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(73) Patenthaver: **Engineered Antigens Inc., 4002 Kovitz Lane N.W., Calgary, AB T3B 6H3, Canada**

(72) Opfinder: **MORAES, Trevor F., 19 Hogarth Avenue, Toronto, ON M4K 1J8, Canada**
GRAY-OWEN, Scott, 1201 Jeff Drive, Oakville, ON L6J 7N6, Canada
SCHRYVERS, Anthony B., 4002 Kovitz Lane N. W., Calgary, AB T3B 6H3, Canada

(74) Fuldmægtig i Danmark: **RWS Group, Europa House, Chiltern Park, Chiltern Hill, Chalfont St Peter, Bucks SL9 9FG, Storbritannien**

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DESCRIPTION

FIELD OF THE DISCLOSURE

[0001] The present disclosure relates to immunogenic compositions and vaccines and methods of making and evaluating thereof. More in particular, the disclosure relates to immunogenic compositions derived from bacterial surface receptor proteins and to vaccines against Gram-negative bacterial organisms, including, but not limited to, bacterial organisms belonging to the bacterial families of Pasteurellaceae, Neisseriaceae and Moraxellaceae.

BACKGROUND OF THE DISCLOSURE

[0002] The following paragraphs are intended to introduce the reader to the more detailed description that follows and not to define or limit the claimed subject matter of the present disclosure.

[0003] Vaccines capable of mediating an effective immune response are important in health strategies aimed at combating diseases caused by microbial pathogens. The two basic strategies for inducing an effect immune response in the host involve either the administration to a subject (host) of a 'live' agent capable of replicating within the host, or the administration of materials or substances that are not capable of replicating in the host. Administration of a live vaccine may represent a safety risk for immune-compromised individuals if the agent or a contaminating organism replicate and adversely affect the immunized subject. These risks are not associated with vaccines based on killed whole pathogens, based on extracts from pathogens or based on purified components, commonly referred to as subunit vaccines. Subunit vaccines avoid the safety problems associated with live vaccines but the purified components may not by themselves deliver the desired protective effect in the subject against the infective microbial organism and require appropriate components, termed adjuvants, to enhance the immune response.

[0004] Approaches to the design of vaccines against Gram-negative bacterial organisms have commonly focused on the use of proteins that are naturally associated with the outer membrane of the bacteria and exposed on the surface of the bacterial cells. Particularly attractive targets for vaccination are proteins presumed to be critical for survival in the host as they cannot be lost or dramatically altered in order to avoid the host immune response. In this respect the bacterial surface receptor proteins capable of interacting with and binding to the host iron binding proteins, transferrin and lactoferrin, have for some time been considered suitable components for use in the preparation of vaccines (1-3). This group of surface receptor proteins, hereinafter referred to as "HIBP" (host iron binding protein) surface receptor proteins, is present in pathogens of humans and animals belonging to the bacterial families Pasteurellaceae, Moraxellaceae and Neisseriaceae (4). Thus these proteins have been

recognized as potential targets for development of vaccines against a variety of different pathogens of humans and food production animals (5) (6-10).

[0005] The HIBP surface receptors normally are comprised of two proteins, a surface lipoprotein, transferrin binding B (TbpB) or lactoferrin binding protein B (LbpB), and a TonB-dependent, integral membrane protein, transferrin binding protein A (TbpA) or lactoferrin binding protein A (LbpA) (11). Recently the detailed three-dimensional structures of TbpBs from *Actinobacillus pleuropneumoniae, Actinobacillus suis,* and *Neisseria meningitidis* were determined at high resolution (12-14). The intrinsic properties of the TbpB or LbpB proteins are quite different from the integral outer membrane proteins, TbpA and LbpA, and substantially impact on the strategies used for vaccine development. For instance, it is possible to produce and purify TbpB or LbpB at relatively high yields from the *E. coli* cytoplasm for the generation of subunit vaccines. However, these proteins are notably absent or deficient in outer membrane vesicle (OMV) vaccines prepared by selective detergent extraction due to their removal during the extraction process. In contrast, functional TbpA or LbpA can only be produced in the outer membrane, providing limitations for producing high yields of purified proteins to be used in subunit vaccines. The alternate approach of producing misfolded proteins that aggregate into large inclusion bodies and subsequently attempt to refold the protein from the enriched inclusion body preparations, are also problematic for commercial production. Thus most strategies for TbpA or LbpA based vaccines would normally involve production of OMVs or development of attenuated strains.

[0006] An alternate approach that has been used successfully for invasive bacterial pathogens is to use the extracellular capsular polysaccharide as the primary antigen, and couple it to a protein carrier to induce T-cell help. These conjugate capsular vaccines have proven to be very effective at providing protection from infection by strains expressing the specific capsular polysaccharide but provide no cross-protection to other capsular types. Although conjugate capsular vaccines against the human pathogens *H. influenzae, N. meningitidis* and *Streptococcus pneumoniae* were originally developed to prevent invasive infection, post licensure carriage studies have demonstrated that the systemically administered vaccines eliminated colonization by the pathogens expressing the specific targeted polysaccharides (15-17). This had the added benefit of providing herd immunity, providing protection to non-immunized individuals due to reduced carriage frequency within the population. While not the initial intent of these early vaccines, the potential to confer herd immunity has become an important criterion for evaluating new and upcoming bacterial vaccines. However, determining or predicting whether new vaccines will be capable of impacting or preventing colonization (carriage) is a major challenge (18).

[0007] The ability to evaluate whether protein antigens will ultimately be capable of providing broad protection against a diverse set of disease isolates is also a considerable challenge (19). Initial efforts at testing this ability commonly involve immunizing other animal species (mice, rabbits) and then analyzing the cross-reactive and cross-protective properties of the resulting sera. For those surface antigens that can readily be produced in a soluble form, such as surface lipoproteins, a first step is often to produce and purify a set of variant proteins and use

them in a standard ELISA (enzyme linked immunosorbent assay) to evaluate the ability of the antisera to recognize the variant proteins. This is fairly labor intensive making analysis of an extensive set of variants an expensive enterprise and relies on the assumption that the binding of the antigen to the ELISA plate is random so that all protein surfaces can be probed.

[0008] Considering the limitations in the various assays used to evaluate and predict the cross-protective and cross-reactive properties of antisera raised against antigens, the selection and design of new and improved protein-based vaccines should be pursued in conjunction with development of improved assays so that optimizing and improving vaccines in development can be approached on a rational basis.

[0009] Despite considerable efforts over the years since their initial discovery (20, 21), it remains unclear whether and how HIBP surface receptor proteins can be used to prepare efficacious vaccines against Gram-negative bacterial pathogens, and in particular whether and how a broadly protective vaccine can be developed. Thus there is a need in the art to improve immunogenic compositions and vaccines based on HIBP surface receptor proteins against Gram-negative bacterial organisms.

[0010] Frandoloso et al. developed and characterised protective *Haemophilus parasuis* subunit vaccines based on native proteins with affinity to porcine transferrin (Frandoloso et al. 2011 Clinical and Vaccine Immunology 18, 1, 50-58).

SUMMARY OF THE INVENTION

[0011] The invention provides an immunogenic composition comprising a transferrin binding protein B (TbpB) polypeptide obtainable from a Gram-negative pathogenic bacterial species, wherein the TbpB polypeptide comprises the sequence of SEQ.ID NO: 174.

[0012] The invention also provides a vaccine composition comprising an immunogenic composition according to the invention.

[0013] The invention also provides a method for preparing an immunogenic composition comprising:

1. (a) providing a chimeric nucleic acid sequence comprising as operably linked components:
    1. (i) a nucleic acid sequence encoding a TbpB polypeptide obtainable from a Gram-negative pathogenic bacterial species, wherein the TbpB polypeptide comprises the sequence of SEQ.ID NO: 174; and
    2. (ii) a nucleic acid sequence capable of controlling expression in a recombinant host cell;
2. (b) introducing the chimeric nucleic acid sequence into a host cell and growing the host cell to produce the TbpB polypeptide;

3. (c) recovering the TbpB polypeptide from the host cell; and
4. (d) preparing an immunogenic composition.

[0014] The invention also provides an expression vector comprising a nucleic acid sequence encoding a TbpB polypeptide obtainable from a Gram-negative pathogenic bacterial species, wherein the TbpB polypeptide comprises the sequence of SEQ.ID NO: 174.

SUMMARY OF THE DISCLOSURE

[0015] The present disclosure provides novel immunogenic compositions and in particular immunogenic compositions based on HIBP surface receptor proteins from Gram-negative pathogenic bacterial species.

[0016] Accordingly, the present disclosure provides, in at least one aspect, an immunogenic composition comprising an antigen derived from a HIBP surface receptor protein from a Gram-negative pathogenic bacterial species, wherein the protein derived from the HIBP surface receptor protein has been modified in such a manner that it is unable to substantially bind host iron binding protein.

[0017] The present disclosure provides, in at least one aspect, an immunogenic composition comprising a polypeptide comprising a C-lobe domain or an N-lobe domain of a HIBP surface receptor protein obtainable from or obtained from a Gram-negative bacterial species, wherein the polypeptide is unable to substantially bind host iron binding protein. In preferred aspects, the present disclosure provides an immunogenic composition comprising a C-lobe domain of a HIBP surface receptor polypeptide, wherein the polypeptide is unable to substantially bind the host iron binding protein. In further preferred aspects, the present disclosure provides an immunogenic composition comprising a mixture of at least two polypeptides, each polypeptide comprising a C-lobe domain, wherein the C-lobe domains are obtainable or obtained from at least two Gram-negative bacterial species, or from at least two Gram-negative bacterial strains. In further preferred aspects, the C-lobe domains are obtained from the HIBP surface receptor proteins that are antigenically divergent.

[0018] In further aspects, the present disclosure further provides an immunogenic composition comprising a polypeptide comprising an N-lobe domain and/or a C-lobe domain of an HIBP surface receptor protein obtainable from or obtained from a Gram-negative pathogenic bacterial species, wherein the N-lobe domain or the C-lobe domain comprise a plurality of β-strands connected by a plurality of loop domains, and wherein at least one loop domain of the plurality of loop domains of the N-lobe domain or the C-lobe domain has been modified, and wherein the polypeptide is unable to substantially bind host iron binding protein. In preferred aspects, the modification comprises the modification of at least one amino acid residue within a loop domain.

[0019] In further aspects of the disclosure, at least two loop domains of the plurality of loop domains within the C-lobe domain and/or the N-lobe domain of an HIBP surface receptor protein have been modified.

[0020] In further aspects, the present disclosure provides (i) a first polypeptide, comprising an N-lobe domain or a C-lobe domain of an HIBP surface receptor protein obtainable from or obtained from a Gram-negative pathogenic bacterial species, wherein the N-lobe domain or the C-lobe domain comprise a plurality of β-strands connected by a plurality of loop domains, and wherein at least one loop domain of the plurality of loop domains of the N-lobe domain or the C-lobe domain has been modified, linked to (ii) a second polypeptide comprising an HIBP surface receptor protein, or a portion thereof, obtainable from a Gram-negative bacterial species, and wherein the linked polypeptide is unable to substantially bind host iron binding protein. In preferred aspects, the portion of the HIBP surface protein is an N-lobe domain or a C-lobe domain. In further preferred aspects, the portion of the HIBP surface protein is an N-lobe domain or a C-lobe domain of an HIBP surface receptor protein obtainable from or obtained from a Gram-negative pathogenic bacterial species, wherein the N-lobe domain or the C-lobe domain comprise a plurality of β-strands connected by a plurality of loop domains, and wherein at least one loop domain of the plurality of loop domains of the N-lobe domain or the C-lobe domain has been modified.

[0021] In further aspects of the disclosure, the C-lobe domain or the N-lobe domain is a C-lobe domain or an N-lobe domain of an HIBP surface receptor protein obtainable from or obtained from a bacterial species belonging to the bacterial family of Pasteurellaceae, Moraxellaceae or Neisseriaceae, and in further preferred aspects, the C-lobe domain or the N-lobe domain is a C-lobe domain or an N-lobe domain of an HIBP surface receptor polypeptide obtainable from or obtained from a bacterial species belonging to the bacterial genus of *Actinobacillus, Neisseria, Haemophilus, Mannheimia, Histophilus, Pasteurella* or *Moraxella.*

[0022] In further preferred aspects of the disclosure, the HIBP surface receptor protein is modified in such a manner that the N-terminal anchor polypeptide of the HIB surface receptor protein, or a portion thereof, is removed, and wherein the polypeptide is unable to substantially bind host iron binding protein.

