305 310 315 320
 Gln Tyr Lys Asp Ile Phe Glu Glu Ser Thr Phe Thr Ala Val Val Leu
 325 330 335
 Gly Gly Asp Ala Lys Glu His Asn Lys Val Val Thr Lys Asp Phe Asn
 340 345 350
 Glu Ile Arg Asn Ile Ile Lys Asp Asn Ala Glu Leu Ser Phe Lys Asn
 355 360 365
 Pro Ala Tyr Pro Ile Ser Tyr Thr Ser Thr Phe Leu Lys Asp Asn Ala
 370 375 380
 Thr Ala Ala Val His Asn Asn Thr Asp Tyr Ile Glu Thr Thr Thr Thr
 385 390 395 400
 Glu Tyr Ser Ser Ala Lys Met Thr Leu Asp His Tyr Gly Ala Tyr Val
 405 410 415
 Ala Gln Phe Asp Val Ser Trp Asp Glu Phe Thr Phe Asp Gln Asn Gly
 420 425 430
 Lys Glu Val Leu Thr His Lys Thr Trp Glu Gly Ser Gly Lys Asp Lys
 435 440 445
 Thr Ala His Tyr Ser Thr Val Ile Pro Leu Pro Pro Asn Ser Lys Asn
 450 455 460
 Ile Lys Ile Val Ala Arg Glu Cys Thr Gly Leu Ala Trp Glu Trp Trp
 465 470 475 480
 Arg Thr Ile Ile Asn Glu Gln Asn Val Pro Leu Thr Asn Glu Ile Lys
 485 490 495
 Val Ser Ile Gly Gly Thr Thr Leu Tyr Pro Thr Ala Ser Ile Ser His
 500 505 510

<210> 102
 <211> 18
 <212> PRT
 <213> Streptococcus pneumoniae

<400> 102
 Val Pro Ala Arg Met Gln Tyr Glu Lys Ile Thr Ala His Ser Met Glu
 1 5 10 15
 Gln Leu

<210> 103
 <211> 18
 <212> PRT
 <213> Clostridium perfringens

<400> 103
 Leu Pro Ala Arg Thr Gln Tyr Ser Glu Ser Met Val Tyr Ser Lys Ser
 1 5 10 15
 Gln Ile

<210> 104
 <211> 18
 <212> PRT
 <213> Streptococcus intermedius

<400> 104
 Val Pro Ala Arg Met Gln Tyr Glu Ser Ile Ser Ala Gln Ser Met Ser
 1 5 10 15
 Gln Leu

<210> 105
 <211> 18
 <212> PRT
 <213> *Paenibacillus alvei*

<400> 105
 Leu Pro Ala Arg Leu Gln Tyr Ala Glu Ser Met Val Tyr Ser Gln Asn
 1 5 10 15
 Gln Ile

<210> 106
 <211> 18
 <212> PRT
 <213> *Bacillus anthracis*

<400> 106
 Leu Pro Ala Arg Thr Gln Tyr Ser Glu Ser Met Val Tyr Ser Lys Ser
 1 5 10 15
 Gln Leu

<210> 107
 <211> 18
 <212> PRT
 <213> *Bacillus cereus*

<400> 107
 Leu Pro Ala Arg Thr Gln Tyr Ser Glu Ser Met Val Tyr Ser Lys Ser
 1 5 10 15
 Gln Ile

<210> 108
 <211> 18
 <212> PRT
 <213> *Listeria ivanovii*

<400> 108
 Ile Ser Ala Lys Ile Asp Tyr Asp Gln Glu Met Ala Tyr Ser Glu Ser
 1 5 10 15
 Gln Leu

<210> 109
 <211> 18
 <212> PRT
 <213> *Clostridium perfringens*

<400> 109
 Leu Pro Ala Arg Thr Gln Tyr Ser Glu Ser Met Val Tyr Ser Lys Ser
 1 5 10 15
 Gln Ile

<210> 110
 <211> 18
 <212> PRT
 <213> *Listeria seeligeri*

<400> 110
 Ile Asn Ala Lys Ile Asp Tyr Ser Asp Glu Met Ala Tyr Ser Glu Ser
 1 5 10 15
 Gln Leu

<210> 111
 <211> 18
 <212> PRT
 <213> *Streptococcus pyogenes*

<400> 111
 Leu Pro Ala Arg Thr Gln Tyr Thr Glu Ser Met Val Tyr Ser Lys Ser
 1 5 10 15
 Gln Ile

<210> 112
 <211> 18
 <212> PRT
 <213> *Streptococcus suis*

<400> 112
 Thr Gln Ala Glu Leu Gln Tyr Asp Glu Thr Met Ala Tyr Ser Met Ser
 1 5 10 15
 Gln Leu

<210> 113
 <211> 18
 <212> PRT
 <213> *Clostridium tetani*

<400> 113
 Ile Pro Thr Arg Met Ser Tyr Ser Asp Thr Met Val Tyr Ser Gln Ser
 1 5 10 15
 Gln Leu

<210> 114
 <211> 18
 <212> PRT
 <213> *Listeria monocytogenes*

<400> 114

Val Ser Ala Lys Ile Asp Tyr Asp Asp Glu Met Ala Tyr Ser Glu Ser
 1 5 10 15
 Gln Leu

<210> 115

<211> 18

<212> PRT

<213> *Bacillus thuringiensis*

<400> 115

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

<210> 116

<211> 499

<212> PRT

<213> *Clostridium perfringens*

<400> 116

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

Gly Arg Thr Ile Tyr Val Lys Leu Glu Thr Thr Ser Ser Ser Lys Asp
 275 280 285
 Val Gln Ala Ala Phe Lys Ala Leu Ile Lys Asn Thr Asp Ile Lys Asn
 290 295 300
 Ser Gln Gln Tyr Lys Asp Ile Tyr Glu Asn Ser Ser Phe Thr Ala Val
 305 310 315 320
 Val Leu Gly Gly Asp Ala Gln Glu His Asn Lys Val Val Thr Lys Asp
 325 330 335
 Phe Asp Glu Ile Arg Lys Val Ile Lys Asp Asn Ala Thr Phe Ser Thr
 340 345 350
 Lys Asn Pro Ala Tyr Pro Ile Ser Tyr Thr Ser Val Phe Leu Lys Asp
 355 360 365
 Asn Ser Val Ala Ala Val His Asn Lys Thr Asp Tyr Ile Glu Thr Thr
 370 375 380
 Ser Thr Glu Tyr Ser Lys Gly Lys Ile Asn Leu Asp His Ser Gly Ala
 385 390 395 400
 Tyr Val Ala Gln Phe Glu Val Ala Trp Asp Glu Val Ser Tyr Asp Lys
 405 410 415
 Glu Gly Asn Glu Val Leu Thr His Lys Thr Trp Asp Gly Asn Tyr Gln
 420 425 430
 Asp Lys Thr Ala His Tyr Ser Thr Val Ile Pro Leu Glu Ala Asn Ala
 435 440 445
 Arg Asn Ile Arg Ile Lys Ala Arg Glu Cys Thr Gly Leu Ala Trp Glu
 450 455 460
 Trp Trp Arg Asp Val Ile Ser Glu Tyr Asp Val Pro Leu Thr Asn Asn
 465 470 475 480
 Ile Asn Val Ser Ile Trp Gly Thr Thr Leu Tyr Pro Gly Ser Ser Ile
 485 490 495
 Thr Tyr Asn

<210> 117
 <211> 470
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 117
 Ala Asn Lys Ala Val Asn Asp Phe Ile Leu Ala Met Asn Tyr Asp Lys
 1 5 10 15
 Lys Lys Leu Leu Thr His Gln Gly Glu Ser Ile Glu Asn Arg Phe Ile
 20 25 30
 Lys Glu Gly Asn Gln Leu Pro Asp Glu Phe Val Val Ile Glu Arg Lys
 35 40 45
 Lys Arg Ser Leu Ser Thr Asn Thr Ser Asp Ile Ser Val Thr Ala Thr
 50 55 60
 Asn Asp Ser Arg Leu Tyr Pro Gly Ala Leu Leu Val Val Asp Glu Thr
 65 70 75 80
 Leu Leu Glu Asn Asn Pro Thr Leu Leu Ala Val Asp Arg Ala Pro Met
 85 90 95
 Thr Tyr Ser Ile Asp Leu Pro Gly Leu Ala Ser Ser Asp Ser Phe Leu
 100 105 110
 Gln Val Glu Asp Pro Ser Asn Ser Ser Val Arg Gly Ala Val Asn Asp
 115 120 125

Leu Leu Ala Lys Trp His Gln Asp Tyr Gly Gln Val Asn Asn Val Pro
 130 135 140
 Ala Arg Met Gln Tyr Glu Lys Ile Thr Ala His Ser Met Glu Gln Leu
 145 150 155 160
 Lys Val Lys Phe Gly Ser Asp Phe Glu Lys Thr Gly Asn Ser Leu Asp
 165 170 175
 Ile Asp Phe Asn Ser Val His Ser Gly Glu Lys Gln Ile Gln Ile Val
 180 185 190
 Asn Phe Lys Gln Ile Tyr Tyr Thr Val Ser Val Asp Ala Val Lys Asn
 195 200 205
 Pro Gly Asp Val Phe Gln Asp Thr Val Thr Val Glu Asp Leu Lys Gln
 210 215 220
 Arg Gly Ile Ser Ala Glu Arg Pro Leu Val Tyr Ile Ser Ser Val Ala
 225 230 235 240
 Tyr Gly Arg Gln Val Tyr Leu Lys Leu Glu Thr Thr Ser Lys Ser Asp
 245 250 255
 Glu Val Glu Ala Ala Phe Glu Ala Leu Ile Lys Gly Val Lys Val Ala
 260 265 270
 Pro Gln Thr Glu Trp Lys Gln Ile Leu Asp Asn Thr Glu Val Lys Ala
 275 280 285
 Val Ile Leu Gly Gly Asp Pro Ser Ser Gly Ala Arg Val Val Thr Gly
 290 295 300
 Lys Val Asp Met Val Glu Asp Leu Ile Gln Glu Gly Ser Arg Phe Thr
 305 310 315 320
 Ala Asp His Pro Gly Leu Pro Ile Ser Tyr Thr Thr Ser Phe Leu Arg
 325 330 335
 Asp Asn Val Val Ala Thr Phe Gln Asn Ser Thr Asp Tyr Val Glu Thr
 340 345 350
 Lys Val Thr Ala Tyr Arg Asn Gly Asp Leu Leu Leu Asp His Ser Gly
 355 360 365
 Ala Tyr Val Ala Gln Tyr Tyr Ile Thr Trp Asp Glu Leu Ser Tyr Asp
 370 375 380
 His Gln Gly Lys Glu Val Leu Thr Pro Lys Ala Trp Asp Arg Asn Gly
 385 390 395 400
 Gln Asp Leu Thr Ala His Phe Thr Thr Ser Ile Pro Leu Lys Gly Asn
 405 410 415
 Val Arg Asn Leu Ser Val Lys Ile Arg Glu Cys Thr Gly Leu Ala Trp
 420 425 430
 Glu Trp Trp Arg Thr Val Tyr Glu Lys Thr Asp Leu Pro Leu Val Arg
 435 440 445
 Lys Arg Thr Ile Ser Ile Trp Gly Thr Thr Asp Tyr Pro Gln Val Glu
 450 455 460
 Asp Lys Val Glu Asn Asp
 465 470

<210> 118

<211> 470

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence

<400> 118

Ala Asn Lys Ala Val Asn Asp Phe Ile Leu Ala Met Asn Tyr Asp Lys
 1 5 10 15

Lys	Lys	Leu	Leu	Thr	His	Gln	Gly	Glu	Ser	Ile	Glu	Asn	Arg	Phe	Ile		
			20					25					30				
Lys	Glu	Gly	Asn	Gln	Leu	Pro	Asp	Glu	Phe	Val	Val	Ile	Glu	Arg	Lys		
		35					40					45					
Lys	Arg	Ser	Leu	Ser	Thr	Asn	Thr	Ser	Asp	Ile	Ser	Val	Thr	Ala	Thr		
		50				55					60						
Asn	Asp	Ser	Arg	Leu	Tyr	Pro	Gly	Ala	Leu	Leu	Val	Val	Asp	Glu	Thr		
65					70					75					80		
Leu	Leu	Glu	Asn	Asn	Pro	Thr	Leu	Leu	Ala	Val	Asp	Arg	Ala	Pro	Met		
				85					90						95		
Thr	Tyr	Ser	Ile	Asp	Leu	Pro	Gly	Leu	Ala	Ser	Ser	Asp	Ser	Phe	Leu		
			100					105					110				
Gln	Val	Glu	Asp	Pro	Ser	Asn	Ser	Ser	Val	Arg	Gly	Ala	Val	Asn	Asp		
		115					120					125					
Leu	Leu	Ala	Lys	Trp	His	Gln	Asp	Tyr	Gly	Gln	Val	Asn	Asn	Val	Pro		
		130				135					140						
Ala	Arg	Met	Gln	Tyr	Glu	Lys	Ile	Thr	Ala	His	Ser	Met	Glu	Gln	Leu		
145					150				155						160		
Lys	Val	Lys	Phe	Gly	Ser	Asp	Phe	Glu	Lys	Thr	Gly	Asn	Ser	Leu	Asp		
				165				170						175			
Ile	Asp	Phe	Asn	Ser	Val	His	Ser	Gly	Glu	Lys	Gln	Ile	Gln	Ile	Val		
			180					185					190				
Asn	Phe	Lys	Gln	Ile	Tyr	Tyr	Thr	Val	Ser	Val	Asp	Ala	Val	Arg	Asn		
		195					200					205					
Pro	Gly	Asp	Val	Phe	Gln	Asp	Thr	Val	Thr	Val	Glu	Asp	Leu	Lys	Gln		
		210				215					220						
Arg	Gly	Ile	Ser	Ala	Glu	Arg	Pro	Leu	Val	Tyr	Ile	Ser	Ser	Val	Ala		
225					230					235					240		
Tyr	Gly	Arg	Gln	Val	Tyr	Leu	Lys	Leu	Glu	Thr	Thr	Ser	Lys	Ser	Asp		
				245					250					255			
Glu	Val	Glu	Ala	Ala	Phe	Glu	Ala	Leu	Ile	Lys	Gly	Val	Lys	Val	Ala		
			260					265					270				
Pro	Gln	Thr	Glu	Trp	Lys	Gln	Ile	Leu	Asp	Asn	Thr	Glu	Val	Lys	Ala		
		275					280					285					
Val	Ile	Leu	Gly	Gly	Asp	Pro	Ser	Ser	Gly	Ala	Arg	Val	Val	Thr	Gly		
		290				295					300						
Lys	Val	Asp	Met	Val	Glu	Asp	Leu	Ile	Gln	Glu	Gly	Ser	Arg	Phe	Thr		
305					310					315					320		
Ala	Asp	His	Pro	Gly	Leu	Pro	Ile	Ser	Tyr	Thr	Thr	Ser	Phe	Leu	Arg		
				325					330					335			
Asp	Asn	Val	Val	Ala	Thr	Phe	Gln	Asn	Ser	Thr	Asp	Tyr	Val	Glu	Thr		
			340					345					350				
Lys	Val	Thr	Ala	Tyr	Arg	Asn	Gly	Asp	Leu	Leu	Leu	Asp	His	Ser	Gly		
		355					360					365					
Ala	Tyr	Val	Ala	Gln	Tyr	Tyr	Ile	Thr	Trp	Asp	Glu	Leu	Ser	Tyr	Asp		
		370				375					380						
His	Gln	Gly	Lys	Glu	Val	Leu	Thr	Pro	Lys	Ala	Trp	Asp	Arg	Asn	Gly		
385					390					395					400		
Gln	Asp	Leu	Thr	Ala	His	Phe	Thr	Thr	Ser	Ile	Pro	Leu	Lys	Gly	Asn		
				405					410					415			
Val	Arg	Asn	Leu	Ser	Val	Lys	Ile	Arg	Glu	Cys	Thr	Gly	Leu	Ala	Trp		
			420					425				430					
Glu	Trp	Trp	Arg	Thr	Val	Tyr	Glu	Lys	Thr	Asp	Leu	Pro	Leu	Val	Arg		
		435					440					445					

Lys Arg Thr Ile Ser Ile Trp Gly Thr Thr Asp Tyr Pro Gln Val Glu
 450 455 460
 Asp Lys Val Glu Asn Asp
 465 470

<210> 119
 <211> 468
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 119
 Ala Asn Lys Ala Val Asn Asp Phe Ile Leu Ala Met Asn Tyr Asp Lys
 1 5 10 15
 Lys Lys Leu Leu Thr His Gln Gly Glu Ser Ile Glu Asn Arg Phe Ile
 20 25 30
 Lys Glu Gly Asn Gln Leu Pro Asp Glu Phe Val Val Ile Glu Arg Lys
 35 40 45
 Lys Arg Ser Leu Ser Thr Asn Thr Ser Asp Ile Ser Val Thr Ala Thr
 50 55 60
 Asn Asp Ser Arg Leu Tyr Pro Gly Ala Leu Leu Val Val Asp Glu Thr
 65 70 75 80
 Leu Leu Glu Asn Asn Pro Thr Leu Leu Ala Val Asp Arg Ala Pro Met
 85 90 95
 Thr Tyr Ser Ile Asp Leu Pro Gly Leu Ala Ser Ser Asp Ser Phe Leu
 100 105 110
 Gln Val Glu Asp Pro Ser Asn Ser Ser Val Arg Gly Ala Val Asn Asp
 115 120 125
 Leu Leu Ala Lys Trp His Gln Asp Tyr Gly Gln Val Asn Asn Val Pro
 130 135 140
 Met Gln Tyr Glu Lys Ile Thr Ala His Ser Met Glu Gln Leu Lys Val
 145 150 155 160
 Lys Phe Gly Ser Asp Phe Glu Lys Thr Gly Asn Ser Leu Asp Ile Asp
 165 170 175
 Phe Asn Ser Val His Ser Gly Glu Lys Gln Ile Gln Ile Val Asn Phe
 180 185 190
 Lys Gln Ile Tyr Tyr Thr Val Ser Val Asp Ala Val Lys Asn Pro Gly
 195 200 205
 Asp Val Phe Gln Asp Thr Val Thr Val Glu Asp Leu Lys Gln Arg Gly
 210 215 220
 Ile Ser Ala Glu Arg Pro Leu Val Tyr Ile Ser Ser Val Ala Tyr Gly
 225 230 235 240
 Arg Gln Val Tyr Leu Lys Leu Glu Thr Thr Ser Lys Ser Asp Glu Val
 245 250 255
 Glu Ala Ala Phe Glu Ala Leu Ile Lys Gly Val Lys Val Ala Pro Gln
 260 265 270
 Thr Glu Trp Lys Gln Ile Leu Asp Asn Thr Glu Val Lys Ala Val Ile
 275 280 285
 Leu Gly Gly Asp Pro Ser Ser Gly Ala Arg Val Val Thr Gly Lys Val
 290 295 300
 Asp Met Val Glu Asp Leu Ile Gln Glu Gly Ser Arg Phe Thr Ala Asp
 305 310 315 320
 His Pro Gly Leu Pro Ile Ser Tyr Thr Thr Ser Phe Leu Arg Asp Asn
 325 330 335

Val Val Ala Thr Phe Gln Asn Ser Thr Asp Tyr Val Glu Thr Lys Val
 340 345 350
 Thr Ala Tyr Arg Asn Gly Asp Leu Leu Leu Asp His Ser Gly Ala Tyr
 355 360 365
 Val Ala Gln Tyr Tyr Ile Thr Trp Asp Glu Leu Ser Tyr Asn His Gln
 370 375 380
 Gly Lys Glu Val Leu Thr Pro Lys Ala Trp Asp Arg Asn Gly Gln Asp
 385 390 395 400
 Leu Thr Ala His Phe Thr Thr Ser Ile Pro Leu Lys Gly Asn Val Arg
 405 410 415
 Asn Leu Ser Val Lys Ile Arg Glu Cys Thr Gly Leu Ala Trp Glu Trp
 420 425 430
 Trp Arg Thr Val Tyr Glu Lys Thr Asp Leu Pro Leu Val Arg Lys Arg
 435 440 445
 Thr Ile Ser Ile Trp Gly Thr Thr Leu Tyr Pro Gln Val Glu Asp Lys
 450 455 460
 Val Glu Asn Asp
 465

<210> 120
 <211> 470
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

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

Arg Gly Ile Ser Ala Glu Arg Pro Leu Val Tyr Ile Ser Ser Val Ala
 225 230 235 240
 Tyr Gly Arg Gln Val Tyr Leu Lys Leu Glu Thr Thr Ser Lys Ser Asp
 245 250 255
 Glu Val Glu Ala Ala Phe Glu Ala Leu Ile Lys Gly Val Lys Val Ala
 260 265 270
 Pro Gln Thr Glu Trp Lys Gln Ile Leu Asp Asn Thr Glu Val Lys Ala
 275 280 285
 Val Ile Leu Gly Gly Asp Pro Ser Ser Gly Ala Arg Val Val Thr Gly
 290 295 300
 Lys Val Asp Met Val Glu Asp Leu Ile Gln Glu Gly Ser Arg Phe Thr
 305 310 315 320
 Ala Asp His Pro Gly Leu Pro Ile Ser Tyr Thr Thr Ser Phe Leu Arg
 325 330 335
 Asp Asn Val Val Ala Thr Phe Gln Asn Ser Thr Asp Tyr Val Glu Thr
 340 345 350
 Lys Val Thr Ala Tyr Arg Asn Gly Asp Leu Leu Leu Asp His Ser Gly
 355 360 365
 Ala Tyr Val Ala Gln Tyr Tyr Ile Thr Trp Asp Glu Leu Ser Tyr Asp
 370 375 380
 His Gln Gly Lys Glu Val Leu Thr Pro Lys Ala Trp Asp Arg Asn Gly
 385 390 395 400
 Gln Asp Leu Thr Ala His Phe Thr Thr Ser Ile Pro Leu Lys Gly Asn
 405 410 415
 Val Arg Asn Leu Ser Val Lys Ile Arg Glu Cys Thr Gly Leu Ala Phe
 420 425 430
 Glu Trp Trp Arg Thr Val Tyr Glu Lys Thr Asp Leu Pro Leu Val Arg
 435 440 445
 Lys Arg Thr Ile Ser Ile Trp Gly Thr Thr Leu Tyr Pro Gln Val Glu
 450 455 460
 Asp Lys Val Glu Asn Asp
 465 470