[0023] In other aspects, the present disclosure provides methods for preparing an immunogenic composition. Accordingly, the present disclosure provides a method for preparing an immunogenic composition comprising:

1. (a) providing a chimeric nucleic acid sequence comprising as operably linked components:
    1. (i) a nucleic acid sequence encoding a polypeptide comprising a C-lobe domain or an N-lobe domain of an HIBP surface receptor protein obtainable from or obtained from a Gram-negative bacterial species, wherein the polypeptide is unable to substantially bind host iron binding protein; and
    2. (ii) a nucleic acid sequence capable of controlling expression in a recombinant

host cell;

2. (b) introducing the chimeric nucleic acid sequence into a host cell and growing the host cell to produce the polypeptide comprising the C-lobe domain or the N-lobe domain;
3. (c) recovering the polypeptide comprising C-lobe domain or the N-lobe domain from the host cell; and
4. (d) preparing an immunogenic composition.

[0024] In further aspects of the disclosure, the C-lobe domain or the N-lobe domain comprises a plurality of β-strands connected by a plurality of loop domains, wherein at least one loop domain of the plurality of loop domains has been modified.

[0025] In yet further aspects of the disclosure, methods for eliciting an immune response in a vertebrate subject are provided. Accordingly, the present disclosure further provides a method for eliciting an immune response in a vertebrate subject, said method comprising administering to the subject:

1. (a) an immunogen comprising a polypeptide comprising a C-lobe domain or an N-lobe domain of an HIBP surface receptor protein obtainable from or obtained from a Gram-negative bacterial species wherein the polypeptide is unable to substantially bind host iron binding protein; or
2. (b) an expression vector comprising a polynucleotide encoding an immunogen comprising a polypeptide comprising a C-lobe domain or an N-lobe domain of an HIBP surface receptor polypeptide obtainable from a Gram-negative bacterial species; and wherein the immunogen is administered in, or is expressed in, an amount sufficient to elicit an immune response in the vertebrate subject.

[0026] In preferred aspects of the disclosure, the C-lobe domain or the N-lobe domain comprises a plurality of β-strands connected by a plurality of loop domains, wherein at least one loop domain of the plurality of loop domains has been modified.

[0027] The present disclosure further includes an immunogen comprising a C-lobe domain or an N-lobe domain of an HIBP surface receptor polypeptide wherein the C-lobe domain or the N-lobe domain comprises a plurality of β-strands connected by a plurality of loop domains, and wherein at least one loop domain has been modified, for use as a medicament.

[0028] The present disclosure further includes an immunogen comprising a C-lobe domain or an N-lobe domain of an HIBP surface receptor used in the prevention of infection, for example by prevention of colonization, or disease by infectious Gram-negative bacteria, including bacteria belonging to the genus *Actinobacillus, Neisseria, Haemophilus, Mannheimia, Histophilus, Pasteurella* or *Moraxella.* In preferred aspects, the C-lobe domain or the N-lobe domain comprises a plurality of β-strands connected by a plurality of loop domains, wherein at

least one loop domain of the plurality of loop domains has been modified.

[0029] The present disclosure further includes an immunogen comprising a C-lobe domain and/or an N-lobe domain of an HIBP surface receptor polypeptide for use in the manufacture of a medicament for the prevention of infection or disease by infectious Gram-negative bacteria, including bacteria belonging to the genus *Actinobacillus, Neisseria, Haemophilus, Mannheimia, Histophilus, Pasteurella* or *Moraxella.* In preferred aspects, the C-lobe domain or the N-lobe domain comprises a plurality of β-strands connected by a plurality of loop domains, wherein at least one loop domain of the plurality of loop domains has been modified.

[0030] The immunogenic compositions of the present disclosure may be used to prepare a vaccine. Accordingly, the present disclosure further provides a vaccine composition comprising an antigen derived from a HIBP surface receptor protein from a Gram-negative pathogenic bacterial species, wherein the protein derived from the HIBP surface receptor protein has been modified in such a manner that it is unable to substantially bind host iron binding protein.

[0031] In further aspects, the present disclosure further also includes a vaccine composition comprising a polypeptide comprising a C-lobe domain or an N-lobe domain of an HIBP surface receptor protein obtainable from a Gram-negative pathogenic bacterial species wherein the polypeptide is unable to substantially bind host iron binding protein.

[0032] In further aspects of the disclosure, the vaccine composition comprises a polypeptide comprising a C-lobe domain or an N-lobe domain of an HIBP surface receptor polypeptide wherein the C-lobe domain or the N-lobe domain comprises a plurality of β-strands connected by a plurality of loop domains, and wherein at least one loop domain has been modified and wherein the polypeptide is unable to substantially bind host iron binding protein.

[0033] The present disclosure further provides methods for administering a vaccine to a vertebrate subject, the method comprising administering to the subject a vaccine comprising a polypeptide comprising a C-lobe domain or an N-lobe domain of an HIBP surface receptor protein obtainable from a Gram-negative pathogenic bacterial species, wherein the vaccine is administered in an amount sufficient to prevent or treat a disease caused by a Gram-negative bacterial species.

[0034] The present disclosure further includes a vaccine comprising a C-lobe domain or an N-lobe domain of an HIBP surface receptor for use in the prevention of infection or disease by infectious Gram-negative bacteria, including bacteria belonging to the genus *Actinobacillus, Neisseria, Haemophilus, Mannheimia, Histophilus, Pasteurella* or *Moraxella.*

[0035] In preferred aspects of the disclosure, the C-lobe domain or the N-lobe domain comprises a plurality of β-strands connected by a plurality of loop domains, and at least one loop domain of the plurality of loop domains has been modified.

[0036] Other features and advantages of the present disclosure will become apparent from the

following detailed description. It should be understood, however, that the detailed description, while indicating preferred aspects of the disclosure, is given by way of illustration only, since various changes and modifications will become apparent to those of skill in the art from the detailed description.

BRIEF DESCRIPTION OF THE DRAWINGS

[0037] The disclosure is in the hereinafter provided paragraphs described in relation to its Figures. The Figures provided herein are provided for illustration purposes and are not intended to limit the present disclosure.

FIGURE 1 depicts an alignment of the polypeptide sequences of several TbpBs, notably ApH49 TbpB (SEQ.ID NO: 2), *Actinobacillus pleuropneumoniae* ApH87 TbpB (SEQ.ID NO: 12), and AsH57TbpB (SEQ.ID NO: 28), from porcine TbpB pathogens and structural models of the proteins (pdb 3HOL, 3PQS and 3PQU, respectively). These three proteins provide a good representation of the sequence diversity amongst TbpBs from porcine pathogens **(FIG. 4,** large black arrows). The upper panel illustrates the polypeptide sequence alignment, whereas the lower panel illustrates the structural models. In the sequence alignment the domain structure is demarked by background shading and labeled accordingly. The secondary structural elements are illustrated and nomenclature and numbering for the β-strands ("β1" - "β31") and loops (L1-L32) are illustrated immediately above the aligned sequences. The sub-regions for loop 8 (8a; 8b; and 8c) in this figure are referred to due to the large size of loop 8, differences between TbpB variants and secondary structural elements in some loop variants. Further indicated are the C-lobe and N-lobe cap areas labeled as "C-lobe Cap Area" and "N-lobe Cap Area", respectively and the C-lobe handle and N-lobe handle areas labeled as "C-lobe handle" and "N-lobe handle" areas, respectively. The structural models for the three TbpBs in the alignment in the upper panel are depicted in the bottom panel and the domains are labeled for the third structural model (AsH57TbpB), which is depicted in an identical orientation as the other two models.

FIGURE 2 depicts a schematic drawing of certain secondary structural features of the amino acid sequence of a TbpB polypeptide with the recommended nomenclature for this class of proteins. The N and C-termini of the polypeptide are indicated and labeled "N" and "C" respectively. The β-strands are indicated by arrows and sequentially labeled starting from the N-terminus "β1" to "β31". The loop domains are indicated and labeled "L1" to "L32". The sequences of the loops of the TbpB polypeptide from *A. pleuropneumoniae* Strain H49 TbpB (SEQ.ID NO: 2) are included in this patent application (SEQ.ID NO: 41 to SEQ.ID NO: 106). Further indicated are the C-lobe and N-lobe cap areas labeled as C-lobe Cap Area and N-lobe Cap Area, respectively, and the C-lobe handle and N-lobe handle areas labeled as "C-lobe handle" and "N-lobe handle" areas.

FIGURE 3A depicts a comparison of the magnitude of the antibody response against the intact TbpB protein from the human pathogen *Neisseria meningitidis* (strain B16B6 - SEQ.ID NO: 117) or the intact TbpB from the porcine pathogen *Actinobacillus pleuropneumoniae* (strain

H49 - SEQ.ID NO: 2) in different host species (mice, rabbits or pigs) using 33% Emulsigen D as adjuvant. The antibody titre against the TbpB from *Actinobacillus pleuropneumoniae* (grey bar) is slightly higher in mice and rabbits than against the TbpB from *Neisseria meningitidis* (black bar), but substantially lower in pigs. These results infer that binding of host transferrin may be influencing the development of the antibody response.

FIGURE 3B depicts a comparison of the magnitude of the antibody response in pigs against intact TbpB from the bovine pathogen *Mannhemia haemolytica* (strain H196 - SEQ.ID NO: 206) or the intact TbpB (SEQ.ID NO:2), TbpB N-lobe (SEQ.ID NO: 8) or TbpB C-lobe (SEQ.ID NO: 6) from the porcine pathogen *Actinobacillus pleuropneumoniae* (strain H49). The clusters of bars represent serum samples taken from individual pigs immunized on day 0 (prior to the first immunization), day 21 (after the first immunization), day 42 (after the second immunization) and day 56 (after the third immunization). The sera from the pig immunized with intact TbpB from *M. haemolytica* (Mh Intact; strain H196 - SEQ.ID NO: 206), were tested with the intact *M. haemolytica* TbpB bound to the ELISA plate. The sera from the pigs immunized with the *A. pleuropneumoniae* TbpB (Ap Intact), TbpB N -lobe (Ap N Lobe) or the TbpB C-lobe (Ap C Lobe) were analyzed with the intact *A. pleuropneumoniae* TbpB bound to the ELISA plate.

FIGURE 3C depicts a comparison of cross-reactivity of antisera against the C-lobe polypeptide domain of TbpB (SEQ.ID NO: 6), N-lobe polypeptide domain of TbpB (SEQ.ID NO: 8) and intact TbpB (SEQ.ID NO: 2) from the porcine pathogen *Actinobacillus pleuropneumoniae* (strain H49). The cluster of bars represent the reactivity of sera against intact TbpB from three different porcine pathogens; *Actinobacillus pleuropneumoniae* strain H49 (SEQ.ID NO: 2, black bar), *Haemophilus parasuis* strain HP5 (SEQ.ID NO: 115, dark grey bar) and *Actinobacillus pleuropneumoniae* strain H87 (SEQ.ID NO: 12, light grey bar) that were selected to represent antigenically diverse TbpBs **(FIG. 4).** The results illustrate the reactivity of sera immunized with intact TbpB (first cluster from the left, labeled "Intact"), TbpB N-lobe (second cluster from the left, labeled "N lobe"), TbpB C-lobe (third cluster from the left, labeled "C lobe") or a mixture of the N-lobe and the C-lobe (fourth cluster from the left labeled "N+C lobe"). Standard error of the mean (SEM) error bars are shown. The statistics were done via ANOVA with Tukeys HSD (honest significant difference) test done as post hoc. The stars shown on the figure denote specific immunization/protein pairs that differ significantly from the C lobe or N+C lobe tested against H49.

FIGURE 4 depicts the sequence diversity of TbpBs from the porcine pathogens *Actinobacillus pleuropneumoniae, A. suis* and *Haemophilus parasuis* isolated from pigs in North America, Europe and Asia. The maximum likelihood phylogenetic tree illustrates the relationship between 56 TbpBs based on sequences from our collection of clinical isolates or obtained from public databases. The TbpB sequences cluster into 3 main groups with representative isolates indicated by the arrows (SEQ.ID NO: 2; SEQ.ID NO: 12; SEQ.ID NO: 28 and SEQ.ID NO: 107 to SEQ.ID NO: 115). The strains that express the TbpB variants used in the ELISA assay illustrated in **FIG. 3** are indicated by the large black stars; *A. pleuropneumoniae* strain H87 (SEQ.ID NO: 12), *A. pleuropneumoniae* strain H49 (SEQ.ID NO: 2) and *H. parasuis* strain HP5 (SEQ.ID NO: 115). The large black arrows depict the three TbpBs used in the alignment

illustrated in **FIG. 1;** *A. pleuropneumoniae* strain H87 (SEQ.ID NO: 12), *A. pleuropneumoniae* strain H49 (SEQ.ID NO: 2) and *A. suis* strain H57 (SEQ.ID NO: 28).