<210> 121
 <211> 789
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 121
 agctctggag gtggaggaag cgggggcggt ggagttgcag cagacattgg agcaggatta 60
 gcagatgcac tgacggcacc gttggatcat aaagacaaag gcttgaaatc gcttacctta 120
 gaagattcta ttccacaaaa tggcaccctt accttgctcg cgcaaggcgc tgaacgtact 180
 tttaaagccg gtgacaaaga taatagctta aatacaggta aactcaaaaa tgataaaatc 240
 tcgcgttttg atttcattcg tcaaatcgaa gtagatggcc aacttattac attagaaagc 300
 ggtgaattcc aagtatataa acaatcccat tcagcactta cagcattgca aaccgaacag 360
 gtccaagact cagaacattc cggcaaaatg gtagctaaac gtcaattccg catcggtgac 420
 attgtcgggtg aacatacaag cttcggaaaa ttaccaaaag atgtgatggc gacctatcgc 480
 ggtacggcat ttggatcaga tgatgcaggc ggtaaattaa cttatacaat tgactttgca 540
 gcaaaacaag gacatggcaa aattgaacat ttaaaatctc ccgaacttaa cgtagatctc 600
 gcagcagcag atattaaacc agatgaaaaa caccacgcag tcatttcagg ttcagtttta 660
 tacaatcagg cagaaaaagg ttcgtactct ttaggtatctt ttggcgggca agctcaagaa 720
 gttgcaggta gcgcagaagt agaaacggca aatggcattc gtcacattgg gttagcggcg 780
 aaacaataa 789

<210> 122
 <211> 780
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 122
 agctctggag gtggaggaag cgggggcggt ggagttgcag cagacattgg agcaggatta 60
 gcagatgcac tgacggcacc gttggatcat aaagacaaag gcttgcagtc gcttacctta 120
 gatcagLctg tcaggaaaaa tgagaaactt aagttggcgg cgcaaggcgc tgaaaaaact 180
 tatggaaacg gtgacagctt aaatacaggt aaactcaaaa atgataaagt ctgcgcgtttt 240
 gatttcattc gtcaaatcga agtagatggc aagcttatta cattagaaag cgggtgaattc 300
 caagtatata aacaatccca ttcagcactt acagcattgc aaaccgaaca ggtccaagac 360
 tcagaagatt cgggcaaaat ggtagctaaa cgtcaattcc gcatcggtga cattgcgggt 420
 gaacatacaa gcttcgacaa attaccaaaa ggcggcagtg cgacctatcg cggtagcgga 480
 lttggatcag atgatgcagg cggtaaatta acttatataa ttgactttgc agcaaaaaca 540
 ggacatggca aaattgaaca tttaaaatct cccgaactta acgtagagct cgcaaccgca 600
 tatattaaac cagatgaaaa acgccacgca gtcaatttcag gttcagtttt atacaatcag 660
 gacgaaaaag gttcgtactc tttaggtatt tttggcgggc aagctcaaga agttgcaggt 720
 agcgcagaag tagaaacggc aaatggcatt caccacattg ggtagcggc gaaacaataa 780

<210> 123
 <211> 765
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 123
 agctctggag gtggaggagt tgcagcagac attggagcag gattagcaga tgcactgacg 60
 gcaccgttgg atcataaaga caaaggcttg cagtcgctta ccttagatca gtctgtcagg 120
 aaaaatgaga aacttaagtt ggcggcgcaa ggcgctgaaa aaacttatgg aaacggtgac 180
 agcttaaata caggtaaact caaaaatgat aaagtctcgc gttttgattt cattcgtcaa 240
 atcgaagtag atggcaagct tattacatta gaaagcggtg aattccaagt atataaaca 300
 tcccattcag cacttacagc attgcaaacc gaacagggtcc aagactcaga agattccggc 360
 aaaatggtag ctaaacgtca attccgcctc ggtgacattg cgggtgaaca tacaagcttc 420
 gacaaattac caaaaggcgg cagtgcgacc tatcgcggta cggcatttgg atcagatgat 480
 gcaggcggta aarttaacta tacaattgac tttgcagcaa aacaaggaca tggcaaaatt 540
 gaacatttaa aatctcccgga acttaacgta gagctcgcaa ccgcatatat taaaccagat 600
 gaaaaacgcc acgcagtcct ttcagggttc gttttataca atcaggacga aaaagggttcg 660
 tactctttag gtatttttgg cgggcaagct caagaagttg caggtagcgc agaagtagaa 720
 acggcaaatg gcattcacca cattgggtta gcggcgaaac aataa 765

<210> 124
 <211> 765
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 124

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agcagcgggg ggggtggagt tgcagcagac attggagcag gattagcaga tgcactgacg      60
gcaccgttgg atcataaaga caaaggcttg cagtcgctta ccttagatca gtctgtcagg      120
aaaaatgaga aacttaagtt ggcggcgcaa ggcgctgaaa aaacttatgg aaacggtgac      180
agcttaaata caggtaaact caaaaatgat aaagtctcgc gttttgattt cattcgtcaa      240
atcgaagtag atggcaagct tattacatta gaaagcgggt aattccaagt atataaacia      300
tcccattcag cacttacagc attgcaaacc gaacagggtc aagactcaga agattccggc      360
aaaatggtag ctaaacgtca attccgcctc ggtgacattg cgggtgaaca tacaagcttc      420
gacaaattac caaaaggcgg cagtgcgacc tatcgoggta cggcatttgg atcagatgat      480
gcaggcggta aattaactta tacaattgac tttgcagcaa aacaaggaca tggcaaaatt      540
gaacatttaa aatctcccga acttaacgta gagctcgcaa ccgcataat taaaccagat      600
gaaaaacgcc acgcagtcct ttcaggttca gttttataca atcaggacga aaaaggttcg      660
tactctttag gtatttttgg cgggcaagct caagaagttg caggtagcgc agaagtagaa      720
acggcaaatt gcattcacca cattgggtta gcggcgaaac aataa      765

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<210> 125

<211> 786

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence

<400> 125

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atgagctctg gaagcgggaag cgggggcggt ggagttgcag cagacattgg aacaggatta      60
gcagatgcac tgacggcacc gttggatcat aaagacaaag gcttgaaatc gcttacctta      120
gaagattcta tttcacaaaa tggcaccctt accttgctcg cgcaaggcgc tgaaaaaact      180
tttaaagtcg gtgacaaaga taatagctta aatacaggta aactcaaaaa tgataaaatc      240
tcgcgttttg atttcgtgca aaaaatcgaa gtagatggcc aaaccattac attagcaagc      300
ggtgaattcc aaatatataa acaagaccat tcagcagtcg ttgcattgca aattgaaaaa      360
atcaacaacc ccgacaaaat cgacagcctg ataaaccaac gttccttcct tgtcagcggg      420
ttggggcggtg aacatacagc cttcaaccaa ttaccaagcg gcaaagcgga gtatcacggg      480
aaagcattta gctcagatga tgcaggcggg aaattaactt atacaattga ctttgcagca      540
aaacaaggac atggcaaaat tgaacattta aaaacacccg aacagaacgt agagctcgca      600
tcgcgagaac tcaaagcaga tgaaaaatca cagcagtcg ttttgggtga cagcgctac      660
ggcagcgaag aaaaaggtac ttaccactta gctctttttg gcgaccgagc tcaagaaatc      720
gcaggtagcg caaccgtaaa gataagggaa aagggttcacg aaattgggat cgcgggcaaa      780
caataa      786

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<210> 126

<211> 786

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence

<400> 126

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atgtccagcg gttcaggcag cggcgggtgga ggcgtggcag cagatatcgg aacaggttta      60
gcagalgctc tgacagcacc cttagatcac aaagacaaag gacttaaatc actgacattg      120
gaagattcta tctcgcaaaa tgggtactct actcttttcag cccaaggcgc agaaaaaaca      180
tttaaagtag gcgataaaga taactcctta aatacaggta aattaaaaaa tgacaaaatc      240
tcacggtttg atttcgttca gaaaattgaa gtagatggac aaacgattac attagcaagc      300
ggcgaattcc aaatttataa acaagaccat tcagcagtag tagcattaca aatcgaaaaa      360
attaacaacc cggacaaaat tgattctctt attaaccaac gctcttttct cgtatcagga      420

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cttgggtggtg	aacatacagc	gtttaatcaa	ctgccgtcag	gaaaagcaga	atatcatggt	480
aaagcatttt	catcagacga	cgcaggtggc	aaactgacct	atactattga	ctttgcagca	540
aaacagggac	atggaaaaat	tgaacattta	aaaacacccg	aacagaacgt	agaactggcc	600
tcagcagaat	tgaaagctga	tgaaaaatcc	catgcagtaa	ttttaggcga	tacacgttac	660
ggtagcgaag	aaaaaggtac	atatcactta	gctctttttg	gcgatcgtgc	tcaagaaatt	720
gctggttccg	caacagttaa	aatccgtgaa	aaagtacatg	aaatcggcat	tgcaggtaaa	780
caataa						786

<210> 127

<211> 765

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence

<400> 127

atgagctctg	gaggtggagg	agttgcagca	gacattggag	caggattagc	agatgcaactg	60
acggcaccgl	tggatcataa	agacaaaagt	ttgcagtcgc	ttaccttaga	tcagtctgtc	120
aggaaaaatg	agaaacttaa	gttggcggcg	caaggcgctg	aaaaaactta	tggaaacggg	180
gacagcttaa	atacaggtaa	actcaaaaat	gataaagtct	cgcgttttga	tttcattcgt	240
caaategaag	tagatggcca	acttattaca	ttagaaagcg	gtgaattcca	aatatataaa	300
caagaccatt	cagcagtcgt	tgcattgcaa	attgaaaaaa	tcaacaaccc	cgacaaaatc	360
gacagcctga	taaaccaacg	tcccttcctt	gtcagcgggt	tgggcgggtga	acatacagcc	420
ttcaaccaat	taccaagcgg	caaagcggag	tatcacggta	aagcatttag	ctcagatgat	480
gcaggcggta	aattaactta	tacaattgac	tttgcagcaa	aacaaggaca	tggcaaaatt	540
gaacatttaa	aaacacccga	acagaacgta	gagctcgcat	ccgcagaact	caaagcagat	600
gaaaaatcac	acgcagtcac	tttgggtgac	acgcgctacg	gcggcggaaga	aaaaggtaact	660
taccacttag	ctcttttttg	cgaccgagct	caagaaatcg	caggtagcgc	aaccgtaaaag	720
ataagggaaa	aggttcacga	aattgggata	gcgggcacaa	aataa		765

<210> 128

<211> 768

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence

<400> 128

atgagcagcg	gagggggcgg	tgtcgccgcc	gacatcggtg	cggggcettgc	cgatgcacta	60
accgcaccgc	tcgaccataa	agacaaaggt	ttgcagtctt	taacgctgga	tcagtccgtc	120
aggaaaaacg	agaaactgaa	gctggcggca	caagggtgcg	aaaaaactta	tggaaacggc	180
gacagcctta	atacgggcaa	altgaagaac	gacaaggtea	gccgcttcga	ctttatccgt	240
caaategaag	tggacgggaa	gctcattacc	ttggagagcg	gagagttcca	agtgtacaaa	300
caaagccatt	ccgccttaac	cgccttcag	accgagcaag	tacaagactc	ggaggattcc	360
gggaagatgg	ttgcgaaacg	ccagttcaga	atcggcgaca	tagcgggcga	acatacatct	420
tttgacaagc	ttcccaaagg	cggcagtgcg	acatatcgcg	ggacggcggt	cgtttcagac	480
gatgctggcg	gaaaactgac	ctatactata	gatttcgccg	ccaaacaggg	acacggcaaa	540
atcgaacact	tgaaaacacc	cgagcaaaaat	gtcgagcttg	cctccgccga	actcaaagca	600
gatgaaaaat	cacacgccgt	catttttgggc	gacacgcgct	acggcggcga	agaaaaaggc	660
acttaccacc	tcgccctttt	cggcgaccgc	qcccaagaaa	tcgccggctc	ggcaaccgtg	720
aagataaggg	aaaaggttca	cgaaatcggc	atcgccggca	aacagtaa		768

<210> 129
 <211> 780
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 129
 atgagctctg gaggtggagg aagcgggggc ggtggagttg cagcagacat tggagcagga 60
 ttagcagatg cactgacggc accgttggat cataaagaca aaagtttgca gtcgcttacc 120
 ttagatcagt ctgtcaggaa aaatgagaaa cttaagttgg cggcgcaagg cgctgaaaaa 180
 acttatggaa acggtgacag cttaaataca ggtaaactca aaaatgataa agtctcgcg 240
 tttgatttca ttctgtcaa atcgaagtagat ggccaaacca ttacattagc aagcgggtgaa 300
 ttccaaatat ataaacaaaa ccattcagca gtcgttgcat tgcaaattga aaaaatcaac 360
 aaccccgaca aaatcgacag cctgataaac caacgttcct tccttgtcag cggtttgggc 420
 ggtgaacata cagccttcaa ccaattacca gacggcaaag cggagtatca cggtaaagca 480
 tttagctcag atgatecgaa cggtaggtta cactattcca ttgactttac caaaaaacaa 540
 ggatacggca gaattgaaca tttaaaaacg ccggaacaga acgtagagct cgcattccgca 600
 gaactcaaag cagatgaaaa atcacacgca gtcatttttg gtgacacgcg ctacggcggc 660
 gaagaaaaag gtacttacca cttagccctt tttggcgacc gcgctcaaga aatcgaggt 720
 agcgcaaccg taaagataag ggaaaaggtt cacgaaattg ggatcgcggg caaacaataa 780

<210> 130
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

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

Ala Asp Ile Lys Pro Asp Gly Lys Arg His Ala Val Ile Ser Gly Ser
 195 200 205
 Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser Tyr Ser Leu Gly Ile Phe
 210 215 220
 Gly Gly Lys Ala Gln Glu Val Ala Gly Ser Ala Glu Val Lys Thr Val
 225 230 235 240
 Asn Gly Ile Arg His Ile Gly Leu Ala Ala Lys Gln
 245 250

<210> 131
 <211> 765
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 131
 ggcagcagcg gaggcggcgg tgctgcgcgc gacatcggcg cggggccttgc cgatgcacta 60
 accgcaccgc tcgaccataa agacaaaagt ttgcagtctt tgacgctgga tcagtcctgc 120
 aggaaaaacg agaaactgaa gctggcgggc caaggtgcgg aaaaaactta tggaaacggc 180
 gacagcctca atacgggcaa attgaagaac gacaaggtca gccgcttcga ctttatccgt 240
 caaatcgaag tggacgggca gctcattacc ttggagagcg gagagttcca aatatacaaa 300
 caggaccact ccgccgtcgt tgccctacag attgaaaaaa tcaacaaccc cgacaaaatc 360
 gacagcctga taaaccaacg ctccctcctt gtcagcgggt tgggtggaga acataccgcc 420
 ttcaaccaac tgcccagcgg caaagccgag tatcacggca aagcattcag ctccgacgat 480
 gctggcgga aactgaccta taccatagat ttgcgcgcca aacagggaca cggcaaaatc 540
 gaacacttga aaacacccga gcaaaatgtc gagcttgctt ccgcogaact caaagcagat 600
 gaaaaatcac acgccgtcat tttgggcgac acgcgctacg gcggcgaaga aaaaggcact 660
 taccacctcg cccttttcgg cgaccgcgcc caagaaatcg ccggctcggc aaccgtgaag 720
 ataagggaaa aggttcacga aatcggcatc gccggcaaac agtaa 765

<210> 132
 <211> 254
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 132
 Gly Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly Ala Gly Leu
 1 5 10 15
 Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys Ser Leu Gln
 20 25 30
 Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys Leu Lys Leu
 35 40 45
 Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp Ser Leu Asn
 50 55 60
 Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp Phe Ile Arg
 65 70 75 80
 Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser Gly Glu Phe
 85 90 95
 Gln Ile Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu
 100 105 110

Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
115 120 125
Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln Leu
130 135 140
Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser Asp Asp
145 150 155 160
Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly
165 170 175
His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln Asn Val Glu Leu
180 185 190
Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser His Ala Val Ile Leu
195 200 205
Gly Asp Thr Arg Tyr Gly Gly Glu Glu Lys Gly Thr Tyr His Leu Ala
210 215 220
Leu Phe Gly Asp Arg Ala Gln Glu Ile Ala Gly Ser Ala Thr Val Lys
225 230 235 240
Ile Arg Glu Lys Val His Glu Ile Gly Ile Ala Gly Lys Gln
245 250

<210> 133
<211> 765
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence

<400> 133
agcagcggag ggggcggtgt cgccgccgac atcggtgcgg ggcttgccga tgcactaacc 60
gcaccgctcg accataaaga caaaggtttg cagtctttaa cactggatca gtccgtcagg 120
aaaaacgaga aactgaagct ggccgcacaa ggtgcggaaa aaacttatgg aaacggcgac 180
agccttaata cgggcaaatt gaagaacgac aaggtcagcc gcttcgactt tatccgtcaa 240
atcgaagtgg acgggaagct cattacottg gagagcggag agttccaagt gtacaaacaa 300
agccattccg ccttaaccgc ccttcagacc gagcaagtac aagactcgga ggattccggg 360
aagatggttg cgaaacgcca gttcagaatc ggcgacatag cgggcgaaca tacatctttt 420
gacaagcttc ccaaaggcgg cagtgcgaca tatcgcgga cggcggttcg ttcagacgat 480
gctggcgga aactgaccta tactatagat ttgcgcgcca agcagggaca cggcaaaatc 540
gaacatttga aatcgccoga actcaatgtc gagcttgcca ccgcctatat caagccggat 600
gaaaaacgcc atgcggttat cagcggttcc gtccctttaca accaagacga gaaaggcagt 660
tactccctcg gtatcttttg cgggcaagcc caggaagttg ccggcagcgc ggaagtggaa 720
accgcaaacy gcatacacca tatcggtctt gccgccaagc agtaa 765

<210> 134
<211> 789
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence

<400> 134
agcagcggag gcggcggaag cggaggcggc ggtgtcgccg ccgacatcgg cgcggggctt 60
gccgatgcac taaccgcacc gctcgaccat aaagacaaag gtttgaaatc cctgacattg 120
gaagactcca tttcccaaaa cggaacactg accctgtcgg cacaaggtgc ggaaagaact 180
ttcaaagccg gcgacaaaga caacagtctc aacacaggca aactgaagaa cgacaaaatc 240

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agccgcttcg actttatccg tcaaatcgaa gtggacgggc agctcattac cttggagagc 300
ggagagttec aagtgtacaa acaaagccat tccgccttaa ccgcccttca gaccgagcaa 360
gtacaagact cggagcattc cgggaagatg gttgcgaaac gccagttcag aatcggcgac 420
atagtgggcg aacatacatc ttttggcaag cttcccaaag acgtcatggc gacatatcgc 480
gggacggcgt tcggttcaga cgatgccggc ggaaaactga cctacaccat agatttcgcc 540
gccaagcagg gacacggcaa aatcgaacat ttgaaatcgc cagaactcaa tgttgacctg 600
gccgcgcgcg atatcaagcc ggatgaaaaa caccatgccg tcatcagcgg ttccgtcctt 660
tacaaccaag ccgagaaagg cagttactct ctaggcactt ttggcgggca agcccaggaa 720
gttgccggca gcgcggaagt ggaaaccgca aacggcatac gccatatcgg tcttgccgcc 780
aagcaataa 789

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<210> 135

<211> 257

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence

<400> 135

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

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<210> 136
 <211> 727
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 136
 Met Ala Asn Lys Ala Val Asn Asp Phe Ile Leu Ala Met Asn Tyr Asp
 1 5 10 15
 Lys Lys Lys Leu Leu Thr His Gln Gly Glu Ser Ile Glu Asn Arg Phe
 20 25 30
 Ile Lys Glu Gly Asn Gln Leu Pro Asp Glu Phe Val Val Ile Glu Arg
 35 40 45
 Lys Lys Arg Ser Leu Ser Thr Asn Thr Ser Asp Ile Ser Val Thr Ala
 50 55 60
 Thr Asn Asp Ser Arg Leu Tyr Pro Gly Ala Leu Leu Val Val Asp Glu
 65 70 75 80
 Thr Leu Leu Glu Asn Asn Pro Thr Leu Leu Ala Val Asp Arg Ala Pro
 85 90 95
 Met Thr Tyr Ser Ile Asp Leu Pro Gly Leu Ala Ser Ser Asp Ser Phe
 100 105 110
 Leu Gln Val Glu Asp Pro Ser Asn Ser Ser Val Arg Gly Ala Val Asn
 115 120 125
 Asp Leu Leu Ala Lys Trp His Gln Asp Tyr Gly Gln Val Asn Asn Val
 130 135 140
 Pro Met Gln Tyr Glu Lys Ile Thr Ala His Ser Met Glu Gln Leu Lys
 145 150 155 160
 Val Lys Phe Gly Ser Asp Phe Glu Lys Thr Gly Asn Ser Leu Asp Ile
 165 170 175
 Asp Phe Asn Ser Val His Ser Gly Glu Lys Gln Ile Gln Ile Val Asn
 180 185 190
 Phe Lys Gln Ile Tyr Tyr Thr Val Ser Val Asp Ala Val Lys Asn Pro
 195 200 205
 Gly Asp Val Phe Gln Asp Thr Val Thr Val Glu Asp Leu Lys Gln Arg
 210 215 220
 Gly Ile Ser Ala Glu Arg Pro Leu Val Tyr Ile Ser Ser Val Ala Tyr
 225 230 235 240
 Gly Arg Gln Val Tyr Leu Lys Leu Glu Thr Thr Ser Lys Ser Asp Glu
 245 250 255
 Val Glu Ala Ala Phe Glu Ala Leu Ile Lys Gly Val Lys Val Ala Pro
 260 265 270
 Gln Thr Glu Trp Lys Gln Ile Leu Asp Asn Thr Glu Val Lys Ala Val
 275 280 285
 Ile Leu Gly Gly Asp Pro Ser Ser Gly Ala Arg Val Val Thr Gly Lys
 290 295 300
 Val Asp Met Val Glu Asp Leu Ile Gln Glu Gly Ser Arg Phe Thr Ala
 305 310 315 320
 Asp His Pro Gly Leu Pro Ile Ser Tyr Thr Thr Ser Phe Leu Arg Asp
 325 330 335
 Asn Val Val Ala Thr Phe Gln Asn Ser Thr Asp Tyr Val Glu Thr Lys
 340 345 350
 Val Thr Ala Tyr Arg Asn Gly Asp Leu Leu Leu Asp His Ser Gly Ala
 355 360 365
 Tyr Val Ala Gln Tyr Tyr Ile Thr Trp Asp Glu Leu Ser Tyr Asp His
 370 375 380