FIGURE 5 depicts the nonrandom binding of the TbpB N-lobe (SEQ.ID NO: 8) from *A. pleuropneumoniae* H49 to ELISA plates illustrated by the substantial reduction in binding of labeled transferrin when the purified TbpB protein is used to coat the ELISA plate rather than the fusion protein (i.e. maltose binding protein (Mbp) fused to the TbpB N-lobe) precursor (left portion of Panel A and Panel B). The figure also illustrates how the use of an N-terminal biotinylated peptide overcomes the random binding (right portion of Panel A and Panel B). The left portion of **Panel A** illustrates the results of an assay using labeled transferrin (Tf) to measure bound purified Mbp-TbpB N-lobe or TbpB N-lobe to regular ELISA plates. The right portion illustrates the results when the recombinant proteins contain a biotinylated N-terminal peptide tag that is used to attach to streptavidin-coated ELISA plates. **Panel B** is a cartoon illustrating what is believed to occur in the different ELISA wells for the corresponding results shown immediately above in **Panel A.** *** indicates statistical significance $p < 0.001$ between MBP N lobe and N lobe, ns - not statistically significant.

FIGURE 6 depicts the design and production of a multimer comprised of the TbpB C-lobe from three different porcine pathogens. Panel A shows the DNA and protein sequence for the trimer (SEQ.ID NO: 39; SEQ.ID NO: 40) of C-lobes from *A. pleuropneumoniae* strain H49 (SEQ.ID NO: 6), *A. suis* strain H57 (SEQ.ID NO: 35) and *A. pleuropneumoniae* strain H87 (SEQ.ID NO: 22), in that order. The underline indicates the peptide sequence connecting the individual C-lobes or preceding the first C-lobe. Panel B illustrates SDS-PAGE analysis of a preparation of the C-lobe trimer compared to preparations of the N-lobe and C-lobe from *N. meningitidis* strain M982. 1 µl of sample was applied to lanes 1, 4 & 7, 5 µls to lanes 2, 5 & 8 and 10 µls to lanes 3, 6 & 9. Protein molecular weight standards (MWS) observed on these gels are 93, 70, 63, 41, 30 and 22.

FIGURE 7 depicts the immune response against the TbpB C-lobe from *A. pleuropneumoniae* (H49 C-lobe, SEQ.ID NO: 6) compared to the immune response against a trimer comprised of C-lobes from TbpB C-lobes from *A. pleuropneumoniae* H49, *A. suis* H57 and *A. pleuropneumoniae* H87 (C-lobe trimer, SEQ.ID NO: 40). The cluster of bars on the left side of the figure represent the immune response against H49 C-lobe whereas the cluster of bars on the left side of the figure represents the immune response against the C-lobe trimer. The black bar represents the immune response against the TbpB from *A. pleuropneumoniae* strain H49 (SEQ.ID NO: 2), the dark grey bar represents the immune response against the TbpB from *H. parasuis* strain HP5 (SEQ.ID NO: 115) and the light grey bar represents the immune response against the TbpB from *A. pleuropneumoniae* strain H87 (SEQ.ID NO: 22).

FIGURE 8 depicts **the** loop regions of the *Actinobacillus pleuropneumoniae* strain H49 TbpB N-lobe (labeled "loop 1"; "loop 5"; "loop 8a"; "loop 8c" and "loop 12") (SEQ ID. NO: 41; SEQ.ID NO: 49; SEQ.ID NO: 55; and SEQ.ID NO: 63, respectively) targeted for loop reduction and the sequences of the original and modified loops. Loop 8a and loop 8c refer to portions of loop 8 present in the TbpB from strain H49. **Panel A** is a structural model of the *Actinobacillus pleuropneumoniae* TbpB N-lobe viewed from the side (relative to the predicted dominant

orientation at the cell surface) with the targeted regions labeled. **Panel B** is the same structural model viewed from the top to illustrate the association of loops 1 and 5 with the handle domain and loops 8a, 8c and 12 associated with the barrel domain. **Panel C** is an alignment of the native TbpB and the TbpB with reductions in the targeted loop regions. The regions of the sequence encoding the loops are highlighted in grey and labeled with the loop numbers.

FIGURE 9 illustrates that the engineered loop reduction of the TbpB N-lobes from *A. pleuropneumoniae* strain H49 (SEQ.ID NO: 10), *A. suis* strain H57 (SEQ.ID NO: 38) and *A. pleuropneumoniae* strain H87 (SEQ.ID NO: 26) did not adversely affect their production or stability but eliminated binding by porcine Tf. The upper panel illustrates the production of intact H49 TbpB (SEQ.ID NO: 2), native h49 TbpB N-lobe (SEQ.ID NO: 8) and the engineered TbpB N-lobes from *A. pleuropneumoniae* strain H49 (SEQ.ID NO: 10), *A. suis* strain H57 (SEQ.ID NO: 38) or *A. pleuropneumoniae* strain H87(SEQ.ID NO:26). They were expressed as fusion proteins with an N-terminal maltose binding protein with a polyhistidine tag and captured on a Ni-NTA resin. The bound proteins were released in SDS-PAGE buffer and analyzed on a 10% SDS-PAGE gel. The middle panel represents the same preparations captured with an affinity resin consisting of porcine transferrin coupled to Sepharose (pTf-Sepharose) and eluted in SDS-PAGE buffer. The bottom panel illustrates a dot assay with the material from the upper panel eluted from the Ni-NTA resin and spotted onto a nitrocellulose resin, blocked and exposed to horse-radish peroxidase conjugated porcine transferrin (HRP-pTf) in blocking solution, and the bound HRP detected with incubation in HRP substrate.

FIGURE 10 depicts the sequence diversity of TbpBs from the human pathogen *Neisseria meningitidis.* A subset of *tbpB* genes sequenced from a collection of over 100 strains combined with a large collection of sequences available in the BIGSDB public database (http://pubmlst.org/software/database/bigsdb/ - Bacterial Isolate Genome Sequence Database) are represented in this figure. The collection of sequences represents a global collection of isolates over an extended time period of nearly 50 years, and thus this is a fairly comprehensive representation of the overall TbpB diversity. **FIG. 10A** illustrates the sequence diversity of the intact TbpBs. The sequences for TbpBs from strains indicated by arrows, double arrows, or lines are appended (SEQ.ID NO: 117; SEQ.ID NO: 124; SEQ.ID NO: 132 to SEQ.ID NO: 147; SEQ.ID NO: 177; and SEQ.ID NO: 178) to provide representative sequences for the identified groups. Two primary clades represented by Group 1 and by Groups 2-4 are identified within this tree corresponding to isotype I and isotype II TbpB lineages (22). Support values for primary branches are depicted, and a "*" identifies branches with 100% support. Antigens derived from the TbpB from strain B16B6 [SEQ.ID NO: 117, black arrow) were used to generate the antisera analyzed in **FIG. 11** and were screened for reactivity against TbpBs from the strains illustrated by the grey arrows (SEQ.ID NOs: 123; and SEQ.ID NO: 132 to SEQ.ID NO: 139) using our custom ELISA assay **(FIG. 5). FIG. 10B** depicts the sequence diversity of TbpBs C-lobes that were derived from the TbpB sequences. The sequences for TbpB C-lobes from strains indicated by arrows or lines are appended (SEQ.ID NO: 119; SEQ.ID NO: 125; and SEQ.ID NO: 179 to SEQ.ID NO: 195) to provide representative sequences. The two strains indicated by the double-headed arrows were included to provide a more comprehensive representation of the C-lobe diversity but were not available for the

analysis of antisera illustrated in **FIG**. **11.**

FIGURE 11 depicts the reactivity of antisera directed against truncated intact TbpB (SEQ.ID NO: 148, aa 43-575) and TbpB C-lobe (SEQ.ID NO: 119 aa 342- 575) derived from B16B6, a representative isotype I strain of *N. meningitidis.* The antisera were tested in our custom ELISA assay **(FIG. 5)** against a panel of TbpBs that represent the overall sequence diversity of TbpBs in *N. meningitidis* (arrows, **FIG**. **10**). The panel of TbpBs are from *N. meningitidis* strains B16B6 (SEQ.ID NO: 117), H44/76 (SEQ.ID NO: 133), S3131 (SEQ.ID NO: 132), M990 (SEQ.ID NO: 134), M978 (SEQ.ID NO: 135), M992 (SEQ.ID NO: 138), P3006 (SEQ.ID NO: 139), 120M (SEQ.ID NO: 137), MC58 (SEQ.ID NO: 136) and M982 (SEQ.ID NO: 123). The results demonstrate that the C-lobe antiserum had higher titres than the TbpB antiserum against all of the TbpBs except the TbpBs from B16B6 and H44/76.

FIGURE 12 depicts the design and production of a dimer comprised of the TbpB C-lobe from two different strains of the human pathogen *Neisseria meningitidis* (SEQ.ID NO: 118). **Panel A** shows the DNA and protein sequence for the dimer of C-lobes from *N. meningitidis* strains B16B6 (SEQ.ID NO: 118; and SEQ.ID NO: 119) and M982 (SEQ.ID NOS: 124; and SEQ.ID NO: 125), in that order. The underline indicates the DNA sequence of the peptide region connecting the individual C-lobes. **Panel B** illustrates SDS-PAGE analysis of a preparation of the C-lobe dimer compared to preparations of the individual C-lobes from *N. meningitidis* strains M982 and B16B6.

FIGURE 13 depicts the analysis of the immune response against a dimer comprised of the TbpB C-lobe from two different strains of the human pathogen *Neisseria meningitidis* (SEQ.ID NO: 150). The pairs of bars represent sera obtained from rabbits immunized with adjuvant alone (naive), with B16B6 C-lobe (SEQ.ID NO: 119), with M982 C-lobe (SEQ.ID NO: 125) or the dimer of B16B6 and M982 C-lobes (SEQ.ID NO: 150) illustrated in **FIG. 12.** The white bars represent results of the novel, custom ELISA assay with immobilized intact M982 TbpB (SEQ.ID NO: 123) and the black bar represents the results with immobilized intact B16B6 protein (SEQ.ID NO: 117).

FIGURE 14 depicts the reduction of loop domains of the C-lobe of the TbpB polypeptide of *N. meningitidis* M982. In **Panel A,** structural models of the native C-lobe (SEQ.ID NO: 125) and modified C-lobe (SEQ.ID NO: 129) are shown to illustrate the reduction of the four loops (L18, L21, L23 and L27). In the model on the left hand side (SEQ.ID NO: 125) the loops targeted for reduction are indicated with a dotted black line. The middle model (SEQ.ID NO: 129) illustrates the modified loop domains. In the model on the right hand side, the two prior structures are superimposed to show how the large variable loops have been removed without affecting overall protein structure. **Panel B** is a polypeptide sequence alignment comparing sequences of the native C-lobe, the engineered C-lobes with those from which a single loop has been modified and the C-lobe in which all four loops (L18, L21, L23 and L27); have been modified (the sequence labeled "loopless"). The regions of the sequence encompassing the targeted loops are highlighted in grey and the loop number is indicated in grey font.

FIGURE 15 depicts the microbial production of the modified C-lobes of *N. meningitidis* M982 described in **FIG. 14.** The wild-type (WT) C-lobe (SEQ.ID NO: 125) corresponds to the model

on the left hand side in **Panel A** of **FIG. 14.** The other samples represent proteins with truncations in the loops L18, L21, L23, and L27 and the protein with all four loops removed [all loops). The structural model for this protein (SEQ.ID NO: 129) is illustrated in the middle of **Panel A** in **FIG. 14.** Protein molecular weight standards (MWS) observed on this gel are 93, 70 and 41 kDa.

FIGURE 16 depicts the immunogenicity of the modified C-lobe of *N. meningitidis* strain M982 relative to the native C-lobes from strain M982 and B16B6. The endpoint titres of mouse antisera were determined with our custom ELISA assay. Mice were either immunized with the C-lobe from strain M982 (SEQ.ID NO: 125, first bar), the C-lobe TbpB from strain B16B6 (SEQ.ID NO: 119, second bar) or the 'loopless' M982 C-lobe (SEQ.ID NO: 129, last two bars). The sera were tested against immobilized intact TbpB from strain M982 (SEQ.ID NO: 123) (first and third bars) or strain B16B6 (SEQ.ID NO: 117) (second and fourth bars). The results show that the modified C-lobe was more immunogenic as it resulted in a higher titre against intact TbpB from strain M982 than the parent C-lobe protein (compare bars 3 and 1). Surprisingly the modified C-lobe even produced a similar level of reactivity to the heterologous B16B6 TbpB as the C-lobe from that strain (compare bars 4 and 2).