Gln Gly Lys Glu Val Leu Thr Pro Lys Ala Trp Asp Arg Asn Gly Gln
 385 390 395 400
 Asp Leu Thr Ala His Phe Thr Thr Ser Ile Pro Leu Lys Gly Asn Val
 405 410 415
 Arg Asn Leu Ser Val Lys Ile Arg Glu Cys Thr Gly Leu Ala Trp Glu
 420 425 430
 Trp Trp Arg Thr Val Tyr Glu Lys Thr Asp Leu Pro Leu Val Arg Lys
 435 440 445
 Arg Thr Ile Ser Ile Trp Gly Thr Thr Leu Tyr Pro Gln Val Glu Asp
 450 455 460
 Lys Val Glu Asn Asp Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 465 470 475 480
 Val Ala Ala Asp Ile Gly Ala Gly Leu Ala Asp Ala Leu Thr Ala Pro
 485 490 495
 Leu Asp His Lys Asp Lys Ser Leu Gln Ser Leu Thr Leu Asp Gln Ser
 500 505 510
 Val Arg Lys Asn Glu Lys Leu Lys Leu Ala Ala Gln Gly Ala Glu Lys
 515 520 525
 Thr Tyr Gly Asn Gly Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp
 530 535 540
 Lys Val Ser Arg Phe Asp Phe Ile Arg Gln Ile Glu Val Asp Gly Gln
 545 550 555 560
 Thr Ile Thr Leu Ala Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asn His
 565 570 575
 Ser Ala Val Val Ala Leu Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys
 580 585 590
 Ile Asp Ser Leu Ile Asn Gln Arg Ser Phe Leu Val Ser Gly Leu Gly
 595 600 605
 Gly Glu His Thr Ala Phe Asn Gln Leu Pro Asp Gly Lys Ala Glu Tyr
 610 615 620
 His Gly Lys Ala Phe Ser Ser Asp Asp Pro Asn Gly Arg Leu His Tyr
 625 630 635 640
 Ser Ile Asp Phe Thr Lys Lys Gln Gly Tyr Gly Arg Ile Glu His Leu
 645 650 655
 Lys Thr Pro Glu Gln Asn Val Glu Leu Ala Ser Ala Glu Leu Lys Ala
 660 665 670
 Asp Glu Lys Ser His Ala Val Ile Leu Gly Asp Thr Arg Tyr Gly Gly
 675 680 685
 Glu Glu Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln
 690 695 700
 Glu Ile Ala Gly Ser Ala Thr Val Lys Ile Arg Glu Lys Val His Glu
 705 710 715 720
 Ile Gly Ile Ala Gly Lys Gln
 725

<210> 137

<211> 726

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence

<400> 137

Ala Asn Lys Ala Val Asn Asp Phe Ile Leu Ala Met Asn Tyr Asp Lys
 1 5 10 15

Lys	Lys	Leu	Leu	Thr	His	Gln	Gly	Glu	Ser	Ile	Glu	Asn	Arg	Phe	Ile		
			20					25					30				
Lys	Glu	Gly	Asn	Gln	Leu	Pro	Asp	Glu	Phe	Val	Val	Ile	Glu	Arg	Lys		
		35					40					45					
Lys	Arg	Ser	Leu	Ser	Thr	Asn	Thr	Ser	Asp	Ile	Ser	Val	Thr	Ala	Thr		
		50				55					60						
Asn	Asp	Ser	Arg	Leu	Tyr	Pro	Gly	Ala	Leu	Leu	Val	Val	Asp	Glu	Thr		
65					70					75					80		
Leu	Leu	Glu	Asn	Asn	Pro	Thr	Leu	Leu	Ala	Val	Asp	Arg	Ala	Pro	Met		
				85					90					95			
Thr	Tyr	Ser	Ile	Asp	Leu	Pro	Gly	Leu	Ala	Ser	Ser	Asp	Ser	Phe	Leu		
			100					105					110				
Gln	Val	Glu	Asp	Pro	Ser	Asn	Ser	Ser	Val	Arg	Gly	Ala	Val	Asn	Asp		
		115					120					125					
Leu	Leu	Ala	Lys	Trp	His	Gln	Asp	Tyr	Gly	Gln	Val	Asn	Asn	Val	Pro		
		130				135					140						
Met	Gln	Tyr	Glu	Lys	Ile	Thr	Ala	His	Ser	Met	Glu	Gln	Leu	Lys	Val		
145					150					155					160		
Lys	Phe	Gly	Ser	Asp	Phe	Glu	Lys	Thr	Gly	Asn	Ser	Leu	Asp	Ile	Asp		
				165					170					175			
Phe	Asn	Ser	Val	His	Ser	Gly	Glu	Lys	Gln	Ile	Gln	Ile	Val	Asn	Phe		
			180					185					190				
Lys	Gln	Ile	Tyr	Tyr	Thr	Val	Ser	Val	Asp	Ala	Val	Lys	Asn	Pro	Gly		
		195					200					205					
Asp	Val	Phe	Gln	Asp	Thr	Val	Thr	Val	Glu	Asp	Leu	Lys	Gln	Arg	Gly		
		210				215					220						
Ile	Ser	Ala	Glu	Arg	Pro	Leu	Val	Tyr	Ile	Ser	Ser	Val	Ala	Tyr	Gly		
225					230					235					240		
Arg	Gln	Val	Tyr	Leu	Lys	Leu	Glu	Thr	Thr	Ser	Lys	Ser	Asp	Glu	Val		
				245					250					255			
Glu	Ala	Ala	Phe	Glu	Ala	Leu	Ile	Lys	Gly	Val	Lys	Val	Ala	Pro	Gln		
			260					265					270				
Thr	Glu	Trp	Lys	Gln	Ile	Leu	Asp	Asn	Thr	Glu	Val	Lys	Ala	Val	Ile		
		275					280					285					
Leu	Gly	Gly	Asp	Pro	Ser	Ser	Gly	Ala	Arg	Val	Val	Thr	Gly	Lys	Val		
		290				295					300						
Asp	Met	Val	Glu	Asp	Leu	Ile	Gln	Glu	Gly	Ser	Arg	Phe	Thr	Ala	Asp		
305					310					315					320		
His	Pro	Gly	Leu	Pro	Ile	Ser	Tyr	Thr	Thr	Ser	Phe	Leu	Arg	Asp	Asn		
				325					330					335			
Val	Val	Ala	Thr	Phe	Gln	Asn	Ser	Thr	Asp	Tyr	Val	Glu	Thr	Lys	Val		
			340					345					350				
Thr	Ala	Tyr	Arg	Asn	Gly	Asp	Leu	Leu	Leu	Asp	His	Ser	Gly	Ala	Tyr		
		355				360						365					
Val	Ala	Gln	Tyr	Tyr	Ile	Thr	Trp	Asp	Glu	Leu	Ser	Tyr	Asp	His	Gln		
		370				375					380						
Gly	Lys	Glu	Val	Leu	Thr	Pro	Lys	Ala	Trp	Asp	Arg	Asn	Gly	Gln	Asp		
385					390					395					400		
Leu	Thr	Ala	His	Phe	Thr	Thr	Ser	Ile	Pro	Leu	Lys	Gly	Asn	Val	Arg		
			405					410					415				
Asn	Leu	Ser	Val	Lys	Ile	Arg	Glu	Cys	Thr	Gly	Leu	Ala	Trp	Glu	Trp		
			420					425					430				
Trp	Arg	Thr	Val	Tyr	Glu	Lys	Thr	Asp	Leu	Pro	Leu	Val	Arg	Lys	Arg		
		435					440					445					
Thr	Ile	Ser	Ile	Trp	Gly	Thr	Thr	Leu	Tyr	Pro	Gln	Val	Glu	Asp	Lys		
					455						460						

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Val Glu Asn Asp Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Val
465                               470                               475                               480
Ala Ala Asp Ile Gly Ala Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu
                               485                               490                               495
Asp His Lys Asp Lys Ser Leu Gln Ser Leu Thr Leu Asp Gln Ser Val
                               500                               505                               510
Arg Lys Asn Glu Lys Leu Lys Leu Ala Ala Gln Gly Ala Glu Lys Thr
                               515                               520                               525
Tyr Gly Asn Gly Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys
                               530                               535                               540
Val Ser Arg Phe Asp Phe Ile Arg Gln Ile Glu Val Asp Gly Gln Thr
545                               550                               555                               560
Ile Thr Leu Ala Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asn His Ser
                               565                               570                               575
Ala Val Val Ala Leu Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys Ile
                               580                               585                               590
Asp Ser Leu Ile Asn Gln Arg Ser Phe Leu Val Ser Gly Leu Gly Gly
                               595                               600                               605
Glu His Thr Ala Phe Asn Gln Leu Pro Asp Gly Lys Ala Glu Tyr His
                               610                               615                               620
Gly Lys Ala Phe Ser Ser Asp Asp Pro Asn Gly Arg Leu His Tyr Ser
625                               630                               635                               640
Ile Asp Phe Thr Lys Lys Gln Gly Tyr Gly Arg Ile Glu His Leu Lys
                               645                               650                               655
Thr Pro Glu Gln Asn Val Glu Leu Ala Ser Ala Glu Leu Lys Ala Asp
                               660                               665                               670
Glu Lys Ser His Ala Val Ile Leu Gly Asp Thr Arg Tyr Gly Gly Glu
                               675                               680                               685
Glu Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln Glu
                               690                               695                               700
Ile Ala Gly Ser Ala Thr Val Lys Ile Arg Glu Lys Val His Glu Ile
705                               710                               715                               720
Gly Ile Ala Gly Lys Gln
                               725

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<210> 138
<211> 728
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetic sequence

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<400> 138
Met Ala Asn Lys Ala Val Asn Asp Phe Ile Leu Ala Met Asn Tyr Asp
1                               5                               10                               15
Lys Lys Lys Leu Leu Thr His Gln Gly Glu Ser Ile Glu Asn Arg Phe
                               20                               25                               30
Ile Lys Glu Gly Asn Gln Leu Pro Asp Glu Phe Val Val Ile Glu Arg
                               35                               40                               45
Lys Lys Arg Ser Leu Ser Thr Asn Thr Ser Asp Ile Ser Val Thr Ala
                               50                               55                               60
Thr Asn Asp Ser Arg Leu Tyr Pro Gly Ala Leu Leu Val Val Asp Glu
65                               70                               75                               80
Thr Leu Leu Glu Asn Pro Thr Leu Leu Ala Val Asp Arg Ala Pro
                               85                               90                               95

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Met	Thr	Tyr	Ser	Ile	Asp	Leu	Pro	Gly	Leu	Ala	Ser	Ser	Asp	Ser	Phe	100	105	110
Leu	Gln	Val	Glu	Asp	Pro	Ser	Asn	Ser	Ser	Val	Arg	Gly	Ala	Val	Asn	115	120	125
Asp	Leu	Leu	Ala	Lys	Trp	His	Gln	Asp	Tyr	Gly	Gln	Val	Asn	Asn	Val	130	135	140
Pro	Met	Gln	Tyr	Glu	Lys	Ile	Thr	Ala	His	Ser	Met	Glu	Gln	Leu	Lys	145	150	155
Val	Lys	Phe	Gly	Ser	Asp	Phe	Glu	Lys	Thr	Gly	Asn	Ser	Leu	Asp	Ile	165	170	175
Asp	Phe	Asn	Ser	Val	His	Ser	Gly	Glu	Lys	Gln	Ile	Gln	Ile	Val	Asn	180	185	190
Phe	Lys	Gln	Ile	Tyr	Tyr	Thr	Val	Ser	Val	Asp	Ala	Val	Lys	Asn	Pro	195	200	205
Gly	Asp	Val	Phe	Gln	Asp	Thr	Val	Thr	Val	Glu	Asp	Leu	Lys	Gln	Arg	210	215	220
Gly	Ile	Ser	Ala	Glu	Arg	Pro	Leu	Val	Tyr	Ile	Ser	Ser	Val	Ala	Tyr	225	230	235
Gly	Arg	Gln	Val	Tyr	Leu	Lys	Leu	Glu	Thr	Thr	Ser	Lys	Ser	Asp	Glu	245	250	255
Val	Glu	Ala	Ala	Phe	Glu	Ala	Leu	Ile	Lys	Gly	Val	Lys	Val	Ala	Pro	260	265	270
Gln	Thr	Glu	Trp	Lys	Gln	Ile	Leu	Asp	Asn	Thr	Glu	Val	Lys	Ala	Val	275	280	285
Ile	Leu	Gly	Gly	Asp	Pro	Ser	Ser	Gly	Ala	Arg	Val	Val	Thr	Gly	Lys	290	295	300
Val	Asp	Met	Val	Glu	Asp	Leu	Ile	Gln	Glu	Gly	Ser	Arg	Phe	Thr	Ala	305	310	315
Asp	His	Pro	Gly	Leu	Pro	Ile	Ser	Tyr	Thr	Thr	Ser	Phe	Leu	Arg	Asp	325	330	335
Asn	Val	Val	Ala	Thr	Phe	Gln	Asn	Ser	Thr	Asp	Tyr	Val	Glu	Thr	Lys	340	345	350
Val	Thr	Ala	Tyr	Arg	Asn	Gly	Asp	Leu	Leu	Leu	Asp	His	Ser	Gly	Ala	355	360	365
Tyr	Val	Ala	Gln	Tyr	Tyr	Ile	Thr	Trp	Asp	Glu	Leu	Ser	Tyr	Asp	His	370	375	380
Gln	Gly	Lys	Glu	Val	Leu	Thr	Pro	Lys	Ala	Trp	Asp	Arg	Asn	Gly	Gln	385	390	395
Asp	Leu	Thr	Ala	His	Phe	Thr	Thr	Ser	Ile	Pro	Leu	Lys	Gly	Asn	Val	405	410	415
Arg	Asn	Leu	Ser	Val	Lys	Ile	Arg	Glu	Cys	Thr	Gly	Leu	Ala	Trp	Glu	420	425	430
Trp	Trp	Arg	Thr	Val	Tyr	Glu	Lys	Thr	Asp	Leu	Pro	Leu	Val	Arg	Lys	435	440	445
Arg	Thr	Ile	Ser	Ile	Trp	Gly	Thr	Thr	Leu	Tyr	Pro	Gln	Val	Glu	Asp	450	455	460
Lys	Val	Glu	Asn	Asp	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	465	470	475
Val	Thr	Ala	Asp	Ile	Gly	Thr	Gly	Leu	Ala	Asp	Ala	Leu	Thr	Ala	Pro	485	490	495
Leu	Asp	His	Lys	Asp	Lys	Gly	Leu	Lys	Ser	Leu	Thr	Leu	Glu	Asp	Ser	500	505	510
Ile	Ser	Gln	Asn	Gly	Thr	Leu	Thr	Leu	Ser	Ala	Gln	Gly	Ala	Glu	Lys	515	520	525
Thr	Tyr	Gly	Asn	Gly	Asp	Ser	Leu	Asn	Thr	Gly	Lys	Leu	Lys	Asn	Asp	530	535	540

Lys Val Ser Arg Phe Asp Phe Ile Arg Gln Ile Glu Val Asp Gly Gln
 545 550 555 560
 Leu Ile Thr Leu Glu Ser Gly Glu Phe Gln Val Tyr Lys Gln Ser His
 565 570 575
 Ser Ala Leu Thr Ala Leu Gln Thr Glu Gln Glu Gln Asp Pro Glu His
 580 585 590
 Ser Glu Lys Met Val Ala Lys Arg Arg Phe Arg Ile Gly Asp Ile Ala
 595 600 605
 Gly Glu His Thr Ser Phe Asp Lys Leu Pro Lys Asp Val Met Ala Thr
 610 615 620
 Tyr Arg Gly Thr Ala Phe Gly Ser Asp Asp Ala Gly Gly Lys Leu Thr
 625 630 635 640
 Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly His Gly Lys Ile Glu His
 645 650 655
 Leu Lys Ser Pro Glu Leu Asn Val Asp Leu Ala Val Ala Tyr Ile Lys
 660 665 670
 Pro Asp Glu Lys His His Ala Val Ile Ser Gly Ser Val Leu Tyr Asn
 675 680 685
 Gln Asp Glu Lys Gly Ser Tyr Ser Leu Gly Ile Phe Gly Glu Lys Ala
 690 695 700
 Gln Glu Val Ala Gly Ser Ala Glu Val Glu Thr Ala Asn Gly Ile His
 705 710 715 720
 His Ile Gly Leu Ala Ala Lys Gln
 725

<210> 139
 <211> 727
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 139
 Ala Asn Lys Ala Val Asn Asp Phe Ile Leu Ala Met Asn Tyr Asp Lys
 1 5 10 15
 Lys Lys Leu Leu Thr His Gln Gly Glu Ser Ile Glu Asn Arg Phe Ile
 20 25 30
 Lys Glu Gly Asn Gln Leu Pro Asp Glu Phe Val Val Ile Glu Arg Lys
 35 40 45
 Lys Arg Ser Leu Ser Thr Asn Thr Ser Asp Ile Ser Val Thr Ala Thr
 50 55 60
 Asn Asp Ser Arg Leu Tyr Pro Gly Ala Leu Leu Val Val Asp Glu Thr
 65 70 75 80
 Leu Leu Glu Asn Asn Pro Thr Leu Leu Ala Val Asp Arg Ala Pro Met
 85 90 95
 Thr Tyr Ser Ile Asp Leu Pro Gly Leu Ala Ser Ser Asp Ser Phe Leu
 100 105 110
 Gln Val Glu Asp Pro Ser Asn Ser Ser Val Arg Gly Ala Val Asn Asp
 115 120 125
 Leu Leu Ala Lys Trp His Gln Asp Tyr Gly Gln Val Asn Asn Val Pro
 130 135 140
 Met Gln Tyr Glu Lys Ile Thr Ala His Ser Met Glu Gln Leu Lys Val
 145 150 155 160
 Lys Phe Gly Ser Asp Phe Glu Lys Thr Gly Asn Ser Leu Asp Ile Asp
 165 170 175

Phe	Asn	Ser	Val	His	Ser	Gly	Glu	Lys	Gln	Ile	Gln	Ile	Val	Asn	Phe	180	185	190
Lys	Gln	Ile	Tyr	Tyr	Thr	Val	Ser	Val	Asp	Ala	Val	Lys	Asn	Pro	Gly	195	200	205
Asp	Val	Phe	Gln	Asp	Thr	Val	Thr	Val	Glu	Asp	Leu	Lys	Gln	Arg	Gly	210	215	220
Ile	Ser	Ala	Glu	Arg	Pro	Leu	Val	Tyr	Ile	Ser	Ser	Val	Ala	Tyr	Gly	225	230	235
Arg	Gln	Val	Tyr	Leu	Lys	Leu	Glu	Thr	Thr	Ser	Lys	Ser	Asp	Glu	Val	245	250	255
Glu	Ala	Ala	Phe	Glu	Ala	Leu	Ile	Lys	Gly	Val	Lys	Val	Ala	Pro	Gln	260	265	270
Thr	Glu	Trp	Lys	Gln	Ile	Leu	Asp	Asn	Thr	Glu	Val	Lys	Ala	Val	Ile	275	280	285
Leu	Gly	Gly	Asp	Pro	Ser	Ser	Gly	Ala	Arg	Val	Val	Thr	Gly	Lys	Val	290	295	300
Asp	Met	Val	Glu	Asp	Leu	Ile	Gln	Glu	Gly	Ser	Arg	Phe	Thr	Ala	Asp	305	310	315
His	Pro	Gly	Leu	Pro	Ile	Ser	Tyr	Thr	Thr	Ser	Phe	Leu	Arg	Asp	Asn	325	330	335
Val	Val	Ala	Thr	Phe	Gln	Asn	Ser	Thr	Asp	Tyr	Val	Glu	Thr	Lys	Val	340	345	350
Thr	Ala	Tyr	Arg	Asn	Gly	Asp	Leu	Leu	Leu	Asp	His	Ser	Gly	Ala	Tyr	355	360	365
Val	Ala	Gln	Tyr	Tyr	Ile	Thr	Trp	Asp	Glu	Leu	Ser	Tyr	Asp	His	Gln	370	375	380
Gly	Lys	Glu	Val	Leu	Thr	Pro	Lys	Ala	Trp	Asp	Arg	Asn	Gly	Gln	Asp	385	390	395
Leu	Thr	Ala	His	Phe	Thr	Thr	Ser	Ile	Pro	Leu	Lys	Gly	Asn	Val	Arg	405	410	415
Asn	Leu	Ser	Val	Lys	Ile	Arg	Glu	Cys	Thr	Gly	Leu	Ala	Trp	Glu	Trp	420	425	430
Trp	Arg	Thr	Val	Tyr	Glu	Lys	Thr	Asp	Leu	Pro	Leu	Val	Arg	Lys	Arg	435	440	445
Thr	Ile	Ser	Ile	Trp	Gly	Thr	Thr	Leu	Tyr	Pro	Gln	Val	Glu	Asp	Lys	450	455	460
Val	Glu	Asn	Asp	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Val	465	470	475
Thr	Ala	Asp	Ile	Gly	Thr	Gly	Leu	Ala	Asp	Ala	Leu	Thr	Ala	Pro	Leu	485	490	495
Asp	His	Lys	Asp	Lys	Gly	Leu	Lys	Ser	Leu	Thr	Leu	Glu	Asp	Ser	Ile	500	505	510
Ser	Gln	Asn	Gly	Thr	Leu	Thr	Leu	Ser	Ala	Gln	Gly	Ala	Glu	Lys	Thr	515	520	525
Tyr	Gly	Asn	Gly	Asp	Ser	Leu	Asn	Thr	Gly	Lys	Leu	Lys	Asn	Asp	Lys	530	535	540
Val	Ser	Arg	Phe	Asp	Phe	Ile	Arg	Gln	Ile	Glu	Val	Asp	Gly	Gln	Leu	545	550	555
Ile	Thr	Leu	Glu	Ser	Gly	Glu	Phe	Gln	Val	Tyr	Lys	Gln	Ser	His	Ser	565	570	575
Ala	Leu	Thr	Ala	Leu	Gln	Thr	Glu	Gln	Glu	Gln	Asp	Pro	Glu	His	Ser	580	585	590
Glu	Lys	Met	Val	Ala	Lys	Arg	Arg	Phe	Arg	Ile	Gly	Asp	Ile	Ala	Gly	595	600	605
Glu	His	Thr	Ser	Phe	Asp	Lys	Leu	Pro	Lys	Asp	Val	Met	Ala	Thr	Tyr	610	615	620