FIGURE 17 depicts the design of hybrid proteins displaying regions of TbpA on the TbpB C-lobe scaffold. **Panel A** is a structural model of TbpA (SEQ.ID NO: 152) highlighting the regions selected to 'transplant' onto the TbpB C-lobe. The TbpA loop 3 helix, loop 10, loop 11 and plug loop are shown as space-filled regions. **Panel B** shows an alignment of the native C-lobe (C-lobe) (SEQ.ID NO: 125), the loopless C-lobe scaffold (loopless C) (SEQ.ID NO: 129) and a hybrid protein with the all the regions of TbpA displayed (SEQ.ID NO: 131). In the hybrid protein the TbpA loop 3 helix replaces loop 18 of the TbpB C-lobe, TbpA loop 10 replaces loop 21 of the TbpB C-lobe, TbpA loop 11 replaces loop 23 of the TbpB C-lobe, and the TbpA plug loop replaces loop 27 of the TbpB C-lobe.

FIGURE 18 depicts the microbial production of hybrid TbpA-TbpB C-lobes that were produced using the strategy described in **FIG 17. Panel A** illustrates the production of the recombinant fusion proteins with an N-terminal maltose binding protein (Mbp) fusion partner and **Panel B** illustrates the proteins after cleavage with TEV protease. The wild-type (WT) protein is the native M982 C-lobe (SEQ.ID NO: 125) and the Minus Loops is the C-lobe with all four loops removed (SEQ.ID NO: 129) that effectively serves as the scaffold for displaying the TbpA regions. Loop 10 refers to the protein with the extracellular loop region of TbpA inserted into the TbpB C-lobe loop 21 (SEQ.ID NO: 154). Loop 11 refers to the protein with the extracellular loop region of TbpA that was inserted into the TbpB C-lobe loop 23 (SEQ.ID NO: 156). Helix 3 refers to the segment of extracellular loop 3 of TbpA that was inserted into the TbpB C-lobe loop 27 (SEQ.ID NO: 158). Plug loop refers to the region from the plug domain of TbpA that was inserted into the TbpB C-lobe loop 18 (SEQ.ID NO: 160). Protein molecular weight standards (MWS) observed on these gels are 93, 70, 53, 41 and 22.

FIGURE 19 depicts the immunogenicity of the modified C-lobe of *N. meningitidis* strain M982 compared to the modified C-lobe with foreign loop regions from TbpA spliced into the modified loop sites. The endpoint titres of mouse antisera were determined with our custom ELISA

assay. Mice were either immunized with; (i) the 'loopless' C-lobe with all four loops removed (SEQ.ID NO: 129), (ii) the 'loopless' C-lobe with TbpA loop 10 inserted into the TbpB C-lobe loop 21(SEQ.ID NO: 154), (iii) the 'loopless' C-lobe with TbpA loop 11 inserted into the TbpB C-lobe loop 23 (SEQ.ID NO: 156), (iv) the 'loopless' C-lobe with TbpA loop 3 helix inserted into the TbpB C-lobe loop 27 (SEQ.ID NO: 158), or (v) the 'loopless' C-lobe with TbpA plug loop inserted into the TbpB C-lobe loop 18 (SEQ.ID NO: 160). The sera were tested against the hybrid TbpA-TbpB antigen in which the 'loopless' C-lobe has all four of the TbpA loops inserted (SEQ.ID NO: 131). The results show that all the hybrid antigens were immunogenic, at least as immunogenic as the 'loopless' C-lobe.

FIGURE 20 depicts the design and production of hybrid proteins displaying regions of LbpA (SEQ.ID NO: 162) on the TbpB C-lobe scaffold. **Panel A** is a structural model of LbpA highlighting the regions selected to 'transplant' onto the TbpB C-lobe. The LbpA loop 3 helix is colored darker grey and loop 2 is colored black. **Panel B** shows an alignment of the native C-lobe (C-lobe, SEQ.ID NO: 125), the loopless C-lobe scaffold (loopless C, SEQ.ID NO: 129) and the hybrid protein with the regions of LbpA displayed. In the hybrid protein the LbpA loop 2 replaces loop 21 of the TbpB C-lobe (SEQ.ID NO: 164) and the LbpA loop 3 helix replaces loop 18 of the TbpB C-lobe (SEQ.ID NO: 166). Protein molecular weight standards (MWS) observed on these gels are 100, 75, 63, and 48.

FIGURE 21 depicts the design of a 'conjugation loop' in the TbpB C-lobe from the human pathogen Haemophilus *influenzae.* **Panel A** shows the DNA and protein sequence for the gene encoding the hybrid gene with the DNA region encoding the conjugation loop shown in larger font (SEQ.ID NO: 167). The amino acids are shown in single letter code in which lysine is indicated by the letter K, of which there are 42 in the conjugation loop compared to 24 in the entire C-lobe (SEQ.ID NO: 168). **Panel B** illustrates a structural model of the *H. influenzae* TbpB C-lobe indicating the position for insertion of the conjugation loop. As illustrated, the conjugation loop is inserted into the handle domain of the C-lobe replacing loop L23 of the C-lobe (using the loop nomenclature used throughout this disclosure) **(FIG. 2).** It is noted that for illustrative purposes the model was created with a conjugation loop of 11 amino acids instead of the 91 in the actual protein.

FIGURE 22 depicts the transferrin binding properties of site-directed mutant TbpB proteins derived from recombinant truncated TbpB proteins from *A. pleuropneumoniae, A. suis* and *H. parasuis.* The recombinant truncated TbpB proteins were expressed as fusion proteins and tested for binding activity. Recombinant fusion proteins were initially screened for transferrin binding by a solid-phase binding assay and an affinity capture assay. The purified mutant proteins were then evaluated for binding to pTf either by isothermal calorimetry, surface plasmon resonance or biolayer interferomety(23-25). Several of the mutations resulted in a ≥ 100 fold increase in the affinity constant (Kd), such as the F171A mutation in the TbpB from *A. pleuropneumoniae* strain H49, the Y174A mutation in the TbpB from *A. pleuropneumoniae* strain H49 or the Y167A or W176A mutations in the TbpB from *H. parasuis* strain HP5. It is interesting to note that these mutants all map to loop 8.

FIGURE 23 depicts the enhanced ability of a site-directed mutant protein to induce a protective

immune response in the native host. In this figure the ability of the site-directed Y167A TbpB from *H. parasuis* strain HP5 (SEQ.ID NO: 174) is compared to the wild-type TbpB (SEQ.ID NO: 115), and controls including a commercial vaccine (Porcillis Glasser) and adjuvant alone. The pigs were challenged by intratracheal inoculation with 10^8 colony-forming units (cfus) of the Hp5 (Nagasaki) strain and were monitored for clinical signs and symptoms throughout the duration of the experiment. Animals with severe symptomatology were euthanized prior to the end of the experiment. The graph shows the survival curve from 24 to 108 hrs at 12 hr increments, and then connects to the final time point at 14 days.

FIGURE 24 depicts the cellular immune response induced by the native and mutant TbpB antigens. Panel A and Panel B illustrate the B-cell response on the day of challenge (after two IM immunizations) and 4 days (96 hrs) after challenge, respectively. Panel C and Panel D illustrate the T-helper cell response on the day of challenge and 4 days after challenge. The diamonds, triangles and squares represent pigs immunized with native TbpB, the Y167A mutant TbpB and the Porcilis Glässer (PG) vaccine, respectively. There are reduced numbers of samples for the native TbpB and PG vaccine treated pigs on the 4th day after challenge. The analysis was performed by FACS analysis with peripheral blood mononuclear cells. Significant differences between groups: *$p<0.05$, *** $p<0.001$.

FIGURE 25 depicts that immunization with recombinant truncated TbpB, recombinant truncated TbpB N-lobe or recombinant TbpB C-lobe from *N. meningitidis* provides protection from colonization in a humanized transgenic mouse model. In the experiment illustrated in **Panel A,** transgenic C57 black mice expressing the human CEACAM1 receptor were immunized with recombinant truncated TbpB from *N. meningitidis* strain M982 or with adjuvant alone on day 1 and day 21. Mice were subjected to intranasal inoculation with approximately 1×10^7 CFU of *N. meningitidis* strain M982 on day 35. The squares and circles represent the CFU recovered from individual mice 3 days after challenge (day 38). **Panel B** illustrates a follow up experiment in which mice were immunized either with recombinant truncated TbpB, recombinant truncated TbpB N-lobe, recombinant TbpB C-lobe, recombinant factor H binding protein or adjuvant alone on day 1 and day 21. As in Panel A, the number of CFUs of *N. meningitidis* strain M982 recovered 3 days after challenge in individual mice are plotted on the graph.

FIGURE 26 depicts the sequence diversity of TbpBs and TbpB C-lobes from the human pathogen Neisseria *gonorrhoeae.* **Panel A (FIG. 26A)** illustrates the sequence diversity of the intact TbpBs and **Panel B (FIG. 26B)** represents the sequence diversity for the TbpB C-lobes. Sequences for representative *N. meningitidis* TbpBs and TbpB C-lobes **(FIG. 10,** arrows and double arrows) were included in this analysis to determine to what extent the sequences for TbpBs and TbpB C-lobes from *N. gonorrhoeae* is a subset of the sequence diversity of that present in *N. meningitidis.* As for **FIG. 10,** representative *N. gonorrhoeae* TbpB sequences (SEQ ID NO: 207 to SEQ ID NO: 212) and TbpB C-lobe sequences (SEQ ID NO: 213 to SEQ ID NO: 218) indicated by arrows are included in appendix to provide a representation of the overall sequence diversity. As illustrated in **Panel A** there are two clusters of *N. gonorrhoeae* TbpBs that are sub-branches of meningococcal isotype 2 TbpBs. There is one larger cluster

most closely related to TbpB from meningococcal strain H44/76 and a smaller cluster most closely related to TbpB from strain P3306. The C-lobe tree in **Panel B** reveals that the *N. gonorrhoeae* TbpB C-lobes form a distinct cluster from the meningococcal TbpB C-lobes that are most closely related to the meningococcal isotype 2 TbpBs.

FIGURE 27 depicts the sequence diversity of TbpBs and TbpB C-lobes from the human pathogen *Haemophilus influenzae.* **Panel A (FIG. 27A)** illustrates the sequence diversity of the intact TbpBs and **Panel B (FIG. 27B)** represents the sequence diversity for the TbpB C-lobes. Representative *H. influenzae* TbpB sequences (SEQ ID NO: 196-204) indicated by arrows are included in the appendix to provide a representation of the overall sequence diversity. As illustrated in **Panel A** there are three main clusters (groups) of *H. influenzae* TbpBs that include type b and non-typeable *H. influenzae* strains intermixed, indicating that the TbpB diversity is not linked to any other attribute such as presence of capsule. There are also three main groups of C-lobe diversity.

FIGURE 28 depicts the sequence diversity of TbpBs amongst the ruminant pathogens *Mannheimia haemolytica, Mannheimia glucosida* and *Bibersteinia trehalosi* (also known to the art as *Pasteurella haemolytica* and P. *trehalosi,* respectively). Arrows indicate representative sequences included in the SEQ.ID NO: listing.

FIGURE 29 depicts the sequence diversity of TbpBs from *Moraxella catarrhalis.* Arrows indicate the representative sequences of TbpBs from the three main clusters that are included in the SEQ.ID NO: listing.

FIGURE 30 depicts an illustrative phylogenetic tree.

[0038] TABLES 1-3 represent combinations of 1, 2 or 3 loop domains, respectively, selected from the loop domains L1-L32 of HIBP polypeptides, which may be modified in accordance with the present disclosure.

☑

signifies a loop domain or combination of loop domains that may be modified in accordance with certain aspects of the current disclosure.

☒

signifies a non-permitted combination of loop domains in accordance with certain aspects of the current disclosure.

☐

signifies a combination of permitted loop domains, displayed however by a

☑

elsewhere in the same table, in accordance with certain aspects of the current disclosure.

DETAILED DESCRIPTION OF THE DISCLOSURE

[0039] Various compositions and methods are described below. No disclosure below limits any

claimed subject matter and any claimed subject matter may cover methods, processes, compositions or systems that differ from those described below. The claimed subject matter is not limited to compositions or methods having all of the features of any one composition, method, system or process described below or to features common to multiple or all of the compositions, systems or methods described below. It is possible that a composition, system, method or process described below is not an embodiment of any claimed subject matter. Any subject matter disclosed in a composition, system, method or process described below that is not claimed in this document may be the subject matter of another protective instrument, for example, a continuing patent application, and the applicants, inventors or owners do not intend to abandon, disclaim or dedicate to the public any such subject matter by its disclosure in this document.