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Arg Gly Thr Ala Phe Gly Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr
625          630          635          640
Thr Ile Asp Phe Ala Ala Lys Gln Gly His Gly Lys Ile Glu His Leu
          645          650          655
Lys Ser Pro Glu Leu Asn Val Asp Leu Ala Val Ala Tyr Ile Lys Pro
          660          665          670
Asp Glu Lys His His Ala Val Ile Ser Gly Ser Val Leu Tyr Asn Gln
          675          680          685
Asp Glu Lys Gly Ser Tyr Ser Leu Gly Ile Phe Gly Glu Lys Ala Gln
          690          695          700
Glu Val Ala Gly Ser Ala Glu Val Glu Thr Ala Asn Gly Ile His His
705          710          715          720
Ile Gly Leu Ala Ala Lys Gln
          725

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<210> 140
<211> 723
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetic sequence

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<400> 140
Met Ala Asn Lys Ala Val Asn Asp Phe Ile Leu Ala Met Asn Tyr Asp
1          5          10          15
Lys Lys Lys Leu Leu Thr His Gln Gly Glu Ser Ile Glu Asn Arg Phe
          20          25          30
Ile Lys Glu Gly Asn Gln Leu Pro Asp Glu Phe Val Val Ile Glu Arg
          35          40          45
Lys Lys Arg Ser Leu Ser Thr Asn Thr Ser Asp Ile Ser Val Thr Ala
          50          55          60
Thr Asn Asp Ser Arg Leu Tyr Pro Gly Ala Leu Leu Val Val Asp Glu
65          70          75          80
Thr Leu Leu Glu Asn Asn Pro Thr Leu Leu Ala Val Asp Arg Ala Pro
          85          90          95
Met Thr Tyr Ser Ile Asp Leu Pro Gly Leu Ala Ser Ser Asp Ser Phe
          100          105          110
Leu Gln Val Glu Asp Pro Ser Asn Ser Ser Val Arg Gly Ala Val Asn
          115          120          125
Asp Leu Leu Ala Lys Trp His Gln Asp Tyr Gly Gln Val Asn Asn Val
          130          135          140
Pro Met Gln Tyr Glu Lys Ile Thr Ala His Ser Met Glu Gln Leu Lys
145          150          155          160
Val Lys Phe Gly Ser Asp Phe Glu Lys Thr Gly Asn Ser Leu Asp Ile
          165          170          175
Asp Phe Asn Ser Val His Ser Gly Glu Lys Gln Ile Gln Ile Val Asn
          180          185          190
Phe Lys Gln Ile Tyr Tyr Thr Val Ser Val Asp Ala Val Lys Asn Pro
          195          200          205
Gly Asp Val Phe Gln Asp Thr Val Thr Val Glu Asp Leu Lys Gln Arg
          210          215          220
Gly Ile Ser Ala Glu Arg Pro Leu Val Tyr Ile Ser Ser Val Ala Tyr
225          230          235          240
Gly Arg Gln Val Tyr Leu Lys Leu Glu Thr Thr Ser Lys Ser Asp Glu
          245          250          255

```

Val	Glu	Ala	Ala	Phe	Glu	Ala	Leu	Ile	Lys	Gly	Val	Lys	Val	Ala	Pro	260	265	270
Gln	Thr	Glu	Trp	Lys	Gln	Ile	Leu	Asp	Asn	Thr	Glu	Val	Lys	Ala	Val	275	280	285
Ile	Leu	Gly	Gly	Asp	Pro	Ser	Ser	Gly	Ala	Arg	Val	Val	Thr	Gly	Lys	290	295	300
Val	Asp	Met	Val	Glu	Asp	Leu	Ile	Gln	Glu	Gly	Ser	Arg	Phe	Thr	Ala	305	310	315
Asp	His	Pro	Gly	Leu	Pro	Ile	Ser	Tyr	Thr	Thr	Ser	Phe	Leu	Arg	Asp	325	330	335
Asn	Val	Val	Ala	Thr	Phe	Gln	Asn	Ser	Thr	Asp	Tyr	Val	Glu	Thr	Lys	340	345	350
Val	Thr	Ala	Tyr	Arg	Asn	Gly	Asp	Leu	Leu	Leu	Asp	His	Ser	Gly	Ala	355	360	365
Tyr	Val	Ala	Gln	Tyr	Tyr	Ile	Thr	Trp	Asp	Glu	Leu	Ser	Tyr	Asp	His	370	375	380
Gln	Gly	Lys	Glu	Val	Leu	Thr	Pro	Lys	Ala	Trp	Asp	Arg	Asn	Gly	Gln	385	390	395
Asp	Leu	Thr	Ala	His	Phe	Thr	Thr	Ser	Ile	Pro	Leu	Lys	Gly	Asn	Val	405	410	415
Arg	Asn	Leu	Ser	Val	Lys	Ile	Arg	Glu	Cys	Thr	Gly	Leu	Ala	Trp	Glu	420	425	430
Trp	Trp	Arg	Thr	Val	Tyr	Glu	Lys	Thr	Asp	Leu	Pro	Leu	Val	Arg	Lys	435	440	445
Arg	Thr	Ile	Ser	Ile	Trp	Gly	Thr	Thr	Leu	Tyr	Pro	Gln	Val	Glu	Asp	450	455	460
Lys	Val	Glu	Asn	Asp	Ser	Ser	Gly	Gly	Gly	Gly	Val	Ala	Ala	Asp	Ile	465	470	475
Gly	Ala	Gly	Leu	Ala	Asp	Ala	Leu	Thr	Ala	Pro	Leu	Asp	His	Lys	Asp	485	490	495
Lys	Gly	Leu	Gln	Ser	Leu	Thr	Leu	Asp	Gln	Ser	Val	Arg	Lys	Asn	Glu	500	505	510
Lys	Leu	Lys	Leu	Ala	Ala	Gln	Gly	Ala	Glu	Lys	Thr	Tyr	Gly	Asn	Gly	515	520	525
Asp	Ser	Leu	Asn	Thr	Gly	Lys	Leu	Lys	Asn	Asp	Lys	Val	Ser	Arg	Phe	530	535	540
Asp	Phe	Ile	Arg	Gln	Ile	Glu	Val	Asp	Gly	Lys	Leu	Ile	Thr	Leu	Glu	545	550	555
Ser	Gly	Glu	Phe	Gln	Val	Tyr	Lys	Gln	Ser	His	Ser	Ala	Leu	Thr	Ala	565	570	575
Leu	Gln	Thr	Glu	Gln	Val	Gln	Asp	Ser	Glu	Asp	Ser	Gly	Lys	Met	Val	580	585	590
Ala	Lys	Arg	Gln	Phe	Arg	Ile	Gly	Asp	Ile	Ala	Gly	Glu	His	Thr	Ser	595	600	605
Phe	Asp	Lys	Leu	Pro	Lys	Gly	Gly	Ser	Ala	Thr	Tyr	Arg	Gly	Thr	Ala	610	615	620
Phe	Gly	Ser	Asp	Asp	Ala	Gly	Gly	Lys	Leu	Thr	Tyr	Thr	Ile	Asp	Phe	625	630	635
Ala	Ala	Lys	Gln	Gly	His	Gly	Lys	Ile	Glu	His	Leu	Lys	Ser	Pro	Glu	645	650	655
Leu	Asn	Val	Glu	Leu	Ala	Thr	Ala	Tyr	Ile	Lys	Pro	Asp	Glu	Lys	Arg	660	665	670
His	Ala	Val	Ile	Ser	Gly	Ser	Val	Leu	Tyr	Asn	Gln	Asp	Glu	Lys	Gly	675	680	685
Ser	Tyr	Ser	Leu	Gly	Ile	Phe	Gly	Gly	Gln	Ala	Gln	Glu	Val	Ala	Gly	690	695	700

Ser Ala Glu Val Glu Thr Ala Asn Gly Ile His His Ile Gly Leu Ala
 705 710 715 720
 Ala Lys Gln

<210> 141
 <211> 722
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 141
 Ala Asn Lys Ala Val Asn Asp Phe Ile Leu Ala Met Asn Tyr Asp Lys
 1 5 10 15
 Lys Lys Leu Leu Thr His Gln Gly Glu Ser Ile Glu Asn Arg Phe Ile
 20 25 30
 Lys Glu Gly Asn Gln Leu Pro Asp Glu Phe Val Val Ile Glu Arg Lys
 35 40 45
 Lys Arg Ser Leu Ser Thr Asn Thr Ser Asp Ile Ser Val Thr Ala Thr
 50 55 60
 Asn Asp Ser Arg Leu Tyr Pro Gly Ala Leu Leu Val Val Asp Glu Thr
 65 70 75 80
 Leu Leu Glu Asn Asn Pro Thr Leu Leu Ala Val Asp Arg Ala Pro Met
 85 90 95
 Thr Tyr Ser Ile Asp Leu Pro Gly Leu Ala Ser Ser Asp Ser Phe Leu
 100 105 110
 Gln Val Glu Asp Pro Ser Asn Ser Ser Val Arg Gly Ala Val Asn Asp
 115 120 125
 Leu Leu Ala Lys Trp His Gln Asp Tyr Gly Gln Val Asn Asn Val Pro
 130 135 140
 Met Gln Tyr Glu Lys Ile Thr Ala His Ser Met Glu Gln Leu Lys Val
 145 150 155 160
 Lys Phe Gly Ser Asp Phe Glu Lys Thr Gly Asn Ser Leu Asp Ile Asp
 165 170 175
 Phe Asn Ser Val His Ser Gly Glu Lys Gln Ile Gln Ile Val Asn Phe
 180 185 190
 Lys Gln Ile Tyr Tyr Thr Val Ser Val Asp Ala Val Lys Asn Pro Gly
 195 200 205
 Asp Val Phe Gln Asp Thr Val Thr Val Glu Asp Leu Lys Gln Arg Gly
 210 215 220
 Ile Ser Ala Glu Arg Pro Leu Val Tyr Ile Ser Ser Val Ala Tyr Gly
 225 230 235 240
 Arg Gln Val Tyr Leu Lys Leu Glu Thr Thr Ser Lys Ser Asp Glu Val
 245 250 255
 Glu Ala Ala Phe Glu Ala Leu Ile Lys Gly Val Lys Val Ala Pro Gln
 260 265 270
 Thr Glu Trp Lys Gln Ile Leu Asp Asn Thr Glu Val Lys Ala Val Ile
 275 280 285
 Leu Gly Gly Asp Pro Ser Ser Gly Ala Arg Val Val Thr Gly Lys Val
 290 295 300
 Asp Met Val Glu Asp Leu Ile Gln Glu Gly Ser Arg Phe Thr Ala Asp
 305 310 315 320
 His Pro Gly Leu Pro Ile Ser Tyr Thr Thr Ser Phe Leu Arg Asp Asn
 325 330 335

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Val Val Ala Thr Phe Gln Asn Ser Thr Asp Tyr Val Glu Thr Lys Val
      340                      345                      350
Thr Ala Tyr Arg Asn Gly Asp Leu Leu Leu Asp His Ser Gly Ala Tyr
      355                      360                      365
Val Ala Gln Tyr Tyr Ile Thr Trp Asp Glu Leu Ser Tyr Asp His Gln
      370                      375                      380
Gly Lys Glu Val Leu Thr Pro Lys Ala Trp Asp Arg Asn Gly Gln Asp
385                      390                      395                      400
Leu Thr Ala His Phe Thr Thr Ser Ile Pro Leu Lys Gly Asn Val Arg
      405                      410                      415
Asn Leu Ser Val Lys Ile Arg Glu Cys Thr Gly Leu Ala Trp Glu Trp
      420                      425                      430
Trp Arg Thr Val Tyr Glu Lys Thr Asp Leu Pro Leu Val Arg Lys Arg
      435                      440                      445
Thr Ile Ser Ile Trp Gly Thr Thr Leu Tyr Pro Gln Val Glu Asp Lys
      450                      455                      460
Val Glu Asn Asp Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly
465                      470                      475                      480
Ala Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys
      485                      490                      495
Gly Leu Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys
      500                      505                      510
Leu Lys Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp
      515                      520                      525
Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp
      530                      535                      540
Phe Ile Arg Gln Ile Glu Val Asp Gly Lys Leu Ile Thr Leu Glu Ser
545                      550                      555                      560
Gly Glu Phe Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Leu
      565                      570                      575
Gln Thr Glu Gln Val Gln Asp Ser Glu Asp Ser Gly Lys Met Val Ala
      580                      585                      590
Lys Arg Gln Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe
      595                      600                      605
Asp Lys Leu Pro Lys Gly Gly Ser Ala Thr Tyr Arg Gly Thr Ala Phe
      610                      615                      620
Gly Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala
625                      630                      635                      640
Ala Lys Gln Gly His Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu
      645                      650                      655
Asn Val Glu Leu Ala Thr Ala Tyr Ile Lys Pro Asp Glu Lys Arg His
      660                      665                      670
Ala Val Ile Ser Gly Ser Val Leu Tyr Asn Gln Asp Glu Lys Gly Ser
      675                      680                      685
Tyr Ser Leu Gly Ile Phe Gly Gly Gln Ala Gln Glu Val Ala Gly Ser
      690                      695                      700
Ala Glu Val Glu Thr Ala Asn Gly Ile His His Ile Gly Leu Ala Ala
705                      710                      715                      720
Lys Gln

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<210> 142

<211> 723

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence

<400> 142

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Met Ala Asn Lys Ala Val Asn Asp Phe Ile Leu Ala Met Asn Tyr Asp
1      5      10      15
Lys Lys Lys Leu Leu Thr His Gln Gly Glu Ser Ile Glu Asn Arg Phe
20      25      30
Ile Lys Glu Gly Asn Gln Leu Pro Asp Glu Phe Val Val Ile Glu Arg
35      40      45
Lys Lys Arg Ser Leu Ser Thr Asn Thr Ser Asp Ile Ser Val Thr Ala
50      55      60
Thr Asn Asp Ser Arg Leu Tyr Pro Gly Ala Leu Leu Val Val Asp Glu
65      70      75      80
Thr Leu Leu Glu Asn Asn Pro Thr Leu Leu Ala Val Asp Arg Ala Pro
85      90      95
Met Thr Tyr Ser Ile Asp Leu Pro Gly Leu Ala Ser Ser Asp Ser Phe
100     105     110
Leu Gln Val Glu Asp Pro Ser Asn Ser Ser Val Arg Gly Ala Val Asn
115     120     125
Asp Leu Leu Ala Lys Trp His Gln Asp Tyr Gly Gln Val Asn Asn Val
130     135     140
Pro Met Gln Tyr Glu Lys Ile Thr Ala His Ser Met Glu Gln Leu Lys
145     150     155     160
Val Lys Phe Gly Ser Asp Phe Glu Lys Thr Gly Asn Ser Leu Asp Ile
165     170     175
Asp Phe Asn Ser Val His Ser Gly Glu Lys Gln Ile Gln Ile Val Asn
180     185     190
Phe Lys Gln Ile Tyr Tyr Thr Val Ser Val Asp Ala Val Lys Asn Pro
195     200     205
Gly Asp Val Phe Gln Asp Thr Val Thr Val Glu Asp Leu Lys Gln Arg
210     215     220
Gly Ile Ser Ala Glu Arg Pro Leu Val Tyr Ile Ser Ser Val Ala Tyr
225     230     235     240
Gly Arg Gln Val Tyr Leu Lys Leu Glu Thr Thr Ser Lys Ser Asp Glu
245     250     255
Val Glu Ala Ala Phe Glu Ala Leu Ile Lys Gly Val Lys Val Ala Pro
260     265     270
Gln Thr Glu Trp Lys Gln Ile Leu Asp Asn Thr Glu Val Lys Ala Val
275     280     285
Ile Leu Gly Gly Asp Pro Ser Ser Gly Ala Arg Val Val Thr Gly Lys
290     295     300
Val Asp Met Val Glu Asp Leu Ile Gln Glu Gly Ser Arg Phe Thr Ala
305     310     315     320
Asp His Pro Gly Leu Pro Ile Ser Tyr Thr Thr Ser Phe Leu Arg Asp
325     330     335
Asn Val Val Ala Thr Phe Gln Asn Ser Thr Asp Tyr Val Glu Thr Lys
340     345     350
Val Thr Ala Tyr Arg Asn Gly Asp Leu Leu Leu Asp His Ser Gly Ala
355     360     365
Tyr Val Ala Gln Tyr Tyr Ile Thr Trp Asp Glu Leu Ser Tyr Asp His
370     375     380
Gln Gly Lys Glu Val Leu Thr Pro Lys Ala Trp Asp Arg Asn Gly Gln
385     390     395     400
Asp Leu Thr Ala His Phe Thr Thr Ser Ile Pro Leu Lys Gly Asn Val
405     410     415

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Arg Asn Leu Ser Val Lys Ile Arg Glu Cys Thr Gly Leu Ala Trp Glu
 420 425 430
 Trp Trp Arg Thr Val Tyr Glu Lys Thr Asp Leu Pro Leu Val Arg Lys
 435 440 445
 Arg Thr Ile Ser Ile Trp Gly Thr Thr Leu Tyr Pro Gln Val Glu Asp
 450 455 460
 Lys Val Glu Asn Asp Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile
 465 470 475 480
 Gly Ala Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp
 485 490 495
 Lys Gly Leu Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu
 500 505 510
 Lys Leu Lys Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly
 515 520 525
 Asp Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe
 530 535 540
 Asp Phe Ile Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu
 545 550 555 560
 Ser Gly Glu Phe Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala
 565 570 575
 Phe Gln Thr Glu Gln Ile Gln Asp Ser Glu His Ser Gly Lys Met Val
 580 585 590
 Ala Lys Arg Gln Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser
 595 600 605
 Phe Asp Lys Leu Pro Glu Gly Gly Arg Ala Thr Tyr Arg Gly Thr Ala
 610 615 620
 Phe Gly Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe
 625 630 635 640
 Ala Ala Lys Gln Gly Asn Gly Lys Ile Glu His Leu Lys Ser Pro Glu
 645 650 655
 Leu Asn Val Asp Leu Ala Ala Ala Asp Ile Lys Pro Asp Gly Lys Arg
 660 665 670
 His Ala Val Ile Ser Gly Ser Val Leu Tyr Asn Gln Ala Glu Lys Gly
 675 680 685
 Ser Tyr Ser Leu Gly Ile Phe Gly Gly Lys Ala Gln Glu Val Ala Gly
 690 695 700
 Ser Ala Glu Val Lys Thr Val Asn Gly Ile Arg His Ile Gly Leu Ala
 705 710 715 720
 Ala Lys Gln

<210> 143
 <211> 722
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 143
 Ala Asn Lys Ala Val Asn Asp Phe Ile Leu Ala Met Asn Tyr Asp Lys
 1 5 10 15
 Lys Lys Leu Leu Thr His Gln Gly Glu Ser Ile Glu Asn Arg Phe Ile
 20 25 30
 Lys Glu Gly Asn Gln Leu Pro Asp Glu Phe Val Val Ile Glu Arg Lys
 35 40 45

Lys	Arg	Ser	Leu	Ser	Thr	Asn	Thr	Ser	Asp	Ile	Ser	Val	Thr	Ala	Thr	50	55	60
Asn	Asp	Ser	Arg	Leu	Tyr	Pro	Gly	Ala	Leu	Leu	Val	Val	Asp	Glu	Thr	65	70	75
Leu	Leu	Glu	Asn	Asn	Pro	Thr	Leu	Leu	Ala	Val	Asp	Arg	Ala	Pro	Met	85	90	95
Thr	Tyr	Ser	Ile	Asp	Leu	Pro	Gly	Leu	Ala	Ser	Ser	Asp	Ser	Phe	Leu	100	105	110
Gln	Val	Glu	Asp	Pro	Ser	Asn	Ser	Ser	Val	Arg	Gly	Ala	Val	Asn	Asp	115	120	125
Leu	Leu	Ala	Lys	Trp	His	Gln	Asp	Tyr	Gly	Gln	Val	Asn	Asn	Val	Pro	130	135	140
Met	Gln	Tyr	Glu	Lys	Ile	Thr	Ala	His	Ser	Met	Glu	Gln	Leu	Lys	Val	145	150	155
Lys	Phe	Gly	Ser	Asp	Phe	Glu	Lys	Thr	Gly	Asn	Ser	Leu	Asp	Ile	Asp	165	170	175
Phe	Asn	Ser	Val	His	Ser	Gly	Glu	Lys	Gln	Ile	Gln	Ile	Val	Asn	Phe	180	185	190
Lys	Gln	Ile	Tyr	Tyr	Thr	Val	Ser	Val	Asp	Ala	Val	Lys	Asn	Pro	Gly	195	200	205
Asp	Val	Phe	Gln	Asp	Thr	Val	Thr	Val	Glu	Asp	Leu	Lys	Gln	Arg	Gly	210	215	220
Ile	Ser	Ala	Glu	Arg	Pro	Leu	Val	Tyr	Ile	Ser	Ser	Val	Ala	Tyr	Gly	225	230	235
Arg	Gln	Val	Tyr	Leu	Lys	Leu	Glu	Thr	Thr	Ser	Lys	Ser	Asp	Glu	Val	245	250	255
Glu	Ala	Ala	Phe	Glu	Ala	Leu	Ile	Lys	Gly	Val	Lys	Val	Ala	Pro	Gln	260	265	270
Thr	Glu	Trp	Lys	Gln	Ile	Leu	Asp	Asn	Thr	Glu	Val	Lys	Ala	Val	Ile	275	280	285
Leu	Gly	Gly	Asp	Pro	Ser	Ser	Gly	Ala	Arg	Val	Val	Thr	Gly	Lys	Val	290	295	300
Asp	Met	Val	Glu	Asp	Leu	Ile	Gln	Glu	Gly	Ser	Arg	Phe	Thr	Ala	Asp	305	310	315
His	Pro	Gly	Leu	Pro	Ile	Ser	Tyr	Thr	Thr	Ser	Phe	Leu	Arg	Asp	Asn	325	330	335
Val	Val	Ala	Thr	Phe	Gln	Asn	Ser	Thr	Asp	Tyr	Val	Glu	Thr	Lys	Val	340	345	350
Thr	Ala	Tyr	Arg	Asn	Gly	Asp	Leu	Leu	Leu	Asp	His	Ser	Gly	Ala	Tyr	355	360	365
Val	Ala	Gln	Tyr	Tyr	Ile	Thr	Trp	Asp	Glu	Leu	Ser	Tyr	Asp	His	Gln	370	375	380
Gly	Lys	Glu	Val	Leu	Thr	Pro	Lys	Ala	Trp	Asp	Arg	Asn	Gly	Gln	Asp	385	390	395
Leu	Thr	Ala	His	Phe	Thr	Thr	Ser	Ile	Pro	Leu	Lys	Gly	Asn	Val	Arg	405	410	415
Asn	Leu	Ser	Val	Lys	Ile	Arg	Glu	Cys	Thr	Gly	Leu	Ala	Trp	Glu	Trp	420	425	430
Trp	Arg	Thr	Val	Tyr	Glu	Lys	Thr	Asp	Leu	Pro	Leu	Val	Arg	Lys	Arg	435	440	445
Thr	Ile	Ser	Ile	Trp	Gly	Thr	Thr	Leu	Tyr	Pro	Gln	Val	Glu	Asp	Lys	450	455	460
Val	Glu	Asn	Asp	Ser	Ser	Gly	Gly	Gly	Gly	Val	Ala	Ala	Asp	Ile	Gly	465	470	475
Ala	Gly	Leu	Ala	Asp	Ala	Leu	Thr	Ala	Pro	Leu	Asp	His	Lys	Asp	Lys	485	490	495

Gly Leu Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys
 500 505 510
 Leu Lys Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp
 515 520 525
 Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp
 530 535 540
 Phe Ile Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser
 545 550 555 560
 Gly Glu Phe Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Phe
 565 570 575
 Gln Thr Glu Gln Ile Gln Asp Ser Glu His Ser Gly Lys Met Val Ala
 580 585 590
 Lys Arg Gln Phe Arg Ile Gly Asp Ile Ala Gly Glu His Thr Ser Phe
 595 600 605
 Asp Lys Leu Pro Glu Gly Gly Arg Ala Thr Tyr Arg Gly Thr Ala Phe
 610 615 620
 Gly Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala
 625 630 635 640
 Ala Lys Gln Gly Asn Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu
 645 650 655
 Asn Val Asp Leu Ala Ala Ala Asp Ile Lys Pro Asp Gly Lys Arg His
 660 665 670
 Ala Val Ile Ser Gly Ser Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser
 675 680 685
 Tyr Ser Leu Gly Ile Phe Gly Gly Lys Ala Gln Glu Val Ala Gly Ser
 690 695 700
 Ala Glu Val Lys Thr Val Asn Gly Ile Arg His Ile Gly Leu Ala Ala
 705 710 715 720
 Lys Gln

<210> 144
 <211> 731
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 144
 Met Ala Asn Lys Ala Val Asn Asp Phe Ile Leu Ala Met Asn Tyr Asp
 1 5 10 15
 Lys Lys Lys Leu Leu Thr His Gln Gly Glu Ser Ile Glu Asn Arg Phe
 20 25 30
 Ile Lys Glu Gly Asn Gln Leu Pro Asp Glu Phe Val Val Ile Glu Arg
 35 40 45
 Lys Lys Arg Ser Leu Ser Thr Asn Thr Ser Asp Ile Ser Val Thr Ala
 50 55 60
 Thr Asn Asp Ser Arg Leu Tyr Pro Gly Ala Leu Leu Val Val Asp Glu
 65 70 75 80
 Thr Leu Leu Glu Asn Asn Pro Thr Leu Leu Ala Val Asp Arg Ala Pro
 85 90 95
 Met Thr Tyr Ser Ile Asp Leu Pro Gly Leu Ala Ser Ser Asp Ser Phe
 100 105 110
 Leu Gln Val Glu Asp Pro Ser Asn Ser Ser Val Arg Gly Ala Val Asn
 115 120 125

Asp	Leu	Leu	Ala	Lys	Trp	His	Gln	Asp	Tyr	Gly	Gln	Val	Asn	Asn	Val
130						135					140				
Pro	Met	Gln	Tyr	Glu	Lys	Ile	Thr	Ala	His	Ser	Met	Glu	Gln	Leu	Lys
145					150					155					160
Val	Lys	Phe	Gly	Ser	Asp	Phe	Glu	Lys	Thr	Gly	Asn	Ser	Leu	Asp	Ile
				165					170					175	
Asp	Phe	Asn	Ser	Val	His	Ser	Gly	Glu	Lys	Gln	Ile	Gln	Ile	Val	Asn
			180					185					190		
Phe	Lys	Gln	Ile	Tyr	Tyr	Thr	Val	Ser	Val	Asp	Ala	Val	Lys	Asn	Pro
		195					200					205			
Gly	Asp	Val	Phe	Gln	Asp	Thr	Val	Thr	Val	Glu	Asp	Leu	Lys	Gln	Arg
210					215					220					
Gly	Ile	Ser	Ala	Glu	Arg	Pro	Leu	Val	Tyr	Ile	Ser	Ser	Val	Ala	Tyr
225					230					235					240
Gly	Arg	Gln	Val	Tyr	Leu	Lys	Leu	Glu	Thr	Thr	Ser	Lys	Ser	Asp	Glu
				245					250					255	
Val	Glu	Ala	Ala	Phe	Glu	Ala	Leu	Ile	Lys	Gly	Val	Lys	Val	Ala	Pro
			260					265					270		
Gln	Thr	Glu	Trp	Lys	Gln	Ile	Leu	Asp	Asn	Thr	Glu	Val	Lys	Ala	Val
		275					280					285			
Ile	Leu	Gly	Gly	Asp	Pro	Ser	Ser	Gly	Ala	Arg	Val	Val	Thr	Gly	Lys
290					295					300					
Val	Asp	Met	Val	Glu	Asp	Leu	Ile	Gln	Glu	Gly	Ser	Arg	Phe	Thr	Ala
305					310					315					320
Asp	His	Pro	Gly	Leu	Pro	Ile	Ser	Tyr	Thr	Thr	Ser	Phe	Leu	Arg	Asp
				325					330					335	
Asn	Val	Val	Ala	Thr	Phe	Gln	Asn	Ser	Thr	Asp	Tyr	Val	Glu	Thr	Lys
			340					345					350		
Val	Thr	Ala	Tyr	Arg	Asn	Gly	Asp	Leu	Leu	Leu	Asp	His	Ser	Gly	Ala
		355					360					365			
Tyr	Val	Ala	Gln	Tyr	Tyr	Ile	Thr	Trp	Asp	Glu	Leu	Ser	Tyr	Asp	His
370					375					380					
Gln	Gly	Lys	Glu	Val	Leu	Thr	Pro	Lys	Ala	Trp	Asp	Arg	Asn	Gly	Gln
385					390					395					400
Asp	Leu	Thr	Ala	His	Phe	Thr	Thr	Ser	Ile	Pro	Leu	Lys	Gly	Asn	Val
				405					410					415	
Arg	Asn	Leu	Ser	Val	Lys	Ile	Arg	Glu	Cys	Thr	Gly	Leu	Ala	Trp	Glu
			420					425					430		
Trp	Trp	Arg	Thr	Val	Tyr	Glu	Lys	Thr	Asp	Leu	Pro	Leu	Val	Arg	Lys
		435					440					445			
Arg	Thr	Ile	Ser	Ile	Trp	Gly	Thr	Thr	Leu	Tyr	Pro	Gln	Val	Glu	Asp
450					455					460					
Lys	Val	Glu	Asn	Asp	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly
465					470					475					480
Val	Ala	Ala	Asp	Ile	Gly	Ala	Gly	Leu	Ala	Asp	Ala	Leu	Thr	Ala	Pro
				485					490					495	
Leu	Asp	His	Lys	Asp	Lys	Gly	Leu	Lys	Ser	Leu	Thr	Leu	Glu	Asp	Ser
			500					505					510		
Ile	Ser	Gln	Asn	Gly	Thr	Leu	Thr	Leu	Ser	Ala	Gln	Gly	Ala	Glu	Arg
		515					520					525			
Thr	Phe	Lys	Ala	Gly	Asp	Lys	Asp	Asn	Ser	Leu	Asn	Thr	Gly	Lys	Leu
530					535					540					
Lys	Asn	Asp	Lys	Ile	Ser	Arg	Phe	Asp	Phe	Ile	Arg	Gln	Ile	Glu	Val
545					550					555					560
Asp	Gly	Gln	Leu	Ile	Thr	Leu	Glu	Ser	Gly	Glu	Phe	Gln	Val	Tyr	Lys
				565					570					575	

Gln Ser His Ser Ala Leu Thr Ala Leu Gln Thr Glu Gln Val Gln Asp
 580 585 590
 Ser Glu His Ser Gly Lys Met Val Ala Lys Arg Gln Phe Arg Ile Gly
 595 600 605
 Asp Ile Val Gly Glu His Thr Ser Phe Gly Lys Leu Pro Lys Asp Val
 610 615 620
 Met Ala Thr Tyr Arg Gly Thr Ala Phe Gly Ser Asp Asp Ala Gly Gly
 625 630 635 640
 Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly His Gly Lys
 645 650 655
 Ile Glu His Leu Lys Ser Pro Glu Leu Asn Val Asp Leu Ala Ala Ala
 660 665 670
 Asp Ile Lys Pro Asp Glu Lys His His Ala Val Ile Ser Gly Ser Val
 675 680 685
 Leu Tyr Asn Gln Ala Glu Lys Gly Ser Tyr Ser Leu Gly Ile Phe Gly
 690 695 700
 Gly Gln Ala Gln Glu Val Ala Gly Ser Ala Glu Val Glu Thr Ala Asn
 705 710 715 720
 Gly Ile Arg His Ile Gly Leu Ala Ala Lys Gln
 725 730

<210> 145
 <211> 730
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

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

Asp	Val	Phe	Gln	Asp	Thr	Val	Thr	Val	Glu	Asp	Leu	Lys	Gln	Arg	Gly	210	215	220
Ile	Ser	Ala	Glu	Arg	Pro	Leu	Val	Tyr	Ile	Ser	Ser	Val	Ala	Tyr	Gly	225	230	235
Arg	Gln	Val	Tyr	Leu	Lys	Leu	Glu	Thr	Thr	Ser	Lys	Ser	Asp	Glu	Val	245	250	255
Glu	Ala	Ala	Phe	Glu	Ala	Leu	Ile	Lys	Gly	Val	Lys	Val	Ala	Pro	Gln	260	265	270
Thr	Glu	Trp	Lys	Gln	Ile	Leu	Asp	Asn	Thr	Glu	Val	Lys	Ala	Val	Ile	275	280	285
Leu	Gly	Gly	Asp	Pro	Ser	Ser	Gly	Ala	Arg	Val	Val	Thr	Gly	Lys	Val	290	295	300
Asp	Met	Val	Glu	Asp	Leu	Ile	Gln	Glu	Gly	Ser	Arg	Phe	Thr	Ala	Asp	305	310	315
His	Pro	Gly	Leu	Pro	Ile	Ser	Tyr	Thr	Thr	Ser	Phe	Leu	Arg	Asp	Asn	325	330	335
Val	Val	Ala	Thr	Phe	Gln	Asn	Ser	Thr	Asp	Tyr	Val	Glu	Thr	Lys	Val	340	345	350
Thr	Ala	Tyr	Arg	Asn	Gly	Asp	Leu	Leu	Leu	Asp	His	Ser	Gly	Ala	Tyr	355	360	365
Val	Ala	Gln	Tyr	Tyr	Ile	Thr	Trp	Asp	Glu	Leu	Ser	Tyr	Asp	His	Gln	370	375	380
Gly	Lys	Glu	Val	Leu	Thr	Pro	Lys	Ala	Trp	Asp	Arg	Asn	Gly	Gln	Asp	385	390	395
Leu	Thr	Ala	His	Phe	Thr	Thr	Ser	Ile	Pro	Leu	Lys	Gly	Asn	Val	Arg	405	410	415
Asn	Leu	Ser	Val	Lys	Ile	Arg	Glu	Cys	Thr	Gly	Leu	Ala	Trp	Glu	Trp	420	425	430
Trp	Arg	Thr	Val	Tyr	Glu	Lys	Thr	Asp	Leu	Pro	Leu	Val	Arg	Lys	Arg	435	440	445
Thr	Ile	Ser	Ile	Trp	Gly	Thr	Thr	Leu	Tyr	Pro	Gln	Val	Glu	Asp	Lys	450	455	460
Val	Glu	Asn	Asp	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Val	465	470	475
Ala	Ala	Asp	Ile	Gly	Ala	Gly	Leu	Ala	Asp	Ala	Leu	Thr	Ala	Pro	Leu	485	490	495
Asp	His	Lys	Asp	Lys	Gly	Leu	Lys	Ser	Leu	Thr	Leu	Glu	Asp	Ser	Ile	500	505	510
Ser	Gln	Asn	Gly	Thr	Leu	Thr	Leu	Ser	Ala	Gln	Gly	Ala	Glu	Arg	Thr	515	520	525
Phe	Lys	Ala	Gly	Asp	Lys	Asp	Asn	Ser	Leu	Asn	Thr	Gly	Lys	Leu	Lys	530	535	540
Asn	Asp	Lys	Ile	Ser	Arg	Phe	Asp	Phe	Ile	Arg	Gln	Ile	Glu	Val	Asp	545	550	555
Gly	Gln	Leu	Ile	Thr	Leu	Glu	Ser	Gly	Glu	Phe	Gln	Val	Tyr	Lys	Gln	565	570	575
Ser	His	Ser	Ala	Leu	Thr	Ala	Leu	Gln	Thr	Glu	Gln	Val	Gln	Asp	Ser	580	585	590
Glu	His	Ser	Gly	Lys	Met	Val	Ala	Lys	Arg	Gln	Phe	Arg	Ile	Gly	Asp	595	600	605
Ile	Val	Gly	Glu	His	Thr	Ser	Phe	Gly	Lys	Leu	Pro	Lys	Asp	Val	Met	610	615	620
Ala	Thr	Tyr	Arg	Gly	Thr	Ala	Phe	Gly	Ser	Asp	Asp	Ala	Gly	Gly	Lys	625	630	635
Leu	Thr	Tyr	Thr	Ile	Asp	Phe	Ala	Ala	Lys	Gln	Gly	His	Gly	Lys	Ile	645	650	655

Glu His Leu Lys Ser Pro Glu Leu Asn Val Asp Leu Ala Ala Ala Asp
 660 665 670
 Ile Lys Pro Asp Glu Lys His His Ala Val Ile Ser Gly Ser Val Leu
 675 680 685
 Tyr Asn Gln Ala Glu Lys Gly Ser Tyr Ser Leu Gly Ile Phe Gly Gly
 690 695 700
 Gln Ala Gln Glu Val Ala Gly Ser Ala Glu Val Glu Thr Ala Asn Gly
 705 710 715 720
 Ile Arg His Ile Gly Leu Ala Ala Lys Gln
 725 730

<210> 146
 <211> 180
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 146
 Met Val Ser Ala Val Ile Gly Ser Ala Ala Val Gly Ala Lys Ser Ala
 1 5 10 15
 Val Asp Arg Arg Thr Thr Gly Ala Gln Thr Asp Asp Asn Val Met Ala
 20 25 30
 Leu Arg Ile Glu Thr Thr Ala Arg Ser Tyr Leu Arg Gln Asn Asn Gln
 35 40 45
 Thr Lys Gly Tyr Thr Pro Gln Ile Ser Val Val Gly Tyr Asn Arg His
 50 55 60
 Leu Leu Leu Leu Gly Gln Val Ala Thr Glu Gly Glu Lys Gln Phe Val
 65 70 75 80
 Gly Gln Ile Ala Arg Ser Glu Gln Ala Ala Glu Gly Val Tyr Asn Tyr
 85 90 95
 Ile Thr Val Ala Ser Leu Pro Arg Thr Ala Gly Asp Ile Ala Gly Asp
 100 105 110
 Thr Trp Asn Thr Ser Lys Val Arg Ala Thr Leu Leu Gly Ile Ser Pro
 115 120 125
 Ala Thr Gln Ala Arg Val Lys Ile Val Thr Tyr Gly Asn Val Thr Tyr
 130 135 140
 Val Met Gly Ile Leu Thr Pro Glu Glu Gln Ala Gln Ile Thr Gln Lys
 145 150 155 160
 Val Ser Thr Thr Val Gly Val Gln Lys Val Ile Thr Leu Tyr Gln Asn
 165 170 175
 Tyr Val Gln Arg
 180

<210> 147
 <211> 179
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 147

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

<210> 148

<211> 440

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence

<400> 148

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

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Tyr Val Gln Arg Ser Ser Gly Ser Gly Ser Gly Gly Gly Gly Val Ala
      180      185      190
Ala Asp Ile Gly Thr Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp
      195      200      205
His Lys Asp Lys Gly Leu Lys Ser Leu Thr Leu Glu Asp Ser Ile Ser
      210      215      220
Gln Asn Gly Thr Leu Thr Leu Ser Ala Gln Gly Ala Glu Lys Thr Phe
      225      230      235      240
Lys Val Gly Asp Lys Asp Asn Ser Leu Asn Thr Gly Lys Leu Lys Asn
      245      250      255
Asp Lys Ile Ser Arg Phe Asp Phe Val Gln Lys Ile Glu Val Asp Gly
      260      265      270
Gln Thr Ile Thr Leu Ala Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asp
      275      280      285
His Ser Ala Val Val Ala Leu Gln Ile Glu Lys Ile Asn Asn Pro Asp
      290      295      300
Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser Phe Leu Val Ser Gly Leu
      305      310      315      320
Gly Gly Glu His Thr Ala Phe Asn Gln Leu Pro Ser Gly Lys Ala Glu
      325      330      335
Tyr His Gly Lys Ala Phe Ser Ser Asp Asp Ala Gly Gly Lys Leu Thr
      340      345      350
Tyr Thr Ile Asp Phe Ala Ala Lys Gln Gly His Gly Lys Ile Glu His
      355      360      365
Leu Lys Thr Pro Glu Gln Asn Val Glu Leu Ala Ser Ala Glu Leu Lys
      370      375      380
Ala Asp Glu Lys Ser His Ala Val Ile Leu Gly Asp Thr Arg Tyr Gly
      385      390      395      400
Ser Glu Glu Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp Arg Ala
      405      410      415
Gln Glu Ile Ala Gly Ser Ala Thr Val Lys Ile Arg Glu Lys Val His
      420      425      430
Glu Ile Gly Ile Ala Gly Lys Gln
      435      440

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<210> 149
 <211> 439
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 149
 Val Ser Ala Val Ile Gly Ser Ala Ala Val Gly Ala Lys Ser Ala Val
 1 5 10 15
 Asp Arg Arg Thr Thr Gly Ala Gln Thr Asp Asp Asn Val Met Ala Leu
 20 25 30
 Arg Ile Glu Thr Thr Ala Arg Ser Tyr Leu Arg Gln Asn Asn Gln Thr
 35 40 45
 Lys Gly Tyr Thr Pro Gln Ile Ser Val Val Gly Tyr Asn Arg His Leu
 50 55 60
 Leu Leu Leu Gly Gln Val Ala Thr Glu Gly Glu Lys Gln Phe Val Gly
 65 70 75 80
 Gln Ile Ala Arg Ser Glu Gln Ala Ala Glu Gly Val Tyr Asn Tyr Ile
 85 90 95

Thr Val Ala Ser Leu Pro Arg Thr Ala Gly Asp Ile Ala Gly Asp Thr
 100 105 110
 Trp Asn Thr Ser Lys Val Arg Ala Thr Leu Leu Gly Ile Ser Pro Ala
 115 120 125
 Thr Gln Ala Arg Val Lys Ile Val Thr Tyr Gly Asn Val Thr Tyr Val
 130 135 140
 Met Gly Ile Leu Thr Pro Glu Glu Gln Ala Gln Ile Thr Gln Lys Val
 145 150 155 160
 Ser Thr Thr Val Gly Val Gln Lys Val Ile Thr Leu Tyr Gln Asn Tyr
 165 170 175
 Val Gln Arg Ser Ser Gly Ser Gly Ser Gly Gly Gly Gly Val Ala Ala
 180 185 190
 Asp Ile Gly Thr Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His
 195 200 205
 Lys Asp Lys Gly Leu Lys Ser Leu Thr Leu Glu Asp Ser Ile Ser Gln
 210 215 220
 Asn Gly Thr Leu Thr Leu Ser Ala Gln Gly Ala Glu Lys Thr Phe Lys
 225 230 235 240
 Val Gly Asp Lys Asp Asn Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp
 245 250 255
 Lys Ile Ser Arg Phe Asp Phe Val Gln Lys Ile Glu Val Asp Gly Gln
 260 265 270
 Thr Ile Thr Leu Ala Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asp His
 275 280 285
 Ser Ala Val Val Ala Leu Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys
 290 295 300
 Ile Asp Ser Leu Ile Asn Gln Arg Ser Phe Leu Val Ser Gly Leu Gly
 305 310 315 320
 Gly Glu His Thr Ala Phe Asn Gln Leu Pro Ser Gly Lys Ala Glu Tyr
 325 330 335
 His Gly Lys Ala Phe Ser Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr
 340 345 350
 Thr Ile Asp Phe Ala Ala Lys Gln Gly His Gly Lys Ile Glu His Leu
 355 360 365
 Lys Thr Pro Glu Gln Asn Val Glu Leu Ala Ser Ala Glu Leu Lys Ala
 370 375 380
 Asp Glu Lys Ser His Ala Val Ile Leu Gly Asp Thr Arg Tyr Gly Ser
 385 390 395 400
 Glu Glu Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln
 405 410 415
 Glu Ile Ala Gly Ser Ala Thr Val Lys Ile Arg Glu Lys Val His Glu
 420 425 430
 Ile Gly Ile Ala Gly Lys Gln
 435

<210> 150

<211> 950

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence

<400> 150

Met Ala Lys Thr Ala Asp Thr Pro Ala Thr Ser Lys Ala Thr Ile Arg
 1 5 10 15

Asp	Leu	Asn	Asp	Pro	Ser	Gln	Val	Lys	Thr	Leu	Gln	Glu	Lys	Ala	Gly	20	25	30
Lys	Gly	Ala	Gly	Thr	Val	Val	Ala	Val	Ile	Ala	Ala	Gly	Phe	Asp	Lys	35	40	45
Asn	His	Glu	Ala	Trp	Arg	Leu	Thr	Asp	Lys	Ala	Lys	Ala	Arg	Tyr	Gln	50	55	60
Ser	Lys	Glu	Asp	Leu	Glu	Lys	Ala	Lys	Lys	Glu	His	Gly	Ile	Thr	Tyr	65	70	75
Gly	Glu	Trp	Val	Asn	Asp	Lys	Val	Ala	Tyr	Tyr	His	Asp	Tyr	Ser	Lys	85	90	95
Asp	Gly	Lys	Thr	Ala	Val	Asp	Gln	Glu	His	Gly	Thr	His	Val	Ser	Gly	100	105	110