[0040] It should be noted that terms of degree such as "substantially", "essentially" "about" and "approximately" as used herein mean a reasonable amount of deviation of the modified term such that the end result is not significantly changed. These terms of degree should be construed as including a deviation of the modified term if this deviation would not negate the meaning of the term it modifies.

[0041] As used herein, the wording "and/or" is intended to represent an inclusive-or. That is, "X and/or Y" is intended to mean X or Y or both, for example. As a further example, "X, Y, and/or Z" is intended to mean X or Y or Z or any combination thereof.

[0042] As hereinbefore mentioned, the present disclosure provides novel immunogenic compositions, and in particular immunogenic compositions based on the HIBP surface receptor proteins from Gram-negative pathogenic bacterial species, such as *Neisseria meningitidis.* The immunogenic compositions of the present disclosure are useful in that they may be employed to prepare novel vaccine formulations to protect humans and animals against infective pathogenic Gram-negative bacterial species. In accordance with the present disclosure, the HIBP surface receptor proteins of the present disclosure are modified in such a manner that they are unable to substantially bind host iron binding proteins. Such modified HIBP surface receptor proteins exhibit unexpectedly strong immunogenic properties. Furthermore the immunogenic compositions of the present disclosure are substantially stable polypeptides and therefore may readily be manufactured. Moreover, and importantly, the immunogenic compositions of the present disclosure are unexpectedly effective, for example by inducing a cross-reactive immune response, thus permitting protection against multiple pathogenic microbial organisms by the administration of a single efficacious vaccinating compound. The vaccines prepared in accordance with the present disclosure do not contain live organisms or crude extracts, thereby representing a very limited health risk.

[0043] Accordingly, the present disclosure provides, in at least one aspect, an immunogenic composition comprising an HIBP surface receptor protein from a Gram-negative pathogenic bacterial species, wherein the HIBP surface receptor protein has been modified in such a manner that it is unable to substantially bind host iron binding protein.

[0044] The present disclosure further provides an immunogenic composition comprising a polypeptide comprising a C-lobe domain or an N-lobe domain of an HIBP surface receptor protein obtainable from a Gram-negative pathogenic bacterial species, wherein the polypeptide is unable to substantially bind host iron binding protein. In certain aspects, the N-lobe domain or the C-lobe domain of the HIBP surface receptor protein comprises a plurality of β-strands connected by a plurality of loop domains, and one of more loop domains of the plurality of loop domains has been modified.

Terms and Definitions

[0045] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which the disclosure pertains. It is further noted that, as used in this specification and the appended claims, the singular forms "a", "an", and "the" include plural referents unless the content clearly dictates otherwise. Thus, for example, reference to "an immunogen" includes a mixture of two or more such agents, reference to "a polypeptide" includes reference to mixtures of two or more polypeptides, reference to "a cell" includes two or more such cells, and the like.

[0046] The terms "immunogen" and "immunogenic composition", as interchangeably used herein, are used in their broadest sense to refer to a molecule which contains one or more epitopes that will stimulate the immune response in a host organism to generate a cellular immunogen-specific immune response, and/or a humoral antibody response. Immunogens include nucleic acids, proteins, polypeptides, peptides and immunogenic protein fragments.

[0047] The terms "vaccine" and "vaccine composition", as interchangeably used herein, refer to any pharmaceutical composition containing an immunogen, which composition can be used to prevent or treat a disease or condition in a subject. The terms thus encompass subunit vaccines, i.e., vaccine compositions containing immunogens which are separate and discrete from a whole organism with which the immunogen is associated in nature.

[0048] The term "vertebrate subject" refers to any member of the subphylum Chordata, particularly mammals, including, without limitation, humans and other primates. The term does not denote a particular age. Thus both newborn, infant, child and adult individuals are intended to be covered.

[0049] The interchangeably herein used terms "HIBP surface receptor protein", "HIBP surface receptor polypeptide", "host iron binding protein surface receptor protein" or "host iron binding protein surface polypeptide" refer to any membrane anchored protein or polypeptide obtainable from a Gram-negative bacterial species capable of interacting with host iron-binding proteins. The term includes, any TbpB and LbpB proteins. HIBP surface receptor proteins when folded in their native three-dimensional structure, are comprised of a bi-lobal structure comprising an N-lobe domain and a C-lobe domain, the N-lobe domain and the C-lobe domain each comprising a plurality of β-strands assembled in a β-barrel, and a plurality of β-strands

assembled in a β-sheet structure adjacent to the β-barrel, referred to as the handle domain, wherein the β-strands are connected by a plurality of loop domains (as further illustrated in **FIG. 1).** The terms further refer to any and all HIBP surface receptor polypeptide sequences including all bacterial HIBP surface receptor polypeptides, including, without limitation, those set forth in SEQ.ID NO: 2; SEQ.ID NO: 12; SEQ.ID NO: 28; SEQ.ID NO: 107 to SEQ.ID NO: 115; SEQ ID NO: 117; SEQ.ID NO: 123; SEQ.ID NO: 131 to SEQ.ID NO: 147; SEQ.ID NO: 177; SEQ.ID NO: 178; SEQ.ID NO: 196 to SEQ.ID NO: 204; SEQ.ID NO: 206 to SEQ.ID NO: 212; and SEQ.ID NO: 219 to SEQ.ID NO: 228, and those comprising a sequence of amino acid residues which (i) are substantially identical to the amino acid sequences constituting any HIBP surface receptor protein set forth herein; (ii) are encoded by a nucleic acid sequence capable of hybridizing under at least moderately stringent conditions to any nucleic acid sequence encoding any HIBP surface receptor protein set forth herein or capable of hybridizing under at least moderately stringent conditions to any nucleic acid sequence encoding any HIBP surface receptor protein set forth herein, but for the use of synonymous codons. The terms further include any HIBP surface receptor protein precursor polypeptide; or (iii) will use transferrin binding proteins, lactoferrin binding proteins or their subdomains as templates when submitted to a structural modeling server such as Phyre2 (http://www.sbg.bio.ic.ac.uk/phyre2/) or Swiss-Model (http://swissmodel.expasy.org/), in the latter selecting automated mode. The terms further include mature TbpB polypeptides as well as any HIBP surface receptor polypeptide precursor, including any pre-HIBP surface receptor polypeptide precursor, or HIBP surface receptor polypeptide precursor comprising an N-terminal or other signal sequence.

[0050] The interchangeably herein used terms "integral outer membrane protein" and "IOM protein" refer to any integral outer membrane protein from Gram-negative bacterial species, including any proteins belonging to the TonB dependent subclass of proteins, which when folded in their native 3 dimensional structure comprise a 22-stranded C-terminal beta-barrel domain and N-terminal plug or cork domain capable of filling a channel in the C-terminal beta-barrel domain. The term includes without limitation TbpA and LbpA protein. The terms further refer to any and all IOM polypeptide sequences including those set forth in SEQ.ID NO: 152; and SEQ.ID NO: 162 and those comprising a sequence of amino acid residues which (i) are substantially identical to the amino acid sequences constituting any IOM protein set forth herein; (ii) are encoded by a nucleic acid sequence capable of hybridizing under at least moderately stringent conditions to any nucleic acid sequence encoding any IOM protein set forth herein or capable of hybridizing under at least moderately stringent conditions to any nucleic acid sequence encoding any IOM protein set forth herein, but for the use of synonymous codons. The terms further include any IOM protein precursor polypeptide; or (iii) will use 3V8X or their subdomains as templates when submitted to a structural modeling server such as Phyre2 (http://www.sbg.bio.ic.ac.uk/phyre2/) or Swiss-Model (http://swissmodel.expasy.org/), in the latter selecting automated mode.

[0051] The term "N-lobe domain" as used herein refers to the N-terminal portion of a HIBP surface receptor protein comprising a plurality of β-strands connected by a plurality of loop domains, wherein some of the β-strands are configured to form a β-barrel and an adjacent β-sheet structure, termed a handle domain (see: **FIG 1;** amino acid residue 46 to amino acid

residue 342). The term N-lobe domain further includes, without limitation all polypeptides having the sequence set forth in SEQ.ID NO: 8; SEQ.ID NO: 10; SEQ.ID NO: 24; SEQ.ID NO: 26; SEQ.ID NO: 36; SEQ.ID NO: 38; SEQ.ID NO: 121; SEQ.ID NO: 127; SEQ.ID NO: 229; SEQ.ID NO: 231; and SEQ.ID NO: 233.

[0052] The term "C-lobe domain" as used herein refers to the C-terminal portion of a HIBP surface receptor protein comprising a plurality of β-strands connected by a plurality of loop domains, wherein some of the β-strands are configured to form a β-barrel and an adjacent β-sheet structure termed a handle domain. Referring further to **FIG. 1** and **FIG. 2,** the C-lobe handle domain is the contiguous polypeptide domain from β-strand 16 onwards and up to and including β-strand 23 which, in the case of the in **FIG. 2** depicted ApH49, ApH57 and ApH87 TbpB polypeptides, consists of amino acid residues 344 to 431, and in SEQ.ID. NO: 2 from amino acid residue 314 to amino acid residue 401 (ApH 49), in SEQ.ID. NO: 27 from amino acid residue 363 to amino acid residue 450 (ApH 57), and in SEQ.ID. NO: 12 from amino acid residue 315 to amino acid residue 401 (ApH 87). The C-lobe β-barrel domain is the contiguous polypeptide domain from β-strand 23 onwards through to the C-terminus of the polypeptide, which, in the case of the in **FIG. 2** depicted ApH49, ApH57 and ApH87 TbpB polypeptides, is the polypeptide chain from amino acid reside 443 onwards and up to the C-terminus, and in SEQ.ID. NO: 2 from amino acid residue 413 onwards (ApH 49), in SEQ.ID. NO: 27 from amino acid residue 462 onwards (ApH 57), and in SEQ.ID. NO: 12 from amino acid residue 413 onwards. It is noted that the C-lobe handle domain and the C-lobe β-barrel domain may be connected by a short loop (denoted as "L24" in **FIG. 1** and **FIG. 2).** It is further noted that the term C-lobe domain, as used herein, is specifically intended to include, not only the C-lobe β-barrel domain, but also the handle domain forming a β-sheet structure, comprised typically of approximately 90 or more amino acid residues, and located N-terminally relative to the C-lobe β-barrel structure. The term C-lobe domain, as used herein, further includes, without limitation all polypeptides set forth in SEQ.ID NO: 5; SEQ.ID NO: 6; SEQ.ID NO: 22; SEQ.ID NO: 33; SEQ.ID NO: 34; SEQ.ID NO: 119; SEQ.ID NO: 125; SEQ.ID NO: 179 to SEQ.ID NO: 195; SEQ.ID NO: 213 to SEQ.ID NO: 218; SEQ.ID NO: 230; SEQ.ID NO: 232; SEQ.ID NO: 234 to SEQ.ID NO: 278; and SEQ.ID NO: 288 to SEQ.ID NO: 292.

[0053] The term "loop domain" refers to the polypeptide sequences in a HIBP surface receptor protein that connect two β-strands. These polypeptide sequences may vary considerably in length from several amino acid residues to 150 or more amino acid residues.

[0054] The terms "TbpB", "TbpB protein", "TbpB polypeptide", as interchangeably used herein, refer to any and all transferrin binding protein B sequences, including all bacterial TbpB polypeptides and polypeptides comprising a sequence of amino acid residues which is (i) substantially identical to the amino acid sequences constituting any TbpB polypeptides set forth herein, including, without limitation, SEQ.ID NO: 2; SEQ.ID NO: 12; SEQ.ID NO: 28; SEQ.ID NO: 107 to SEQ.ID NO: 115; SEQ ID NO: 117; SEQ.ID NO: 123; SEQ.ID NO: 131 to SEQ.ID NO: 147; SEQ.ID NO: 177; SEQ.ID NO: 178; SEQ.ID NO: 196 to SEQ.ID NO: 204; SEQ.ID NO: 206 to SEQ.ID NO: 212; and SEQ.ID NO: 219 to SEQ.ID NO: 228, or (ii) encoded by a nucleic acid sequence capable of hybridizing under at least moderately stringent conditions to any

nucleic acid sequence encoding any TbpB polypeptide set forth herein or capable of hybridizing under at least moderately stringent conditions to any nucleic acid sequence encoding any TbpB polypeptide set forth herein, but for the use of synonymous codons. The terms further include mature TbpB polypeptides as as well as any TbpB precursor, including any pre-TbpB, or TbpB comprising an N-terminal or other signal sequence.