Ile	Leu	Ser	Gly	Asn	Ala	Pro	Ser	Glu	Thr	Lys	Glu	Pro	Tyr	Arg	Leu	115	120	125
Glu	Gly	Ala	Met	Pro	Glu	Ala	Gln	Leu	Leu	Leu	Met	Arg	Val	Glu	Ile	130	135	140
Val	Asn	Gly	Leu	Ala	Asp	Tyr	Ala	Arg	Asn	Tyr	Ala	Gln	Ala	Ile	Arg	145	150	155
Asp	Ala	Ile	Asn	Leu	Gly	Ala	Lys	Val	Ile	Asn	Met	Ser	Phe	Gly	Asn	165	170	175
Ala	Ala	Leu	Ala	Tyr	Ala	Asn	Leu	Pro	Asp	Glu	Thr	Lys	Lys	Ala	Phe	180	185	190
Asp	Tyr	Ala	Lys	Ser	Lys	Gly	Val	Ser	Ile	Val	Thr	Ser	Ala	Gly	Asn	195	200	205
Asp	Ser	Ser	Phe	Gly	Gly	Lys	Thr	Arg	Leu	Pro	Leu	Ala	Asp	His	Pro	210	215	220
Asp	Tyr	Gly	Val	Val	Gly	Thr	Pro	Ala	Ala	Ala	Asp	Ser	Thr	Leu	Thr	225	230	235
Val	Ala	Ser	Tyr	Ser	Pro	Asp	Lys	Gln	Leu	Thr	Glu	Thr	Val	Thr	Val	245	250	255
Lys	Thr	Ala	Asp	Gln	Gln	Asp	Lys	Glu	Met	Pro	Val	Leu	Ser	Thr	Asn	260	265	270
Arg	Phe	Glu	Pro	Asn	Lys	Ala	Tyr	Asp	Tyr	Ala	Tyr	Ala	Asn	Arg	Gly	275	280	285
Thr	Lys	Glu	Asp	Asp	Phe	Lys	Asp	Val	Lys	Gly	Lys	Ile	Ala	Leu	Ile	290	295	300
Glu	Arg	Gly	Asp	Ile	Asp	Phe	Lys	Asp	Lys	Ile	Ala	Lys	Ala	Lys	Lys	305	310	315
Ala	Gly	Ala	Val	Gly	Val	Leu	Ile	Tyr	Asp	Asn	Gln	Asp	Lys	Gly	Phe	325	330	335
Pro	Ile	Glu	Leu	Pro	Asn	Val	Asp	Gln	Met	Pro	Ala	Ala	Phe	Ile	Ser	340	345	350
Arg	Lys	Asp	Gly	Leu	Leu	Leu	Lys	Asp	Asn	Pro	Gln	Lys	Thr	Ile	Thr	355	360	365
Phe	Asn	Ala	Thr	Pro	Lys	Val	Leu	Pro	Thr	Ala	Ser	Gly	Thr	Lys	Leu	370	375	380
Ser	Arg	Phe	Ser	Ser	Trp	Gly	Leu	Thr	Ala	Asp	Gly	Asn	Ile	Lys	Pro	385	390	395
Asp	Ile	Ala	Ala	Pro	Gly	Gln	Asp	Ile	Leu	Ser	Ser	Val	Ala	Asn	Asn	405	410	415
Lys	Tyr	Ala	Lys	Leu	Ser	Gly	Thr	Ala	Met	Ser	Ala	Pro	Leu	Val	Ala	420	425	430
Gly	Ile	Met	Gly	Leu	Leu	Gln	Glu	Gln	Tyr	Glu	Thr	Gln	Tyr	Pro	Asp	435	440	445
Met	Thr	Pro	Ser	Glu	Arg	Leu	Asp	Leu	Ala	Lys	Lys	Val	Leu	Met	Ser	450	455	460

Ser	Ala	Thr	Ala	Leu	Tyr	Asp	Glu	Asp	Glu	Lys	Ala	Tyr	Phe	Ser	Pro
465					470					475					480
Arg	Gln	Gln	Gly	Ala	Gly	Ala	Val	Asp	Ala	Lys	Lys	Ala	Ser	Ala	Ala
				485					490						495
Thr	Met	Tyr	Val	Thr	Asp	Lys	Asp	Asn	Thr	Ser	Ser	Lys	Val	His	Leu
			500					505					510		
Asn	Asn	Val	Ser	Asp	Lys	Phe	Glu	Val	Thr	Val	Thr	Val	His	Asn	Lys
		515					520					525			
Ser	Asp	Lys	Pro	Gln	Glu	Leu	Tyr	Tyr	Gln	Ala	Thr	Val	Gln	Thr	Asp
	530					535						540			
Lys	Val	Asp	Gly	Lys	His	Phe	Ala	Leu	Ala	Pro	Lys	Ala	Leu	Tyr	Glu
545					550					555					560
Thr	Ser	Trp	Gln	Lys	Ile	Thr	Ile	Pro	Ala	Asn	Ser	Ser	Lys	Gln	Val
				565					570					575	
Thr	Val	Pro	Ile	Asp	Ala	Ser	Arg	Phe	Ser	Lys	Asp	Leu	Leu	Ala	Gln
			580					585					590		
Met	Lys	Asn	Gly	Tyr	Phe	Leu	Glu	Gly	Phe	Val	Arg	Phe	Lys	Gln	Asp
		595					600					605			
Pro	Lys	Lys	Glu	Glu	Leu	Met	Ser	Ile	Pro	Tyr	Ile	Gly	Phe	Arg	Gly
	610					615					620				
Asp	Phe	Gly	Asn	Leu	Ser	Ala	Leu	Glu	Lys	Pro	Ile	Tyr	Asp	Ser	Lys
625					630					635					640
Asp	Gly	Ser	Ser	Tyr	Tyr	His	Glu	Ala	Asn	Ser	Asp	Ala	Lys	Asp	Gln
				645					650					655	
Leu	Asp	Gly	Asp	Gly	Leu	Gln	Phe	Tyr	Ala	Leu	Lys	Asn	Asn	Phe	Thr
			660					665					670		
Ala	Leu	Thr	Thr	Glu	Ser	Asn	Pro	Trp	Thr	Ile	Ile	Lys	Ala	Val	Lys
		675					680					685			
Glu	Gly	Val	Glu	Asn	Ile	Glu	Asp	Ile	Glu	Ser	Ser	Glu	Ile	Thr	Glu
	690					695					700				
Thr	Ile	Phe	Ala	Gly	Thr	Phe	Ala	Lys	Gln	Asp	Asp	Asp	Ser	His	Tyr
705					710					715					720
Tyr	Ile	His	Arg	His	Ala	Asn	Gly	Lys	Pro	Tyr	Ala	Ala	Ile	Ser	Pro
				725					730					735	
Asn	Gly	Asp	Gly	Asn	Arg	Asp	Tyr	Val	Gln	Phe	Gln	Gly	Thr	Phe	Leu
			740				745						750		
Arg	Asn	Ala	Lys	Asn	Leu	Val	Ala	Glu	Val	Leu	Asp	Lys	Glu	Gly	Asn
		755					760					765			
Val	Val	Trp	Thr	Ser	Glu	Val	Thr	Glu	Gln	Val	Val	Lys	Asn	Tyr	Asn
	770					775						780			
Asn	Asp	Leu	Ala	Ser	Thr	Leu	Gly	Ser	Thr	Arg	Phe	Glu	Lys	Thr	Arg
785					790					795					800
Trp	Asp	Gly	Lys	Asp	Lys	Asp	Gly	Lys	Val	Val	Ala	Asn	Gly	Thr	Tyr
				805					810					815	
Thr	Tyr	Arg	Val	Arg	Tyr	Thr	Pro	Ile	Ser	Ser	Gly	Ala	Lys	Glu	Gln
			820					825					830		
His	Thr	Asp	Phe	Asp	Val	Ile	Val	Asp	Asn	Thr	Thr	Pro	Glu	Val	Ala
		835					840					845			
Thr	Ser	Ala	Thr	Phe	Ser	Thr	Glu	Asp	Arg	Arg	Leu	Thr	Leu	Ala	Ser
						855					860				
Lys	Pro	Lys	Thr	Ser	Gln	Pro	Val	Tyr	Arg	Glu	Arg	Ile	Ala	Tyr	Thr
865					870					875					880
Tyr	Met	Asp	Glu	Asp	Leu	Pro	Thr	Thr	Glu	Tyr	Ile	Ser	Pro	Asn	Glu
				885					890					895	
Asp	Gly	Thr	Phe	Thr	Leu	Pro	Glu	Glu	Ala	Glu	Thr	Met	Glu	Gly	Ala
			900					905					910		

Thr Val Pro Leu Lys Met Ser Asp Phe Thr Tyr Val Val Glu Asp Met
 915 920 925
 Ala Gly Asn Ile Thr Tyr Thr Pro Val Thr Lys Leu Leu Glu Gly His
 930 935 940
 Ser Asn Lys Pro Glu Gln
 945 950

<210> 151
 <211> 949
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 151
 Ala Lys Thr Ala Asp Thr Pro Ala Thr Ser Lys Ala Thr Ile Arg Asp
 1 5 10 15
 Leu Asn Asp Pro Ser Gln Val Lys Thr Leu Gln Glu Lys Ala Gly Lys
 20 25 30
 Gly Ala Gly Thr Val Val Ala Val Ile Ala Ala Gly Phe Asp Lys Asn
 35 40 45
 His Glu Ala Trp Arg Leu Thr Asp Lys Ala Lys Ala Arg Tyr Gln Ser
 50 55 60
 Lys Glu Asp Leu Glu Lys Ala Lys Lys Glu His Gly Ile Thr Tyr Gly
 65 70 75 80
 Glu Trp Val Asn Asp Lys Val Ala Tyr Tyr His Asp Tyr Ser Lys Asp
 85 90 95
 Gly Lys Thr Ala Val Asp Gln Glu His Gly Thr His Val Ser Gly Ile
 100 105 110
 Leu Ser Gly Asn Ala Pro Ser Glu Thr Lys Glu Pro Tyr Arg Leu Glu
 115 120 125
 Gly Ala Met Pro Glu Ala Gln Leu Leu Leu Met Arg Val Glu Ile Val
 130 135 140
 Asn Gly Leu Ala Asp Tyr Ala Arg Asn Tyr Ala Gln Ala Ile Arg Asp
 145 150 155 160
 Ala Ile Asn Leu Gly Ala Lys Val Ile Asn Met Ser Phe Gly Asn Ala
 165 170 175
 Ala Leu Ala Tyr Ala Asn Leu Pro Asp Glu Thr Lys Lys Ala Phe Asp
 180 185 190
 Tyr Ala Lys Ser Lys Gly Val Ser Ile Val Thr Ser Ala Gly Asn Asp
 195 200 205
 Ser Ser Phe Gly Gly Lys Thr Arg Leu Pro Leu Ala Asp His Pro Asp
 210 215 220
 Tyr Gly Val Val Gly Thr Pro Ala Ala Ala Asp Ser Thr Leu Thr Val
 225 230 235 240
 Ala Ser Tyr Ser Pro Asp Lys Gln Leu Thr Glu Thr Val Thr Val Lys
 245 250 255
 Thr Ala Asp Gln Gln Asp Lys Glu Met Pro Val Leu Ser Thr Asn Arg
 260 265 270
 Phe Glu Pro Asn Lys Ala Tyr Asp Tyr Ala Tyr Ala Asn Arg Gly Thr
 275 280 285
 Lys Glu Asp Asp Phe Lys Asp Val Lys Gly Lys Ile Ala Leu Ile Glu
 290 295 300
 Arg Gly Asp Ile Asp Phe Lys Asp Lys Ile Ala Lys Ala Lys Lys Ala
 305 310 315 320

Gly	Ala	Val	Gly	Val	Leu	Ile	Tyr	Asp	Asn	Gln	Asp	Lys	Gly	Phe	Pro	
				325					330					335		
Ile	Glu	Leu	Pro	Asn	Val	Asp	Gln	Met	Pro	Ala	Ala	Phe	Ile	Ser	Arg	
			340					345					350			
Lys	Asp	Gly	Leu	Leu	Leu	Lys	Asp	Asn	Pro	Gln	Lys	Thr	Ile	Thr	Phe	
		355					360					365				
Asn	Ala	Thr	Pro	Lys	Val	Leu	Pro	Thr	Ala	Ser	Gly	Thr	Lys	Leu	Ser	
	370					375					380					
Arg	Phe	Ser	Ser	Trp	Gly	Leu	Thr	Ala	Asp	Gly	Asn	Ile	Lys	Pro	Asp	
385					390					395					400	
Ile	Ala	Ala	Pro	Gly	Gln	Asp	Ile	Leu	Ser	Ser	Val	Ala	Asn	Asn	Lys	
			405						410					415		
Tyr	Ala	Lys	Leu	Ser	Gly	Thr	Ala	Met	Ser	Ala	Pro	Leu	Val	Ala	Gly	
		420						425					430			
Ile	Met	Gly	Leu	Leu	Gln	Glu	Gln	Tyr	Glu	Thr	Gln	Tyr	Pro	Asp	Met	
		435					440					445				
Thr	Pro	Ser	Glu	Arg	Leu	Asp	Leu	Ala	Lys	Lys	Val	Leu	Met	Ser	Ser	
	450					455					460					
Ala	Thr	Ala	Leu	Tyr	Asp	Glu	Asp	Glu	Lys	Ala	Tyr	Phe	Ser	Pro	Arg	
465					470					475					480	
Gln	Gln	Gly	Ala	Gly	Ala	Val	Asp	Ala	Lys	Lys	Ala	Ser	Ala	Ala	Thr	
			485						490					495		
Met	Tyr	Val	Thr	Asp	Lys	Asp	Asn	Thr	Ser	Ser	Lys	Val	His	Leu	Asn	
		500						505					510			
Asn	Val	Ser	Asp	Lys	Phe	Glu	Val	Thr	Val	Thr	Val	His	Asn	Lys	Ser	
		515					520					525				
Asp	Lys	Pro	Gln	Glu	Leu	Tyr	Tyr	Gln	Ala	Thr	Val	Gln	Thr	Asp	Lys	
	530					535					540					
Val	Asp	Gly	Lys	His	Phe	Ala	Leu	Ala	Pro	Lys	Ala	Leu	Tyr	Glu	Thr	
545					550					555					560	
Ser	Trp	Gln	Lys	Ile	Thr	Ile	Pro	Ala	Asn	Ser	Ser	Lys	Gln	Val	Thr	
			565						570					575		
Val	Pro	Ile	Asp	Ala	Ser	Arg	Phe	Ser	Lys	Asp	Leu	Leu	Ala	Gln	Met	
		580						585					590			
Lys	Asn	Gly	Tyr	Phe	Leu	Glu	Gly	Phe	Val	Arg	Phe	Lys	Gln	Asp	Pro	
		595					600					605				
Lys	Lys	Glu	Glu	Leu	Met	Ser	Ile	Pro	Tyr	Ile	Gly	Phe	Arg	Gly	Asp	
	610					615					620					
Phe	Gly	Asn	Leu	Ser	Ala	Leu	Glu	Lys	Pro	Ile	Tyr	Asp	Ser	Lys	Asp	
625					630					635					640	
Gly	Ser	Ser	Tyr	Tyr	His	Glu	Ala	Asn	Ser	Asp	Ala	Lys	Asp	Gln	Leu	
			645						650					655		
Asp	Gly	Asp	Gly	Leu	Gln	Phe	Tyr	Ala	Leu	Lys	Asn	Asn	Phe	Thr	Ala	
		660						665					670			
Leu	Thr	Thr	Glu	Ser	Asn	Pro	Trp	Thr	Ile	Ile	Lys	Ala	Val	Lys	Glu	
		675						680					685			
Gly	Val	Glu	Asn	Ile	Glu	Asp	Ile	Glu	Ser	Ser	Glu	Ile	Thr	Glu	Thr	
	690					695					700					
Ile	Phe	Ala	Gly	Thr	Phe	Ala	Lys	Gln	Asp	Asp	Asp	Ser	His	Tyr	Tyr	
705					710					715					720	
Ile	His	Arg	His	Ala	Asn	Gly	Lys	Pro	Tyr	Ala	Ala	Ile	Ser	Pro	Asn	
			725						730					735		
Gly	Asp	Gly	Asn	Arg	Asp	Tyr	Val	Gln	Phe	Gln	Gly	Thr	Phe	Leu	Arg	
		740						745					750			
Asn	Ala	Lys	Asn	Leu	Val	Ala	Glu	Val	Leu	Asp	Lys	Glu	Gly	Asn	Val	
		755					760					765				

Val Trp Thr Ser Glu Val Thr Glu Gln Val Val Lys Asn Tyr Asn Asn
 770 775 780
 Asp Leu Ala Ser Thr Leu Gly Ser Thr Arg Phe Glu Lys Thr Arg Trp
 785 790 795 800
 Asp Gly Lys Asp Lys Asp Gly Lys Val Val Ala Asn Gly Thr Tyr Thr
 805 810 815
 Tyr Arg Val Arg Tyr Thr Pro Ile Ser Ser Gly Ala Lys Glu Gln His
 820 825 830
 Thr Asp Phe Asp Val Ile Val Asp Asn Thr Thr Pro Glu Val Ala Thr
 835 840 845
 Ser Ala Thr Phe Ser Thr Glu Asp Arg Arg Leu Thr Leu Ala Ser Lys
 850 855 860
 Pro Lys Thr Ser Gln Pro Val Tyr Arg Glu Arg Ile Ala Tyr Thr Tyr
 865 870 875 880
 Met Asp Glu Asp Leu Pro Thr Thr Glu Tyr Ile Ser Pro Asn Glu Asp
 885 890 895
 Gly Thr Phe Thr Leu Pro Glu Glu Ala Glu Thr Met Glu Gly Ala Thr
 900 905 910
 Val Pro Leu Lys Met Ser Asp Phe Thr Tyr Val Val Glu Asp Met Ala
 915 920 925
 Gly Asn Ile Thr Tyr Thr Pro Val Thr Lys Leu Leu Glu Gly His Ser
 930 935 940
 Asn Lys Pro Glu Gln
 945

<210> 152
 <211> 1210
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 152
 Met Ala Lys Thr Ala Asp Thr Pro Ala Thr Ser Lys Ala Thr Ile Arg
 1 5 10 15
 Asp Leu Asn Asp Pro Ser Gln Val Lys Thr Leu Gln Glu Lys Ala Gly
 20 25 30
 Lys Gly Ala Gly Thr Val Val Ala Val Ile Ala Ala Gly Phe Asp Lys
 35 40 45
 Asn His Glu Ala Trp Arg Leu Thr Asp Lys Ala Lys Ala Arg Tyr Gln
 50 55 60
 Ser Lys Glu Asp Leu Glu Lys Ala Lys Lys Glu His Gly Ile Thr Tyr
 65 70 75 80
 Gly Glu Trp Val Asn Asp Lys Val Ala Tyr Tyr His Asp Tyr Ser Lys
 85 90 95
 Asp Gly Lys Thr Ala Val Asp Gln Glu His Gly Thr His Val Ser Gly
 100 105 110
 Ile Leu Ser Gly Asn Ala Pro Ser Glu Thr Lys Glu Pro Tyr Arg Leu
 115 120 125
 Glu Gly Ala Met Pro Glu Ala Gln Leu Leu Leu Met Arg Val Glu Ile
 130 135 140
 Val Asn Gly Leu Ala Asp Tyr Ala Arg Asn Tyr Ala Gln Ala Ile Arg
 145 150 155 160
 Asp Ala Ile Asn Leu Gly Ala Lys Val Ile Asn Met Ser Phe Gly Asn
 165 170 175

Ala	Ala	Leu	Ala	Tyr	Ala	Asn	Leu	Pro	Asp	Glu	Thr	Lys	Lys	Ala	Phe
		180						185					190		
Asp	Tyr	Ala	Lys	Ser	Lys	Gly	Val	Ser	Ile	Val	Thr	Ser	Ala	Gly	Asn
		195					200					205			
Asp	Ser	Ser	Phe	Gly	Gly	Lys	Thr	Arg	Leu	Pro	Leu	Ala	Asp	His	Pro
	210					215					220				
Asp	Tyr	Gly	Val	Val	Gly	Thr	Pro	Ala	Ala	Ala	Asp	Ser	Thr	Leu	Thr
225					230					235					240
Val	Ala	Ser	Tyr	Ser	Pro	Asp	Lys	Gln	Leu	Thr	Glu	Thr	Val	Thr	Val
				245					250						255
Lys	Thr	Ala	Asp	Gln	Gln	Asp	Lys	Glu	Met	Pro	Val	Leu	Ser	Thr	Asn
		260						265					270		
Arg	Phe	Glu	Pro	Asn	Lys	Ala	Tyr	Asp	Tyr	Ala	Tyr	Ala	Asn	Arg	Gly
	275						280					285			
Thr	Lys	Glu	Asp	Asp	Phe	Lys	Asp	Val	Lys	Gly	Lys	Ile	Ala	Leu	Ile
	290					295					300				
Glu	Arg	Gly	Asp	Ile	Asp	Phe	Lys	Asp	Lys	Ile	Ala	Lys	Ala	Lys	Lys
305					310					315					320
Ala	Gly	Ala	Val	Gly	Val	Leu	Ile	Tyr	Asp	Asn	Gln	Asp	Lys	Gly	Phe
				325					330						335
Pro	Ile	Glu	Leu	Pro	Asn	Val	Asp	Gln	Met	Pro	Ala	Ala	Phe	Ile	Ser
		340						345					350		
Arg	Lys	Asp	Gly	Leu	Leu	Leu	Lys	Asp	Asn	Pro	Gln	Lys	Thr	Ile	Thr
	355						360					365			
Phe	Asn	Ala	Thr	Pro	Lys	Val	Leu	Pro	Thr	Ala	Ser	Gly	Thr	Lys	Leu
	370					375					380				
Ser	Arg	Phe	Ser	Ser	Trp	Gly	Leu	Thr	Ala	Asp	Gly	Asn	Ile	Lys	Pro
385					390					395					400
Asp	Ile	Ala	Ala	Pro	Gly	Gln	Asp	Ile	Leu	Ser	Ser	Val	Ala	Asn	Asn
				405					410					415	
Lys	Tyr	Ala	Lys	Leu	Ser	Gly	Thr	Ala	Met	Ser	Ala	Pro	Leu	Val	Ala
		420						425					430		
Gly	Ile	Met	Gly	Leu	Leu	Gln	Glu	Gln	Tyr	Glu	Thr	Gln	Tyr	Pro	Asp
	435						440					445			
Met	Thr	Pro	Ser	Glu	Arg	Leu	Asp	Leu	Ala	Lys	Lys	Val	Leu	Met	Ser
	450					455					460				
Ser	Ala	Thr	Ala	Leu	Tyr	Asp	Glu	Asp	Glu	Lys	Ala	Tyr	Phe	Ser	Pro
465					470					475					480
Arg	Gln	Gln	Gly	Ala	Gly	Ala	Val	Asp	Ala	Lys	Lys	Ala	Ser	Ala	Ala
				485					490						495
Thr	Met	Tyr	Val	Thr	Asp	Lys	Asp	Asn	Thr	Ser	Ser	Lys	Val	His	Leu
		500						505					510		
Asn	Asn	Val	Ser	Asp	Lys	Phe	Glu	Val	Thr	Val	Thr	Val	His	Asn	Lys
		515					520					525			
Ser	Asp	Lys	Pro	Gln	Glu	Leu	Tyr	Tyr	Gln	Ala	Thr	Val	Gln	Thr	Asp
	530					535					540				
Lys	Val	Asp	Gly	Lys	His	Phe	Ala	Leu	Ala	Pro	Lys	Ala	Leu	Tyr	Glu
545					550					555					560
Thr	Ser	Trp	Gln	Lys	Ile	Thr	Ile	Pro	Ala	Asn	Ser	Ser	Lys	Gln	Val
			565						570					575	
Thr	Val	Pro	Ile	Asp	Ala	Ser	Arg	Phe	Ser	Lys	Asp	Leu	Leu	Ala	Gln
		580						585					590		
Met	Lys	Asn	Gly	Tyr	Phe	Leu	Glu	Gly	Phe	Val	Arg	Phe	Lys	Gln	Asp
	595						600					605			
Pro	Lys	Lys	Glu	Glu	Leu	Met	Ser	Ile	Pro	Tyr	Ile	Gly	Phe	Arg	Gly
	610					615					620				

Asp	Phe	Gly	Asn	Leu	Ser	Ala	Leu	Glu	Lys	Pro	Ile	Tyr	Asp	Ser	Lys
625					630					635					640
Asp	Gly	Ser	Ser	Tyr	Tyr	His	Glu	Ala	Asn	Ser	Asp	Ala	Lys	Asp	Gln
				645					650						655
Leu	Asp	Gly	Asp	Gly	Leu	Gln	Phe	Tyr	Ala	Leu	Lys	Asn	Asn	Phe	Thr
			660					665						670	
Ala	Leu	Thr	Thr	Glu	Ser	Asn	Pro	Trp	Thr	Ile	Ile	Lys	Ala	Val	Lys
		675					680					685			
Glu	Gly	Val	Glu	Asn	Ile	Glu	Asp	Ile	Glu	Ser	Ser	Glu	Ile	Thr	Glu
	690					695					700				
Thr	Ile	Phe	Ala	Gly	Thr	Phe	Ala	Lys	Gln	Asp	Asp	Asp	Ser	His	Tyr
705					710					715					720
Tyr	Ile	His	Arg	His	Ala	Asn	Gly	Lys	Pro	Tyr	Ala	Ala	Ile	Ser	Pro
				725					730						735
Asn	Gly	Asp	Gly	Asn	Arg	Asp	Tyr	Val	Gln	Phe	Gln	Gly	Thr	Phe	Leu
			740					745						750	
Arg	Asn	Ala	Lys	Asn	Leu	Val	Ala	Glu	Val	Leu	Asp	Lys	Glu	Gly	Asn
		755					760					765			
Val	Val	Trp	Thr	Ser	Glu	Val	Thr	Glu	Gln	Val	Val	Lys	Asn	Tyr	Asn
	770					775						780			
Asn	Asp	Leu	Ala	Ser	Thr	Leu	Gly	Ser	Thr	Arg	Phe	Glu	Lys	Thr	Arg
785					790					795					800
Trp	Asp	Gly	Lys	Asp	Lys	Asp	Gly	Lys	Val	Val	Ala	Asn	Gly	Thr	Tyr
			805						810						815
Thr	Tyr	Arg	Val	Arg	Tyr	Thr	Pro	Ile	Ser	Ser	Gly	Ala	Lys	Glu	Gln
			820					825						830	
His	Thr	Asp	Phe	Asp	Val	Ile	Val	Asp	Asn	Thr	Thr	Pro	Glu	Val	Ala
		835					840					845			
Thr	Ser	Ala	Thr	Phe	Ser	Thr	Glu	Asp	Arg	Arg	Leu	Thr	Leu	Ala	Ser
	850					855					860				
Lys	Pro	Lys	Thr	Ser	Gln	Pro	Val	Tyr	Arg	Glu	Arg	Ile	Ala	Tyr	Thr
865					870					875					880
Tyr	Met	Asp	Glu	Asp	Leu	Pro	Thr	Thr	Glu	Tyr	Ile	Ser	Pro	Asn	Glu
			885						890						895
Asp	Gly	Thr	Phe	Thr	Leu	Pro	Glu	Glu	Ala	Glu	Thr	Met	Glu	Gly	Ala
		900					905						910		
Thr	Val	Pro	Leu	Lys	Met	Ser	Asp	Phe	Thr	Tyr	Val	Val	Glu	Asp	Met
	915						920						925		
Ala	Gly	Asn	Ile	Thr	Tyr	Thr	Pro	Val	Thr	Lys	Leu	Leu	Glu	Gly	His
	930					935					940				
Ser	Asn	Lys	Pro	Glu	Gln	Ser	Ser	Gly	Ser	Gly	Ser	Gly	Gly	Gly	Gly
945					950					955					960
Val	Ala	Ala	Asp	Ile	Gly	Thr	Gly	Leu	Ala	Asp	Ala	Leu	Thr	Ala	Pro