[0055] The terms "LbpB", "LbpB protein", "LbpB polypeptide", as interchangeably used herein, refer to any and all lactoferrin binding protein B sequences including all bacterial LbpB polypeptides and a polypeptides comprising a sequence of amino acid residues which is (i) substantially identical to the amino acid sequences constituting any LbpB polypeptides set forth herein, including, without limitation, SEQ.ID NO: 285 or (ii) encoded by a nucleic acid sequence capable of hybridizing under at least moderately stringent conditions to any nucleic acid sequence encoding any LbpB polypeptide set forth herein or capable of hybridizing under at least moderately stringent conditions to any nucleic acid sequence encoding any LbpB polypeptide set forth herein, but for the use of synonymous codons. The terms further include any LbpB precursor, including pre-LbpB.

[0056] The terms "TbpA", "TbpA protein", "TbpA polypeptide", as interchangeably used herein, refer to any and all transferrin binding protein A sequences including all bacterial TbpA polypeptides and polypeptides comprising a sequence of amino acid residues which is (i) substantially identical to the amino acid sequences constituting any TbpA polypeptides set forth herein, including, without limitation, SEQ.ID NO: 152 or (ii) encoded by a nucleic acid sequence capable of hybridizing under at least moderately stringent conditions to any nucleic acid sequence encoding any TbpA polypeptide set forth herein or capable of hybridizing under at least moderately stringent conditions to any nucleic acid sequence encoding any TbpA polypeptide set forth herein, but for the use of synonymous codons. The terms further include any TbpA precursor, including pre-TbpA.

[0057] The terms "LbpA", "LbpA protein", "LbpA polypeptide", as interchangeably used herein, refer to any and all lactoferrin binding protein A sequences including all bacterial LbpA polypeptides and a polypeptides comprising a sequence of amino acid residues which is (i) substantially identical to the amino acid sequences constituting any LbpA polypeptides set forth herein, including, without limitation, SEQ.ID NO: 162, or (ii) encoded by a nucleic acid sequence capable of hybridizing under at least moderately stringent conditions to any nucleic acid sequence encoding any LbpA polypeptide set forth herein or capable of hybridizing under at least moderately stringent conditions to any nucleic acid sequence encoding any LbpA polypeptide set forth herein, but for the use of synonymous codons. The terms further include any LbpA precursor, including pre-LbpA.

[0058] The term "nucleic acid sequence" as used herein refers to a sequence of nucleoside or nucleotide monomers consisting of naturally occurring bases, sugars and intersugar (backbone) linkages. The term also includes modified or substituted sequences comprising non-naturally occurring monomers or portions thereof. The nucleic acid sequences of the present disclosure may be deoxyribonucleic acid sequences (DNA) or ribonucleic acid

sequences (RNA) and may include naturally occurring bases including adenine, guanine, cytosine, thymidine and uracil. The sequences may also contain modified bases. Examples of such modified bases include aza and deaza adenine, guanine, cytosine, thymidine and uracil, and xanthine and hypoxanthine.

[0059] The herein interchangeably used terms "nucleic acid sequence encoding a HIBP surface receptor protein" and "nucleic acid sequence encoding a HIBP surface receptor polypeptide", refer to any and all nucleic acid sequences encoding a HIBP surface receptor protein, including any HIBP surface receptor protein and any nucleic acid sequences that encode HIBP surface receptor protein precursors, including, without limitation, those set forth in SEQ.ID NO: 1; SEQ.ID NO: 11; SEQ.ID NO: 27; SEQ.ID NO: 116; SEQ.ID NO: 122; and SEQ.ID NO: 173. As used herein "HIBP surface receptor protein precursor" refers to a HIBP surface receptor protein molecule additionally comprising an N-terminal signal sequence which facilitates export of the polypeptide chain across the cytoplasmic membrane. Nucleic acid sequences encoding a HIBP surface receptor protein further include any and all nucleic acid sequences which (i) encode polypeptides that are substantially identical to the HIBP surface receptor proteins sequences set forth herein; or (ii) hybridize to any HIBP surface receptor protein nucleic acid sequences set forth herein under at least moderately stringent hybridization conditions or which would hybridize thereto under at least moderately stringent conditions but for the use of synonymous codons.

[0060] The herein interchangeably used terms "nucleic acid sequence encoding an IOM protein" and "nucleic acid sequence encoding an IOM polypeptide", refer to any and all nucleic acid sequences encoding an IOM protein, including any IOM protein and any nucleic acid sequences that encode IOM protein precursors, including, without limitation, those set forth in SEQ.ID NO: 151 and SEQ.ID NO: 161. As used herein "IOM protein precursor" refers to an IOM protein molecule additionally comprising an N-terminal signal sequence which facilitates export of the polypeptide chain across the cytoplasmic membrane. Nucleic acid sequences encoding a IOM protein further include any and all nucleic acid sequences which (i) encode polypeptides that are substantially identical to the IOM proteins sequences set forth herein; or (ii) hybridize to any IOM protein nucleic acid sequences set forth herein under at least moderately stringent hybridization conditions or which would hybridize thereto under at least moderately stringent conditions but for the use of synonymous codons.

[0061] The herein interchangeably used terms "nucleic acid sequence encoding TbpB"; "nucleic acid sequence encoding a TbpB polypeptide", refer to any and all nucleic acid sequences encoding a TbpB polypeptide, including any TbpB polypeptide, including, without limitation, the sequences set forth in SEQ.ID NO: 1; SEQ.ID NO: 11; SEQ.ID NO: 27; SEQ.ID NO: 116; SEQ.ID NO: 122; and SEQ.ID NO: 173, and further including any nucleic acid sequences that encode TbpB precursors. As used herein "TbpB precursor" refers to a TbpB molecule additionally comprising an N-terminal signal sequence which facilitates export of the polypeptide chain across the cytoplasmic membrane. Nucleic acid sequences encoding a TbpB polypeptide further include any and all nucleic acid sequences which (i) encode polypeptides that are substantially identical to the TbpB polypeptide sequences set forth herein; or (ii)

hybridize to any TbpB nucleic acid sequences set forth herein under at least moderately stringent hybridization conditions or which would hybridize thereto under at least moderately stringent conditions but for the use of synonymous codons.

[0062] The herein interchangeably used terms "nucleic acid sequence encoding LbpB"; "nucleic acid sequence encoding a LbpB polypeptide", refer to any and all nucleic acid sequences encoding a LbpB polypeptide, including any LbpB polypeptide, including, without limitation the sequence set forth in SEQ.ID NO: 284 and any nucleic acid sequences that encode LbpB precursors. As used herein "LbpB precursor" refers to a LbpB molecule additionally comprising an N-terminal signal sequence which facilitates export of the polypeptide chain across the cytoplasmic membrane. Nucleic acid sequences encoding a LbpB polypeptide further include any and all nucleic acid sequences which (i) encode polypeptides that are substantially identical to the LbpB polypeptide sequences set forth herein; or (ii) hybridize to any LbpB nucleic acid sequences set forth herein under at least moderately stringent hybridization conditions or which would hybridize thereto under at least moderately stringent conditions but for the use of synonymous codons.

[0063] The herein interchangeably used terms "nucleic acid sequence encoding TbpA"; "nucleic acid sequence encoding a TbpA polypeptide", refer to any and all nucleic acid sequences encoding a TbpA polypeptide, including any TbpA polypeptide, including, without limitation, the nucleic acid sequence set forth in SEQ.ID NO: 151, and any nucleic acid sequences that encode TbpA precursors. As used herein "TbpA precursor" refers to a TbpA molecule additionally comprising an N-terminal signal sequence which facilitates export of the polypeptide chain across the cytoplasmic membrane. Nucleic acid sequences encoding a TbpA polypeptide further include any and all nucleic acid sequences which (i) encode polypeptides that are substantially identical to the TbpA polypeptide sequences set forth herein; or (ii) hybridize to any TbpA nucleic acid sequences set forth herein under at least moderately stringent hybridization conditions or which would hybridize thereto under at least moderately stringent conditions but for the use of synonymous codons.

[0064] The herein interchangeably used terms "nucleic acid sequence encoding LbpA"; "nucleic acid sequence encoding a LbpA polypeptide", refer to any and all nucleic acid sequences encoding a LbpA polypeptide, including any LbpA polypeptide, including, without limitation, the nucleic acid sequence set forth in SEQ.ID NO: 161 and any nucleic acid sequences that encode LbpA precursors. As used herein "LbpA precursor" refers to a LbpA molecule additionally comprising an N-terminal signal sequence which facilitates export of the polypeptide chain across the cytoplasmic membrane. Nucleic acid sequences encoding a LbpA polypeptide further include any and all nucleic acid sequences which (i) encode polypeptides that are substantially identical to the LbpA polypeptide sequences set forth herein; or (ii) hybridize to any LbpA nucleic acid sequences set forth herein under at least moderately stringent hybridization conditions or which would hybridize thereto under at least moderately stringent conditions but for the use of synonymous codons.

[0065] By the term "substantially identical" it is meant that two polypeptide sequences

preferably are at least 50% identical, and more preferably are at least 85% identical and most preferably at least 95% identical, for example 96%, 97%, 98% or 99% identical. In order to determine the percentage of identity between two polypeptide sequences the amino acid sequences of such two sequences are aligned, using for example the alignment method of Needleman and Wunsch (26), as revised by Smith and Waterman (27) so that the highest order match is obtained between the two sequences and the number of identical amino acids is determined between the two sequences. A preferred, broadly applicable, method for accurately aligning two polypeptides involves the Clustal W algorithm (28) employed with the BLOSUM 62 scoring matrix (29) using a gap opening penalty of 10 and a gap extension penalty of 0.1. This enables identification of high scoring alignments between two sequences, wherein at least 50% of the total length of one of the two sequences is involved in the alignment. Methods to calculate the percentage identity between two aligned amino acid sequences are generally art recognized and include, for example, those described by Carillo and Lipton (30) and those described in Computational Molecular Biology, Lesk, e.d. Oxford University Press, New York, 1988, Biocomputing: Informatics and Genomics Projects. Generally, computer programs will be employed for such calculations. Computer programs that may be used in this regard include, but are not limited to, GCG (31) BLASTP, BLASTN and FASTA (32).

[0066] By "at least moderately stringent hybridization conditions" it is meant that conditions are selected which promote selective hybridization between two complementary nucleic acid molecules in solution. Hybridization may occur to all or a portion of a nucleic acid sequence molecule. The hybridizing portion is typically at least 15 (e.g. 20, 25, 30, 40 or 50) nucleotides in length. Those skilled in the art will recognize that the stability of a nucleic acid duplex, or hybrids, is determined by the Tm, which in sodium containing buffers is a function of the sodium ion concentration and temperature (Tm=81.5° C.-16.6 (Log10 [Na+])+0.41(% (G+C)-600/l), or similar equation). Accordingly, the parameters in the wash conditions that determine hybrid stability are sodium ion concentration and temperature. In order to identify molecules that are similar, but not identical, to a known nucleic acid molecule a 1% mismatch may be assumed to result in about a 1° C. decrease in Tm, for example if nucleic acid molecules are sought that have a >95% identity, the final wash temperature will be reduced by about 5° C. Based on these considerations those skilled in the art will be able to readily select appropriate hybridization conditions. In preferred aspects of the disclosure, stringent hybridization conditions are selected. By way of example the following conditions may be employed to achieve stringent hybridization: hybridization at 5× sodium chloride/sodium citrate (SSC)/5×Denhardt's solution/1.0% SDS at Tm (based on the above equation) -5° C, followed by a wash of 0.2×SSC/0.1% SDS at 60° C. Moderately stringent hybridization conditions include a washing step in 3×SSC at 42° C. It is understood however that equivalent stringencies may be achieved using alternative buffers, salts and temperatures. Additional guidance regarding hybridization conditions may be found in: Green and Sambrook, Molecular Cloning, a Laboratory Manual, Cold Spring Harbor Laboratory Press, 2012 (33).

[0067] The term "chimeric" as used herein in the context of nucleic acid sequences refers to at least two linked nucleic acid sequences which are not naturally linked. Chimeric nucleic acid

sequences include linked nucleic acid sequences of different natural origins. For example, a nucleic acid sequence constituting a bacterial promoter linked to a nucleic acid sequence of a TbpB polypeptide or a HIBP surface receptor protein is considered chimeric, and a nucleic acid sequence encoding a TbpB polypeptide from which certain portions have been removed and replaced with portions of a TbpA polypeptide is considered chimeric. Chimeric nucleic acid sequences also may comprise nucleic acid sequences of the same natural origin, provided they are not naturally linked. For example a nucleic acid sequence constituting a promoter obtained from a particular cell-type may be linked to a nucleic acid sequence encoding a polypeptide obtained from that same cell-type, but not normally linked to the nucleic acid sequence constituting the promoter. Chimeric nucleic acid sequences also include nucleic acid sequences comprising any naturally occurring nucleic acid sequence linked to any non-naturally occurring nucleic acid sequence.