			965					970						975	
Leu	Asp	His	Lys	Asp	Lys	Gly	Leu	Lys	Ser	Leu	Thr	Leu	Glu	Asp	Ser
		980						985					990		
Ile	Ser	Gln	Asn	Gly	Thr	Leu	Thr	Leu	Ser	Ala	Gln	Gly	Ala	Glu	Lys
		995				1000							1005		
Thr	Phe	Lys	Val	Gly	Asp	Lys	Asp	Asn	Ser	Leu	Asn	Thr	Gly	Lys	
	1010					1015						1020			
Leu	Lys	Asn	Asp	Lys	Ile	Ser	Arg	Phe	Asp	Phe	Val	Gln	Lys	Ile	
	1025					1030						1035			
Glu	Val	Asp	Gly	Gln	Thr	Ile	Thr	Leu	Ala	Ser	Gly	Glu	Phe	Gln	
	1040					1045						1050			
Ile	Tyr	Lys	Gln	Asp	His	Ser	Ala	Val	Val	Ala	Leu	Gln	Ile	Glu	
	1055					1060						1065			

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Lys Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg
1070 1075 1080
Ser Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn
1085 1090 1095
Gln Leu Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser
1100 1105 1110
Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala
1115 1120 1125
Ala Lys Gln Gly His Gly Lys Ile Glu His Leu Lys Thr Pro Glu
1130 1135 1140
Gln Asn Val Glu Leu Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys
1145 1150 1155
Ser His Ala Val Ile Leu Gly Asp Thr Arg Tyr Gly Ser Glu Glu
1160 1165 1170
Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln Glu
1175 1180 1185
Ile Ala Gly Ser Ala Thr Val Lys Ile Arg Glu Lys Val His Glu
1190 1195 1200
Ile Gly Ile Ala Gly Lys Gln
1205 1210

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<210> 153
<211> 1209
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetic sequence

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<400> 153
Ala Lys Thr Ala Asp Thr Pro Ala Thr Ser Lys Ala Thr Ile Arg Asp
1 5 10 15
Leu Asn Asp Pro Ser Gln Val Lys Thr Leu Gln Glu Lys Ala Gly Lys
20 25 30
Gly Ala Gly Thr Val Val Ala Val Ile Ala Ala Gly Phe Asp Lys Asn
35 40 45
His Glu Ala Trp Arg Leu Thr Asp Lys Ala Lys Ala Arg Tyr Gln Ser
50 55 60
Lys Glu Asp Leu Glu Lys Ala Lys Lys Glu His Gly Ile Thr Tyr Gly
65 70 75 80
Glu Trp Val Asn Asp Lys Val Ala Tyr Tyr His Asp Tyr Ser Lys Asp
85 90 95
Gly Lys Thr Ala Val Asp Gln Glu His Gly Thr His Val Ser Gly Ile
100 105 110
Leu Ser Gly Asn Ala Pro Ser Glu Thr Lys Glu Pro Tyr Arg Leu Glu
115 120 125
Gly Ala Met Pro Glu Ala Gln Leu Leu Leu Met Arg Val Glu Ile Val
130 135 140
Asn Gly Leu Ala Asp Tyr Ala Arg Asn Tyr Ala Gln Ala Ile Arg Asp
145 150 155 160
Ala Ile Asn Leu Gly Ala Lys Val Ile Asn Met Ser Phe Gly Asn Ala
165 170 175
Ala Leu Ala Tyr Ala Asn Leu Pro Asp Glu Thr Lys Lys Ala Phe Asp
180 185 190
Tyr Ala Lys Ser Lys Gly Val Ser Ile Val Thr Ser Ala Gly Asn Asp
195 200 205

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Ser	Ser	Phe	Gly	Gly	Lys	Thr	Arg	Leu	Pro	Leu	Ala	Asp	His	Pro	Asp
210						215					220				
Tyr	Gly	Val	Val	Gly	Thr	Pro	Ala	Ala	Ala	Asp	Ser	Thr	Leu	Thr	Val
225					230					235					240
Ala	Ser	Tyr	Ser	Pro	Asp	Lys	Gln	Leu	Thr	Glu	Thr	Val	Thr	Val	Lys
				245					250					255	
Thr	Ala	Asp	Gln	Gln	Asp	Lys	Glu	Met	Pro	Val	Leu	Ser	Thr	Asn	Arg
			260					265					270		
Phe	Glu	Pro	Asn	Lys	Ala	Tyr	Asp	Tyr	Ala	Tyr	Ala	Asn	Arg	Gly	Thr
		275					280					285			
Lys	Glu	Asp	Asp	Phe	Lys	Asp	Val	Lys	Gly	Lys	Ile	Ala	Leu	Ile	Glu
290						295					300				
Arg	Gly	Asp	Ile	Asp	Phe	Lys	Asp	Lys	Ile	Ala	Lys	Ala	Lys	Lys	Ala
305					310					315					320
Gly	Ala	Val	Gly	Val	Leu	Ile	Tyr	Asp	Asn	Gln	Asp	Lys	Gly	Phe	Pro
				325					330					335	
Ile	Glu	Leu	Pro	Asn	Val	Asp	Gln	Met	Pro	Ala	Ala	Phe	Ile	Ser	Arg
			340					345					350		
Lys	Asp	Gly	Leu	Leu	Leu	Lys	Asp	Asn	Pro	Gln	Lys	Thr	Ile	Thr	Phe
		355					360					365			
Asn	Ala	Thr	Pro	Lys	Val	Leu	Pro	Thr	Ala	Ser	Gly	Thr	Lys	Leu	Ser
370						375					380				
Arg	Phe	Ser	Ser	Trp	Gly	Leu	Thr	Ala	Asp	Gly	Asn	Ile	Lys	Pro	Asp
385					390					395					400
Ile	Ala	Ala	Pro	Gly	Gln	Asp	Ile	Leu	Ser	Ser	Val	Ala	Asn	Asn	Lys
				405					410					415	
Tyr	Ala	Lys	Leu	Ser	Gly	Thr	Ala	Met	Ser	Ala	Pro	Leu	Val	Ala	Gly
			420					425					430		
Ile	Met	Gly	Leu	Leu	Gln	Glu	Gln	Tyr	Glu	Thr	Gln	Tyr	Pro	Asp	Met
		435					440					445			
Thr	Pro	Ser	Glu	Arg	Leu	Asp	Leu	Ala	Lys	Lys	Val	Leu	Met	Ser	Ser
450						455					460				
Ala	Thr	Ala	Leu	Tyr	Asp	Glu	Asp	Glu	Lys	Ala	Tyr	Phe	Ser	Pro	Arg
465					470					475					480
Gln	Gln	Gly	Ala	Gly	Ala	Val	Asp	Ala	Lys	Lys	Ala	Ser	Ala	Ala	Thr
				485					490					495	
Met	Tyr	Val	Thr	Asp	Lys	Asp	Asn	Thr	Ser	Ser	Lys	Val	His	Leu	Asn
			500					505					510		
Asn	Val	Ser	Asp	Lys	Phe	Glu	Val	Thr	Val	Thr	Val	His	Asn	Lys	Ser
		515						520				525			
Asp	Lys	Pro	Gln	Glu	Leu	Tyr	Tyr	Gln	Ala	Thr	Val	Gln	Thr	Asp	Lys
530						535					540				
Val	Asp	Gly	Lys	His	Phe	Ala	Leu	Ala	Pro	Lys	Ala	Leu	Tyr	Glu	Thr
545					550					555				560	
Ser	Trp	Gln	Lys	Ile	Thr	Ile	Pro	Ala	Asn	Ser	Ser	Lys	Gln	Val	Thr
				565					570					575	
Val	Pro	Ile	Asp	Ala	Ser	Arg	Phe	Ser	Lys	Asp	Leu	Leu	Ala	Gln	Met
			580					585					590		
Lys	Asn	Gly	Tyr	Phe	Leu	Glu	Gly	Phe	Val	Arg	Phe	Lys	Gln	Asp	Pro
		595					600					605			
Lys	Lys	Glu	Glu	Leu	Met	Ser	Ile	Pro	Tyr	Ile	Gly	Phe	Arg	Gly	Asp
610						615					620				
Phe	Gly	Asn	Leu	Ser	Ala	Leu	Glu	Lys	Pro	Ile	Tyr	Asp	Ser	Lys	Asp
625					630					635					640
Gly	Ser	Ser	Tyr	Tyr	His	Glu	Ala	Asn	Ser	Asp	Ala	Lys	Asp	Gln	Leu
				645					650					655	

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Asp Gly Asp Gly Leu Gln Phe Tyr Ala Leu Lys Asn Asn Phe Thr Ala
660 665 670
Leu Thr Thr Glu Ser Asn Pro Trp Thr Ile Ile Lys Ala Val Lys Glu
675 680 685
Gly Val Glu Asn Ile Glu Asp Ile Glu Ser Ser Glu Ile Thr Glu Thr
690 695 700
Ile Phe Ala Gly Thr Phe Ala Lys Gln Asp Asp Asp Ser His Tyr Tyr
705 710 715 720
Ile His Arg His Ala Asn Gly Lys Pro Tyr Ala Ala Ile Ser Pro Asn
725 730 735
Gly Asp Gly Asn Arg Asp Tyr Val Gln Phe Gln Gly Thr Phe Leu Arg
740 745 750
Asn Ala Lys Asn Leu Val Ala Glu Val Leu Asp Lys Glu Gly Asn Val
755 760 765
Val Trp Thr Ser Glu Val Thr Glu Gln Val Val Lys Asn Tyr Asn Asn
770 775 780
Asp Leu Ala Ser Thr Leu Gly Ser Thr Arg Phe Glu Lys Thr Arg Trp
785 790 795 800
Asp Gly Lys Asp Lys Asp Gly Lys Val Val Ala Asn Gly Thr Tyr Thr
805 810 815
Tyr Arg Val Arg Tyr Thr Pro Ile Ser Ser Gly Ala Lys Glu Gln His
820 825 830
Thr Asp Phe Asp Val Ile Val Asp Asn Thr Thr Pro Glu Val Ala Thr
835 840 845
Ser Ala Thr Phe Ser Thr Glu Asp Arg Arg Leu Thr Leu Ala Ser Lys
850 855 860
Pro Lys Thr Ser Gln Pro Val Tyr Arg Glu Arg Ile Ala Tyr Thr Tyr
865 870 875 880
Met Asp Glu Asp Leu Pro Thr Thr Glu Tyr Ile Ser Pro Asn Glu Asp
885 890 895
Gly Thr Phe Thr Leu Pro Glu Glu Ala Glu Thr Met Glu Gly Ala Thr
900 905 910
Val Pro Leu Lys Met Ser Asp Phe Thr Tyr Val Val Glu Asp Met Ala
915 920 925
Gly Asn Ile Thr Tyr Thr Pro Val Thr Lys Leu Leu Glu Gly His Ser
930 935 940
Asn Lys Pro Glu Gln Ser Ser Gly Ser Gly Ser Gly Gly Gly Val
945 950 955 960
Ala Ala Asp Ile Gly Thr Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu
965 970 975
Asp His Lys Asp Lys Gly Leu Lys Ser Leu Thr Leu Glu Asp Ser Ile
980 985 990
Ser Gln Asn Gly Thr Leu Thr Leu Ser Ala Gln Gly Ala Glu Lys Thr
995 1000 1005
Phe Lys Val Gly Asp Lys Asp Asn Ser Leu Asn Thr Gly Lys Leu
1010 1015 1020
Lys Asn Asp Lys Ile Ser Arg Phe Asp Phe Val Gln Lys Ile Glu
1025 1030 1035
Val Asp Gly Gln Thr Ile Thr Leu Ala Ser Gly Glu Phe Gln Ile
1040 1045 1050
Tyr Lys Gln Asp His Ser Ala Val Val Ala Leu Gln Ile Glu Lys
1055 1060 1065
Ile Asn Asn Pro Asp Lys Ile Asp Ser Leu Ile Asn Gln Arg Ser
1070 1075 1080
Phe Leu Val Ser Gly Leu Gly Gly Glu His Thr Ala Phe Asn Gln
1085 1090 1095

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Leu Pro Ser Gly Lys Ala Glu Tyr His Gly Lys Ala Phe Ser Ser
 1100 1105 1110
 Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala Ala
 1115 1120 1125
 Lys Gln Gly His Gly Lys Ile Glu His Leu Lys Thr Pro Glu Gln
 1130 1135 1140
 Asn Val Glu Leu Ala Ser Ala Glu Leu Lys Ala Asp Glu Lys Ser
 1145 1150 1155
 His Ala Val Ile Leu Gly Asp Thr Arg Tyr Gly Ser Glu Glu Lys
 1160 1165 1170
 Gly Thr Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile
 1175 1180 1185
 Ala Gly Ser Ala Thr Val Lys Ile Arg Glu Lys Val His Glu Ile
 1190 1195 1200
 Gly Ile Ala Gly Lys Gln
 1205

<210> 154
 <211> 536
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 154
 Met Gly Ala Asp Asp Val Val Asp Ser Ser Lys Ser Phe Val Met Glu
 1 5 10 15
 Asn Phe Ser Ser Tyr His Gly Thr Lys Pro Gly Tyr Val Asp Ser Ile
 20 25 30
 Gln Lys Gly Ile Gln Lys Pro Lys Ser Gly Thr Gln Gly Asn Tyr Asp
 35 40 45
 Asp Asp Trp Lys Glu Phe Tyr Ser Thr Asp Asn Lys Tyr Asp Ala Ala
 50 55 60
 Gly Tyr Ser Val Asp Asn Glu Asn Pro Leu Ser Gly Lys Ala Gly Gly
 65 70 75 80
 Val Val Lys Val Thr Tyr Pro Gly Leu Thr Lys Val Leu Ala Leu Lys
 85 90 95
 Val Asp Asn Ala Glu Thr Ile Lys Lys Glu Leu Gly Leu Ser Leu Thr
 100 105 110
 Glu Pro Leu Met Glu Gln Val Gly Thr Glu Glu Phe Ile Lys Arg Phe
 115 120 125
 Gly Asp Gly Ala Ser Arg Val Val Leu Ser Leu Pro Phe Ala Glu Gly
 130 135 140
 Ser Ser Ser Val Glu Tyr Ile Asn Asn Trp Glu Gln Ala Lys Ala Leu
 145 150 155 160
 Ser Val Glu Leu Glu Ile Asn Phe Glu Thr Arg Gly Lys Arg Gly Gln
 165 170 175
 Asp Ala Met Tyr Glu Tyr Met Ala Gln Ala Cys Ala Gly Asn Arg Val
 180 185 190
 Arg Arg Ser Val Gly Ser Ser Leu Ser Cys Ile Asn Leu Asp Trp Asp
 195 200 205
 Val Ile Arg Asp Lys Thr Lys Thr Lys Ile Glu Ser Leu Lys Glu His
 210 215 220
 Gly Pro Ile Lys Asn Lys Met Ser Glu Ser Pro Asn Lys Thr Val Ser
 225 230 235 240

Glu Glu Lys Ala Lys Gln Tyr Leu Glu Glu Phe His Gln Thr Ala Leu
 245 250 255
 Glu His Pro Glu Leu Ser Glu Leu Lys Thr Val Thr Gly Thr Asn Pro
 260 265 270
 Val Phe Ala Gly Ala Asn Tyr Ala Ala Trp Ala Val Asn Val Ala Gln
 275 280 285
 Val Ile Asp Ser Glu Thr Ala Asp Asn Leu Glu Lys Thr Ala Ala Ala
 290 295 300
 Leu Ser Ile Leu Pro Gly Ile Gly Ser Val Met Gly Ile Ala Asp Gly
 305 310 315 320
 Ala Val His His Asn Thr Glu Glu Ile Val Ala Gln Ser Ile Ala Leu
 325 330 335
 Ser Ser Leu Met Val Ala Gln Ala Ile Pro Leu Val Gly Glu Leu Val
 340 345 350
 Asp Ile Gly Phe Ala Ala Tyr Asn Phe Val Glu Ser Ile Ile Asn Leu
 355 360 365
 Phe Gln Val Val His Asn Ser Tyr Asn Arg Pro Ala Tyr Ser Pro Gly
 370 375 380
 His Lys Thr Gln Pro Phe Leu His Asp Gly Tyr Ala Val Ser Trp Asn
 385 390 395 400
 Thr Val Glu Asp Ser Ile Ile Arg Thr Gly Phe Gln Gly Glu Ser Gly
 405 410 415
 His Asp Ile Lys Ile Thr Ala Glu Asn Thr Pro Leu Pro Ile Ala Gly
 420 425 430
 Val Leu Leu Pro Thr Ile Pro Gly Lys Leu Asp Val Asn Lys Ser Lys
 435 440 445
 Thr His Ile Ser Val Asn Gly Arg Lys Ile Arg Met Arg Cys Arg Ala
 450 455 460
 Ile Asp Gly Asp Val Thr Phe Cys Arg Leu Lys Ser Pro Val Tyr Val
 465 470 475 480
 Gly Asn Gly Val His Ala Asn Leu His Val Ala Phe His Arg Ser Ser
 485 490 495
 Ser Glu Lys Ile His Ser Asn Glu Ile Ser Ser Asp Ser Ile Gly Val
 500 505 510
 Leu Gly Tyr Gln Lys Thr Val Asp His Thr Lys Val Asn Ser Lys Leu
 515 520 525
 Ser Leu Phe Phe Glu Ile Lys Ser
 530 535

<210> 155
 <211> 535
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 155
 Gly Ala Asp Asp Val Val Asp Ser Ser Lys Ser Phe Val Met Glu Asn
 1 5 10 15
 Phe Ser Ser Tyr His Gly Thr Lys Pro Gly Tyr Val Asp Ser Ile Gln
 20 25 30
 Lys Gly Ile Gln Lys Pro Lys Ser Gly Thr Gln Gly Asn Tyr Asp Asp
 35 40 45
 Asp Trp Lys Glu Phe Tyr Ser Thr Asp Asn Lys Tyr Asp Ala Ala Gly
 50 55 60

Tyr	Ser	Val	Asp	Asn	Glu	Asn	Pro	Leu	Ser	Gly	Lys	Ala	Gly	Gly	Val	65	70	75	80
Val	Lys	Val	Thr	Tyr	Pro	Gly	Leu	Thr	Lys	Val	Leu	Ala	Leu	Lys	Val	85	90	95	
Asp	Asn	Ala	Glu	Thr	Ile	Lys	Lys	Glu	Leu	Gly	Leu	Ser	Leu	Thr	Glu	100	105	110	
Pro	Leu	Met	Glu	Gln	Val	Gly	Thr	Glu	Glu	Phe	Ile	Lys	Arg	Phe	Gly	115	120	125	
Asp	Gly	Ala	Ser	Arg	Val	Val	Leu	Ser	Leu	Pro	Phe	Ala	Glu	Gly	Ser	130	135	140	
Ser	Ser	Val	Glu	Tyr	Ile	Asn	Asn	Trp	Glu	Gln	Ala	Lys	Ala	Leu	Ser	145	150	155	160
Val	Glu	Leu	Glu	Ile	Asn	Phe	Glu	Thr	Arg	Gly	Lys	Arg	Gly	Gln	Asp	165	170	175	
Ala	Met	Tyr	Glu	Tyr	Met	Ala	Gln	Ala	Cys	Ala	Gly	Asn	Arg	Val	Arg	180	185	190	
Arg	Ser	Val	Gly	Ser	Ser	Leu	Ser	Cys	Ile	Asn	Leu	Asp	Trp	Asp	Val	195	200	205	
Ile	Arg	Asp	Lys	Thr	Lys	Thr	Lys	Ile	Glu	Ser	Leu	Lys	Glu	His	Gly	210	215	220	
Pro	Ile	Lys	Asn	Lys	Met	Ser	Glu	Ser	Pro	Asn	Lys	Thr	Val	Ser	Glu	225	230	235	240
Glu	Lys	Ala	Lys	Gln	Tyr	Leu	Glu	Glu	Phe	His	Gln	Thr	Ala	Leu	Glu	245	250	255	
His	Pro	Glu	Leu	Ser	Glu	Leu	Lys	Thr	Val	Thr	Gly	Thr	Asn	Pro	Val	260	265	270	
Phe	Ala	Gly	Ala	Asn	Tyr	Ala	Ala	Trp	Ala	Val	Asn	Val	Ala	Gln	Val	275	280	285	
Ile	Asp	Ser	Glu	Thr	Ala	Asp	Asn	Leu	Glu	Lys	Thr	Ala	Ala	Ala	Leu	290	295	300	
Ser	Ile	Leu	Pro	Gly	Ile	Gly	Ser	Val	Met	Gly	Ile	Ala	Asp	Gly	Ala	305	310	315	320
Val	His	His	Asn	Thr	Glu	Glu	Ile	Val	Ala	Gln	Ser	Ile	Ala	Leu	Ser	325	330	335	
Ser	Leu	Met	Val	Ala	Gln	Ala	Ile	Pro	Leu	Val	Gly	Glu	Leu	Val	Asp	340	345	350	
Ile	Gly	Phe	Ala	Ala	Tyr	Asn	Phe	Val	Glu	Ser	Ile	Ile	Asn	Leu	Phe	355	360	365	
Gln	Val	Val	His	Asn	Ser	Tyr	Asn	Arg	Pro	Ala	Tyr	Ser	Pro	Gly	His	370	375	380	
Lys	Thr	Gln	Pro	Phe	Leu	His	Asp	Gly	Tyr	Ala	Val	Ser	Trp	Asn	Thr	385	390	395	400
Val	Glu	Asp	Ser	Ile	Ile	Arg	Thr	Gly	Phe	Gln	Gly	Glu	Ser	Gly	His	405	410	415	
Asp	Ile	Lys	Ile	Thr	Ala	Glu	Asn	Thr	Pro	Leu	Pro	Ile	Ala	Gly	Val	420	425	430	
Leu	Leu	Pro	Thr	Ile	Pro	Gly	Lys	Leu	Asp	Val	Asn	Lys	Ser	Lys	Thr	435	440	445	
His	Ile	Ser	Val	Asn	Gly	Arg	Lys	Ile	Arg	Met	Arg	Cys	Arg	Ala	Ile	450	455	460	
Asp	Gly	Asp	Val	Thr	Phe	Cys	Arg	Leu	Lys	Ser	Pro	Val	Tyr	Val	Gly	465	470	475	480
Asn	Gly	Val	His	Ala	Asn	Leu	His	Val	Ala	Phe	His	Arg	Ser	Ser	Ser	485	490	495	
Glu	Lys	Ile	His	Ser	Asn	Glu	Ile	Ser	Ser	Asp	Ser	Ile	Gly	Val	Leu	500	505	510	

Gly Tyr Gln Lys Thr Val Asp His Thr Lys Val Asn Ser Lys Leu Ser
 515 520 525
 Leu Phe Phe Glu Ile Lys Ser
 530 535

<210> 156
 <211> 261
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

<400> 156
 Cys Ser Ser Gly Ser Gly Ser Gly Gly Gly Gly Val Ala Ala Asp Ile
 1 5 10 15
 Gly Thr Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp
 20 25 30
 Lys Gly Leu Lys Ser Leu Thr Leu Glu Asp Ser Ile Ser Gln Asn Gly
 35 40 45
 Thr Leu Thr Leu Ser Ala Gln Gly Ala Glu Lys Thr Phe Lys Val Gly
 50 55 60
 Asp Lys Asp Asn Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Ile
 65 70 75 80
 Ser Arg Phe Asp Phe Val Gln Lys Ile Glu Val Asp Gly Gln Thr Ile
 85 90 95
 Thr Leu Ala Ser Gly Glu Phe Gln Ile Tyr Lys Gln Asp His Ser Ala
 100 105 110
 Val Val Ala Leu Gln Ile Glu Lys Ile Asn Asn Pro Asp Lys Ile Asp
 115 120 125
 Ser Leu Ile Asn Gln Arg Ser Phe Leu Val Ser Gly Leu Gly Gly Glu
 130 135 140
 His Thr Ala Phe Asn Gln Leu Pro Ser Gly Lys Ala Glu Tyr His Gly
 145 150 155 160
 Lys Ala Phe Ser Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile
 165 170 175
 Asp Phe Ala Ala Lys Gln Gly His Gly Lys Ile Glu His Leu Lys Thr
 180 185 190
 Pro Glu Gln Asn Val Glu Leu Ala Ser Ala Glu Leu Lys Ala Asp Glu
 195 200 205
 Lys Ser His Ala Val Ile Leu Gly Asp Thr Arg Tyr Gly Ser Glu Glu
 210 215 220
 Lys Gly Thr Tyr His Leu Ala Leu Phe Gly Asp Arg Ala Gln Glu Ile
 225 230 235 240
 Ala Gly Ser Ala Thr Val Lys Ile Arg Glu Lys Val His Glu Ile Gly
 245 250 255
 Ile Ala Gly Lys Gln
 260

<210> 157
 <211> 260
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic sequence

<400> 157

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