[0068] By the term "substantially unable to bind host iron binding protein" it is meant that the ability of the host iron binding protein to bind to the HIBP surface receptor protein is diminished in such a manner that the value of the binding constant (Kd) or dissociation constant of the binding interaction between the native host iron binding protein (i.e. the host iron binding protein present in the host organism) and the modified HIBP surface receptor protein is at least 10X higher than the value of the binding constant of the binding interaction between the native host iron binding protein and its complementary native HIBP surface receptor protein. In other words, the modified proteins have a 10X lower affinity for binding native host iron binding protein than the native receptor protein. In preferred aspects of the disclosure, the relative affinity for binding native host iron binding protein by the modified protein is 30X lower than that of the native HIBP surface receptor protein, and, in most preferred aspects, the relative affinity for binding native host iron binding protein by the modified protein is 100X lower than that of the native HIBP surface receptor protein. In further preferred aspects, the binding constant between the modified HIBP surface receptor protein and the native host iron binding protein is at least 300 nM. Preferably the binding constant is at least 500 nM, and most preferably at least 1 μM.

[0069] The term "substantially free" as used herein is a term of degree meaning that a composition does not contain significant amounts of a compound of which the composition is said to be substantially free of. When a composition is substantially free of a compound, for example substantially free of N-lobe domain, such composition comprises preferably less than 5.0% of such compound, more preferably less than 1.0 % of such compound, and most preferably less than 0.1% of such compound.

Immunogenic Compositions

[0070] As hereinbefore mentioned, the present disclosure provides, in at least one aspect, an immunogenic composition comprising an HIBP surface receptor protein from a Gram-negative pathogenic bacterial species, wherein the HIBP surface receptor protein has been modified in such a manner that it is unable to substantially bind a host iron binding protein. The term

"modified" in conjunction with a HIBP surface receptor protein is intended to refer to a non-native HIBP surface receptor protein from which at least one amino acid residue has been removed or in which at least one amino acid residue has been replaced by another, or an HIBP surface receptor protein which has been fragmented in two or more separate polypeptides. Thus modified HIBP surface receptor proteins include, without limitation, truncated HIBP surface receptor proteins (e.g. an N-lobe domain or C-lobe domain of an HIBP surface receptor protein); HIBP surface receptor proteins from which one or more amino acid residues have been removed (e.g. an HIBP surface receptor protein from which one or more amino acids from the loop-domains within the N-lobe domain or C-lobe domain have been removed); HIBP surface receptor proteins in which additional amino acids have been inserted (e.g. HIBP surface receptor proteins in which one or more amino acids have been added to the loop-domains within the N-lobe domain or C-lobe domain); multimeric or extended HIBP polypeptides (e.g. dimers and trimers and N-lobe domain or C-lobe domain dimers and trimers); HIBP surface receptor proteins which have been modified by site-directed mutagenesis to alter one or more amino acids; and mixtures of two or more HIBP surface receptor protein polypeptides (e.g. a mixture comprising a separate N-lobe domains and a C-lobe domains of an HIBP surface receptor protein). The modified HIBP surface receptor proteins of the present disclosure are unable to substantially bind native host iron binding protein.

[0071] As hereinbefore mentioned, the present disclosure provides, in one aspect, an immunogenic composition comprising or consisting of a polypeptide comprising a C-lobe domain or an N-lobe domain of an HIBP surface receptor protein obtainable from or obtained from a Gram-negative bacterial species, wherein the polypeptide is unable to substantially bind host iron binding protein. In further aspects, the present disclosure provides a polypeptide comprising a C-lobe domain or an N-lobe domain of an HIBP surface receptor protein wherein the C-lobe domain or the N-lobe domain comprises a plurality of β-strands connected by a plurality of loop domains, and wherein at least one loop domain of the plurality of loop domains has been modified, and wherein the polypeptide is unable to substantially bind host iron binding protein.

[0072] In accordance with the present disclosure, any polypeptide or nucleic acid sequence encoding such polypeptide, comprising or consisting of a C-lobe domain or an N-lobe domain of an HIBP surface receptor protein obtainable from a Gram-negative pathogenic bacterial species may be used.

[0073] In aspects of the disclosure where the native C-lobe domain is used, the polypeptide comprising the native C-lobe domain does not comprise and is not chemically linked via a peptide bond to the native N-lobe domain of the HIBP surface receptor protein, and is thus an isolated native C-lobe domain, i.e. a native C-lobe domain separated from the native N-lobe domain. Thus in certain aspects, preparations comprising a C-lobe domain of an HIBP surface receptor polypeptide free or substantially free of N-lobe domain of an HIBP surface receptor polypeptide, or portions thereof, are provided. In aspects of the disclosure where the native N-lobe domain is used, the polypeptide comprising the native N-lobe domain used herein does

not comprise and is not chemically linked via a peptide bond to the native C-lobe domain of the HIBP surface receptor protein, and is thus an isolated native N-lobe domain, i.e. an N-lobe domain separated from the native C-lobe domain. Thus in certain aspects, preparations comprising an N-lobe domain of an HIBP surface receptor polypeptide free or substantially free of C-lobe domain of an HIBP surface receptor polypeptide, or portions thereof, are provided. In certain aspects however, a mixture of a native C-lobe domain, or portions thereof, and the native N-lobe domain, or portions thereof, may be used, provided however, that the N-lobe domain and the C-lobe domain are not chemically linked, i.e. they are not chemically connected by a peptide bond. Thus the present disclosure includes an immunogenic composition comprising a mixture of polypeptides comprising an N-lobe domain and a polypeptide comprising a C-lobe domain, wherein the N-lobe domain and C-lobe domain are not physically linked.

[0074] To source the polypeptides of the present disclosure any HIBP surface receptor protein, or TbpB polypeptide obtainable from or obtained from any Gram-negative bacterial species may be used, including, but not limited to, any pathogenic bacterial species or strain, and including, but not limited to, any bacterial species belonging to the bacterial families of Pasteurellaceae, Moxarellaceae or Neisseriaceae, and bacterial species belonging to the bacterial genus *Actinobacillus, Neisseria, Haemophilus, Mannheimia, Histophilus, Pasteurella* or *Moraxella.* The polypeptides further include any polypeptides obtainable from or obtained from any HIBP surface receptor protein, or any polypeptides obtainable from or obtained from any TbpB polypeptide obtainable or obtained from the following bacterial species: *Actinobacillus pleuropneumoniae* (12, 34), *Actinobacillus suis, Haemophilus influenzae* (35, 36), *Haemophilus parasuis* (37), *Haemophilus somnus* (also known to the art as *Histophilus somnus)* (38), *Mannheimia haemolytica* (also known to the art as *Pasteurella haemolytica)* (39), *Moraxella catarrhalis* (40), *Moraxella bovis, Neisseria gonorrhoeae, Neisseria meningitidis* (41, 42), *Mannheimia glucosida* (also known to the art as *Pasteurella haemolytica)* and *Bibersteinia trehalosi* (also known to the art as *Pasteurella trehalosi).*

[0075] Exemplary C-lobe domain and N-lobe domain polypeptides that may be used in accordance herewith further include, any C-lobe domain set forth in SEQ.ID NO: 5; SEQ.ID NO: 6; SEQ.ID NO: 22; SEQ.ID NO: 33; SEQ.ID NO: 34; SEQ.ID NO: 119; SEQ.ID NO: 125; SEQ.ID NO: 179 to SEQ.ID NO: 195; SEQ.ID NO: 213 to SEQ.ID NO: 218; SEQ.ID NO: 230; SEQ.ID NO: 232; SEQ.ID NO: 234 to SEQ.ID NO: 278, and SEQ.ID NO: 288 to SEQ.ID NO: 292, and any N-lobe domain set forth in SEQ.ID NO: 8; SEQ.ID NO: 10; SEQ.ID NO: 24; SEQ.ID NO: 26; SEQ.ID NO: 36; SEQ.ID NO: 38; SEQ.ID NO: 121; SEQ.ID NO: 127; SEQ.ID NO: 229; SEQ.ID NO: 231; and SEQ.ID NO: 233, and further include any C-lobe domain or N-lobe domain that may be prepared from a HIBP polypeptide or a TbpB polypeptide including, without limitation the polypeptides set forth in SEQ.ID NO: 2; SEQ.ID NO: 12; SEQ.ID NO: 28; SEQ.ID NO: 107 to SEQ.ID NO: 115; SEQ ID NO: 117; SEQ.ID NO: 123; SEQ.ID NO: 131 to SEQ.ID NO: 147; SEQ.ID NO: 177; SEQ.ID NO: 178; SEQ.ID NO: 196 to SEQ.ID NO: 204; SEQ.ID NO: 206 to SEQ.ID NO: 212; and SEQ.ID NO: 219 to SEQ.ID NO: 228 or by using the nucleic acid sequences encoded by SEQ.ID NO: 1; SEQ.ID NO: 11; SEQ.ID NO: 27; SEQ.ID NO: 116; SEQ.ID NO: 122; and SEQ.ID NO: 173. Using these nucleic acid sequences and

polypeptide sequences, additional novel HIBP surface receptor proteins and TbpB sequences, and C-lobe domains or N-lobe domains may readily be identified by those of skill in the art. For example expression libraries, cDNA libraries and genomic libraries may be screened and databases comprising sequence information may be searched for similar sequences.

[0076] The immunogenic preparations of the present disclosure elicit, upon administration thereof to a vertebrate subject, an immune response in such vertebrate subject, in the form of the stimulation of antibody production by the vertebrate subject. In accordance herewith, such antibodies are reactive against at least one Gram-negative bacterial strain. Preferably, however, the antibodies are cross-reactive and/or cross-protective against a plurality of bacterial strains or species, and preferably such cross-reactivity and/or cross-protection is attained in a host expressing one or more host iron binding proteins, such as transferrin or lactoferrin. The term "cross-reactive" as used herein refers to the ability of the immune response induced by an immunogenic composition obtained from one bacterial strain to stimulate the production of antibodies capable of additionally reacting with a different bacterial strain or different species. The term "cross-protective" as used herein refers to the ability of the immune response, induced by an immunogenic composition obtained from one bacterial strain, to prevent or attenuate infection or disease by at least one additional bacterial strain or bacterial species. In preferred aspects of the present disclosure, the immunogenic compositions of the present disclosure are cross-reactive and/or cross-protective against a plurality of bacterial strains or bacterial species, for example, 2, 3, 4, 5, 6, 7, 8, 9 or 10 bacterial species or bacterial strains. Cross-reactivity is deemed to be an indicator of cross-protection. It will be readily appreciated by those of skill in the art that the foregoing aspect of the present disclosure facilitates vaccine manufacture by permitting the production of one immunogenic compound, i.e. an immunogenic compound obtainable from one HIBP surface receptor protein, which offers protection against multiple infectious bacterial strains or bacterial species.

[0077] The immunogenic preparations of the present disclosure generate an unexpectedly effective immune response in vertebrate subjects, and notably in vertebrate subjects expressing host iron binding proteins, such as transferrin and lactoferrin, exceeding the effectiveness of the immune response generated when immunizing preparations using native HIBP protein are used. One aspect of the effective immune response is the magnitude of the immune response. Preferably the antibody titre obtained using the immunogenic compositions of the present disclosure exceeds the antibody titre of a native HIBP protein by a factor of at least 2X, more preferably by a factor of at least 5X, most preferably by a factor of at least 10X.