```

<210> 158

<211> 260

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic sequence

<400> 158

```

Ser Ser Gly Ser Gly Cys Gly Gly Gly Gly Val Ala Ala Asp Ile Gly
1      5      10      15
Thr Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys
      20      25      30
Gly Leu Lys Ser Leu Thr Leu Glu Asp Ser Ile Ser Gln Asn Gly Thr
      35      40      45
Leu Thr Leu Ser Ala Gln Gly Ala Glu Lys Thr Phe Lys Val Gly Asp
      50      55      60

```

Lys	Asp	Asn	Ser	Leu	Asn	Thr	Gly	Lys	Leu	Lys	Asn	Asp	Lys	Ile	Ser
65					70				75					80	
Arg	Phe	Asp	Phe	Val	Gln	Lys	Ile	Glu	Val	Asp	Gly	Gln	Thr	Ile	Thr
			85					90						95	
Leu	Ala	Ser	Gly	Glu	Phe	Gln	Ile	Tyr	Lys	Gln	Asp	His	Ser	Ala	Val
			100					105						110	
Val	Ala	Leu	Gln	Ile	Glu	Lys	Ile	Asn	Asn	Pro	Asp	Lys	Ile	Asp	Ser
		115					120					125			
Leu	Ile	Asn	Gln	Arg	Ser	Phe	Leu	Val	Ser	Gly	Leu	Gly	Gly	Glu	His
	130					135					140				
Thr	Ala	Phe	Asn	Gln	Leu	Pro	Ser	Gly	Lys	Ala	Glu	Tyr	His	Gly	Lys
145					150					155					160
Ala	Phe	Ser	Ser	Asp	Asp	Ala	Gly	Gly	Lys	Leu	Thr	Tyr	Thr	Ile	Asp
				165					170					175	
Phe	Ala	Ala	Lys	Gln	Gly	His	Gly	Lys	Ile	Glu	His	Leu	Lys	Thr	Pro
			180					185						190	
Glu	Gln	Asn	Val	Glu	Leu	Ala	Ser	Ala	Glu	Leu	Lys	Ala	Asp	Glu	Lys
		195					200					205			
Ser	His	Ala	Val	Ile	Leu	Gly	Asp	Thr	Arg	Tyr	Gly	Ser	Glu	Glu	Lys
	210					215					220				
Gly	Thr	Tyr	His	Leu	Ala	Leu	Phe	Gly	Asp	Arg	Ala	Gln	Glu	Ile	Ala
225					230					235					240
Gly	Ser	Ala	Thr	Val	Lys	Ile	Arg	Glu	Lys	Val	His	Glu	Ile	Gly	Ile
				245					250					255	
Ala	Gly	Lys	Gln												
			260												

CLAIMS:

1. An isolated polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 2.
2. The isolated polypeptide according to claim 1, wherein the amino acid sequence is encoded by SEQ ID NO: 4.
3. An isolated polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 8.
4. An isolated polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 14.
5. An isolated polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 16.
6. An isolated polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 18.

FIG. 1



FIG. 2

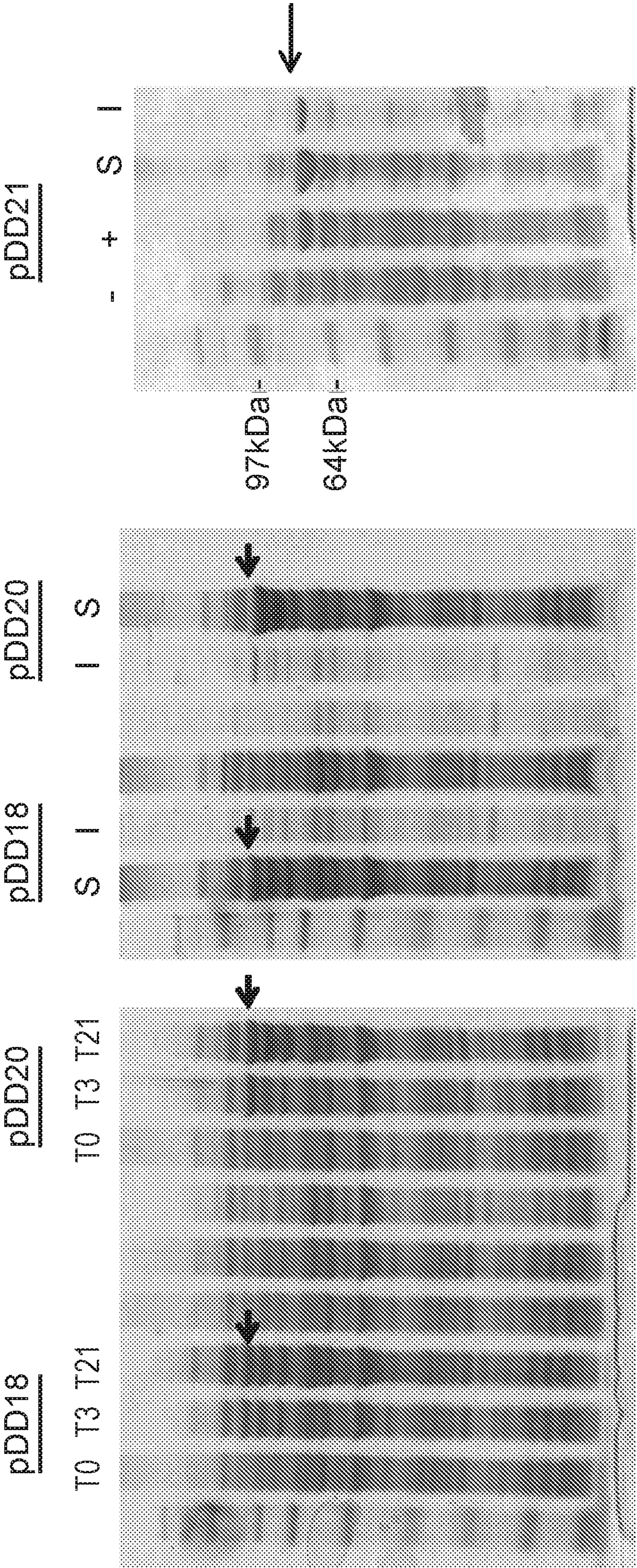


FIG. 3

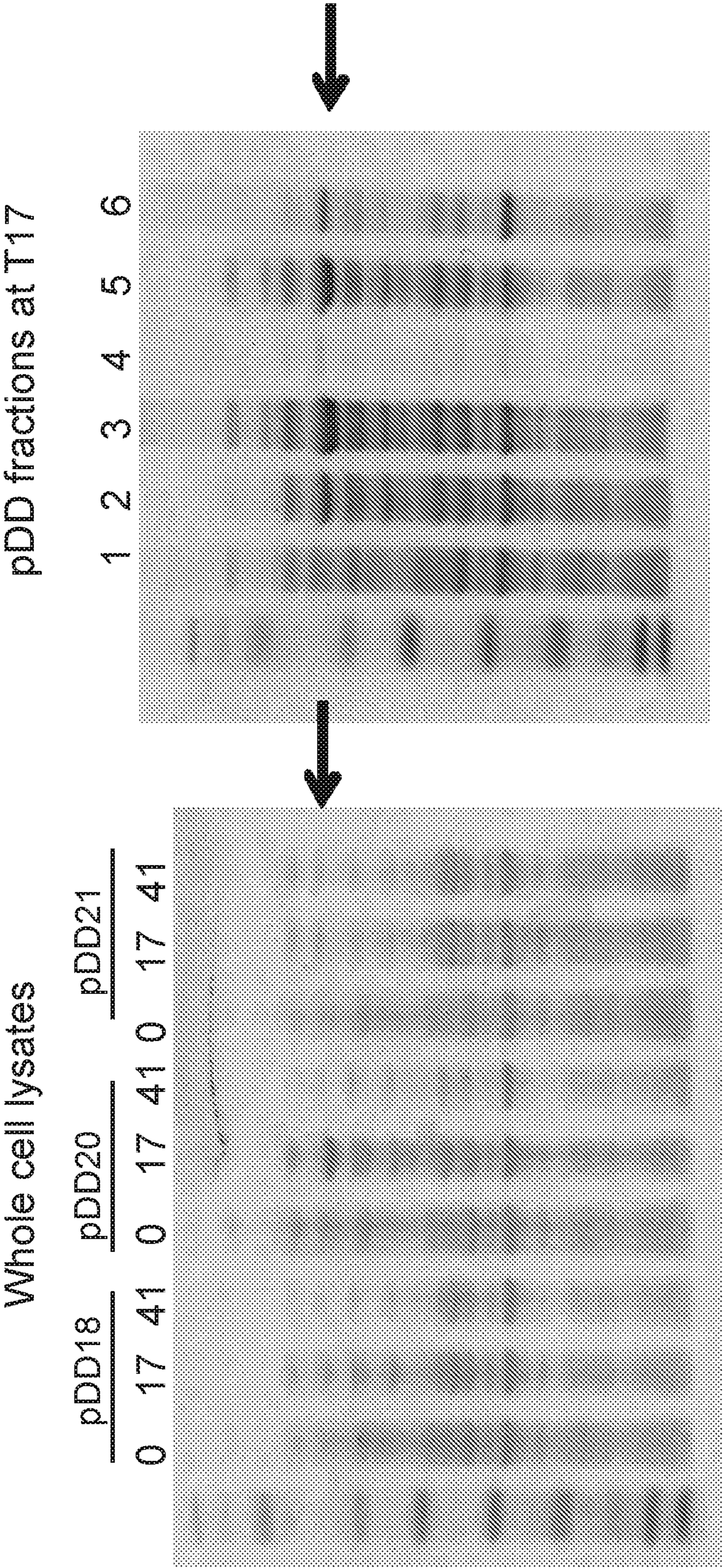
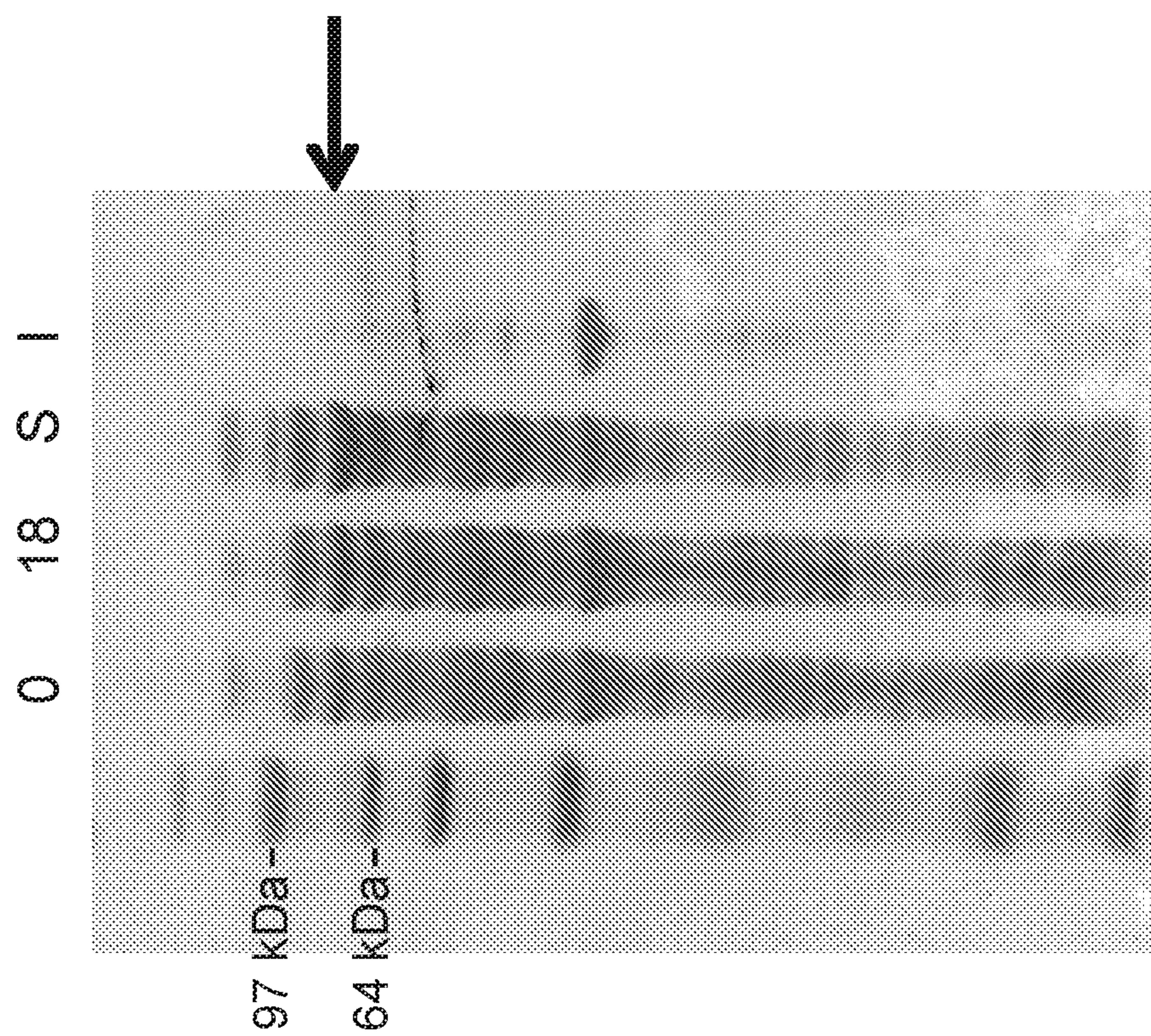


FIG. 4

A. 

B. 

C. 

D. 

E. 