[0078] In preferred aspects of the disclosure, mixtures comprising at least two polypeptides, each polypeptide comprising or consisting of a C-lobe domain are used; or mixtures comprising at least two polypeptides, each polypeptide comprising or consisting of an N-lobe domain, are used; or mixtures comprising at least three polypeptides comprising or consisting of at least two C-lobe domains and at least one N-lobe domain, are used; or mixtures comprising at least three polypeptides comprising or consisting of at least two N-lobe domains and at least one C-lobe domain, are used. In preferred aspects, the at least two polypeptides

are obtainable or obtained from a Gram-negative bacterial genus or species capable of infecting the same vertebrate species. Thus, the at least two polypeptides would be selected from e.g. two C-lobe domains of an TbpB polypeptide, wherein both C-lobe domains are obtainable or obtained from a TbpB polypeptide obtained or obtainable from an *Actinobacillus* strain capable of infecting pigs, or e.g. two C-lobe domains of a TbpB polypeptide, wherein both C-lobe domains are obtainable or obtained from an TbpB polypeptide obtained or obtainable from a *Haemophilus* strain capable of infecting cows. In aspects wherein at least two C-lobe domains are used, the mixtures are preferably free, or substantially free, of N-lobe domains or portions thereof. In aspects wherein at least two N-lobe domains are used the mixtures are preferably free or substantially free of C-lobe domains or portions thereof

[0079] In particularly preferred aspects, in accordance with the present disclosure, mixtures of at least two polypeptides, each polypeptide comprising or consisting of a C-lobe domain of an HIBP surface receptor protein obtainable or obtained from a Gram-negative bacterial species are used. In such aspects, the mixtures are preferably free from N-lobe domains or portions thereof. In particularly preferred aspects, any two C-lobe domains obtainable or obtained from the HIBP surface receptor polypeptides set forth in SEQ.ID NO: 2; SEQ.ID NO: 12; SEQ.ID NO: 28; SEQ.ID NO: 107 to SEQ.ID NO: 115; SEQ ID NO: 117; SEQ.ID NO: 123; SEQ.ID NO: 131 to SEQ.ID NO: 147; SEQ.ID NO: 177; SEQ.ID NO: 178; SEQ.ID NO: 196 to SEQ.ID NO: 204; SEQ.ID NO: 206 to SEQ.ID NO: 212; and SEQ.ID NO: 219 to SEQ.ID NO: 228 are used; or any two C-lobe domains obtainable or obtained from the nucleic acid sequences set forth in SEQ.ID NO: 1; SEQ.ID NO: 11; SEQ.ID NO: 27; SEQ.ID NO: 116; SEQ.ID NO: 122; and SEQ.ID NO: 173 are used. In further preferred aspects, any two C-lobe domains selected from the C-lobe domains set forth in SEQ.ID NO: 5; SEQ.ID NO: 6; SEQ.ID NO: 22; SEQ.ID NO: 33; SEQ.ID NO: 34; SEQ.ID NO: 119; SEQ.ID NO: 125; SEQ.ID NO: 179 to SEQ.ID NO: 195; and SEQ.ID NO: 213 to SEQ.ID NO: 218; SEQ.ID NO: 230: SEQ.ID NO: 232; SEQ.ID NO: 234 to SEQ.ID NO: 278; and SEQ.ID NO: 288 to SEQ.ID NO: 292 are used.

[0080] In further particularly preferred aspects, at least two C-lobe domains obtainable or obtained from an HIBP surface receptor protein are used, wherein at least one C-lobe domain is obtainable or obtained from a bacterial species belonging to the bacterial genus of *Actinobacillus, Haemophilus, Histophilus, Mannheimia, Moraxella, Neisseria, Pasteurella* and *Bibersteinia.*

[0081] In further particularly preferred aspects, at least two C-lobe domains are used, wherein at least one C-lobe domain is obtainable or obtained from an HIBP surface receptor protein obtainable or obtained from *Actinobacillus pleuropneumoniae,* preferably the C-lobe domain set forth in SEQ.ID. NO: 6 or SEQ.ID NO: 22, or wherein at least one C-lobe domain is obtainable or obtained from an HIBP surface receptor protein obtainable or obtained from *Actinobacillus suis* preferably the C-lobe domain set forth in SEQ.ID NO: 34.

[0082] In further particularly preferred aspects, at least two C-lobe domains are used, wherein at least one C-lobe domain is obtainable or obtained from an HIBP surface receptor protein obtainable or obtained from *Mannheimia haemolytica* preferably the C-lobe domain set forth in

SEQ.ID NO: 232; or SEQ.ID NO: 234, or wherein at least one C-lobe domain is obtainable or obtained from an HIBP surface receptor protein obtainable or obtained from *Mannheimia glucosida.*

[0083] In further particularly preferred aspects, at least two C-lobe domains are used, wherein at least one C-lobe domain is obtainable or obtained from an HIBP surface receptor protein obtainable or obtained from *Neisseria gonorrhoeae* preferably one of the C-lobe domains set forth in SEQ.ID NO: 213 to SEQ.ID NO: 218, or wherein at least one C-lobe domain is obtainable or obtained from an HIBP surface receptor protein obtainable or obtained from *Neisseria meningitidis* preferably one of the C-lobe domains set forth in SEQ.ID. NO: 119; SEQ.ID NO: 125; SEQ.ID NO: 128; SEQ.ID NO: 129; SEQ.ID NO: 130; SEQ.ID NO: 131; SEQ.ID NO: 152; SEQ.ID NO: 154; SEQ.ID NO: 156; SEQ.ID NO: 158; SEQ.ID NO: 160; SEQ.ID NO: 164; SEQ.ID NO: 166; SEQ.ID NO: 168; SEQ.ID NO: 179 to SEQ.ID NO: 195; and SEQ.ID NO: 235 to SEQ.ID NO: 278.

[0084] In further particularly preferred aspects of the disclosure, at least two C-lobe domains are used, wherein at least one C-lobe domain is obtainable or obtained from an HIBP surface receptor protein obtainable or obtained from *Bibersteinia trehalosi,* preferably the C-lobe domain set forth in SEQ.ID.NO: 292.

[0085] In further preferred aspects of the disclosure, at least two C-lobe domains obtainable or obtained from a HIBP surface receptor polypeptide are used, wherein both of the two C-lobe domains are obtainable or obtained from two bacterial species selected from *Actinobacillus pleuropneumoniae,* preferably, the C-lobe domain set forth in SEQ.ID NO: 6 or SEQ.ID NO: 22, *Actinobacillus suis,* preferably the C-lobe domain set forth in SEQ.ID NO: 34 and *Haemophilus parasuis,* preferably the C-lobe domain set forth in SEQ.ID NO: 294.

[0086] In further preferred aspects of the disclosure, at least two C-lobe domains obtainable or obtained from a HIPB surface receptor polypeptide are used, wherein one of the two C-lobe domains are obtainable or obtained from *Neisseria gonorrhoeae,* preferably, one of the C-lobe domains set forth in SEQ.ID. NO: 213 to SEQ.ID. NO: 218 and the other C-lobe domain is obtainable from *Neisseria meningitidis* preferably one of the C-lobe domains set forth in. SEQ.ID. NO: 119; SEQ.ID NO: 125; SEQ.ID NO: 128; SEQ.ID NO: 129; SEQ.ID NO: 130; SEQ.ID NO: 131; SEQ.ID NO: 152; SEQ.ID NO: 154; SEQ.ID NO: 156; SEQ.ID NO: 158; SEQ.ID NO: 160; SEQ.ID NO: 164; SEQ.ID NO: 166; SEQ.ID NO: 168; SEQ.ID NO: 179 to SEQ.ID NO: 195; and SEQ.ID NO: 235 to SEQ.ID NO: 278.

[0087] In further preferred aspects of the disclosure, at least two C-lobe domains obtainable or obtained from a HIPB surface receptor polypeptide are used, wherein one of the two C-lobe domains is obtainable or obtained from *Mannheimia haemolytica,* preferably a C-lobe domain set forth in SEQ.ID NO: 232; or SEQ.ID NO: 234, and the other C-lobe is obtainable or obtained from *Bibersteinia trehalosi* preferably a C-lobe domain set forth in SEQ.ID NO: 292.

[0088] In further preferred aspects of the disclosure, at least two C-lobe domains obtainable or

obtained from a TbpB polypeptide are used, wherein both of the two C-lobe domains are obtainable or obtained from one or from two bacterial species, and wherein the TbpB polypeptides or the C-lobe domains obtained therefrom are antigenically divergent. The TbpB or C-lobe domains are preferably obtained from bacterial species or bacterial strains capable of exchanging TbpB variants. The term "antigenically divergent" as used herein in relation to two TbpB polypeptides or C-lobe domains of TbpB polypeptides means that the two TbpB polypeptides or C-lobe domains of TbpB polypeptides when used to construct a phylogenetic tree using a representative number of TbpB polypeptides or C-lobe domain polypeptides belong to divergent branches or groups of a phylogenetic tree. In accordance herewith, a phylogenetic tree with any amount of TbpB or C-lobe domain polypeptides may be constructed, however preferably a phylogenetic tree is constructed using at least 25 TbpB polypeptides or C-lobe domain polypeptides, more preferably at least 30, at least 40, or at least 50 TbpB polypeptides or C-lobe domain polypeptides, and preferably a phylogenetic tree is constructed in such a manner that it comprises at least 2 node orders above the root level, more preferably a phylogenetic tree comprises at least 3, 4, or 5 node orders above the root level, most preferably, at least 6, 7, 8, 9, or 10 node orders above the root level (as further explained below and in **FIG. 30).** Antigenically divergent TbpB polypeptides or C-lobe domain polypeptides preferably belong to distinct branches which (i) diverge at a node at least 2 node orders below the highest order node of the phylogenetic tree (e.g. if the highest order node of a phylogenetic tree is the 9th order node, antigenically divergent polypeptides are those polypeptides diverging at the 7th order node, or a lower order node, i.e. the 6th, 5th, 4th, 3rd, 2nd or 1st order node; and/or (ii) diverge at a 1st, 2nd or 3rd node order of a phylogenetic tree. Several computer programs may be used to facilitate construction of phylogenetic trees using TbpB polypeptides or C-lobe domain polypeptides including: (i) computer programs performing sequence alignments, such as a program using the M-Coffee alignment algorithm as implemented on the T-Coffee server site (http://www.tcoffee.org/) (43); (ii) computer programs editing alignments, such as Geneious Pro (44); (iii) computer programs automatically cleaning alignments, such as GBlocks (45); (iv) computer programs selecting an evolutionary model compatible with the alignment, such as ProtTest v3.2 (Darriba et al, 2011) and (iv) computer programs generating phylogenetic trees such as programs using the Maximum likelihood method, PhyML (46), running on the general time reversible (GTR) model (47) (48, 49), or other model such as the JTT+I+G+F model, or the WAG+G=F model, or programs such as PHYLIP and PAUP (University of Washington). Each of these programs is preferably configured so that the tree branches are deemed to be statistically significant. It is noted however that the more distally located branches may be less statistically significant, thus selection of strains belonging to groups based from the lowest order nodes is preferred.

[0089] Now referring to **FIG. 30,** there is shown, for illustrative purposes, a phylogenetic tree **100** having a root **120,** intermediate branches (as illustrated by **130, 131, 140, 141, 142** and **143),** and a total of 38 distal branches (as illustrated by distal branches **150, 151, 152, 153, 154** and **155),** each distal branch representing a related polypeptide obtained from 1 of 38 bacterial strains (strain 1-38 **(110)).** Each branch shown originates from a node (as illustrated by nodes **161, 171, 172, 181, 182, 183** and **184).** Thus, for example, branch **130** originates

from node **161** and branch **143** originates from node **172.** The node **(161)** most proximal to the tree root **(120)** is more specifically referred to as the first order node **161;** nodes **171** and **172** are more specifically referred to as 2nd order nodes **171** and **172**; nodes **181, 182, 183** and **184** are more specifically referred to as 3rd order nodes **181, 182, 183** and **184,** and further nodes, *mutatis mutandis,* may be referred to as 4th, 5th, 6th, 7th etc. order nodes. Shown in **FIG**. **30** are further four Groups (Group 1 **(105),** polypeptides of bacterial strains **(110)** 1-17; Group 2 **(106),** polypeptides of bacterial strains **(110)** 18-24; Group 3 **(107),** polypeptides of bacterial strains **(110)** 25-30; and Group 4 **(108),** polypeptides of bacterial strains **(110)** 26-38). Polypeptides of bacterial strains belonging to either Group 1 **(105)** or Group 2 **(106)** both belong to a branch **(131)** diverging at the first order node **(161)** of the phylogenetic tree **(100).** Similarly, polypeptides of bacterial strains belonging to either Group 3 **(105)** or Group 4 **(106)** both belong to a branch **(131)** diverging at the first order node **(161)** of the phylogenetic tree **(100).** Thus polypeptides of all bacterial strains belonging to Group 1 **(105)** or Group 2 **(106)** are antigenically divergent from polypeptides of all bacterial strains belonging to Group 3 **(107)** or Group 4 **(108)**. Polypeptides of bacterial strains belonging to Group 1 **(105)** or Group 2 **(106)** belong to groups diverging at the 2nd order node **(172)** of the phylogenetic tree **(100).** Polypeptides of bacterial strains belonging to Group 1 **(105)** are in accordance herewith also antigenically divergent from bacterial strains belonging to Group 2 **(106).** It is noted that phylogenetic trees may be represented in different formats, for example, in a rectangular format, as in **FIG**. **30,** for example, or in circular format as in **FIG**. **10.** Exemplary phylogenetic trees constructed using TbpB polypeptides or C-lobes or TbpB polypeptides are provided in **FIG**. **4** (comprising strains of *Actinobacillus pleuropneumoniae, Actinobacillus suis* and *Haemophilus parasuis),* **FIG**. **10** (comprising strains of *Neisseria meningitidis),* **FIG**. **26** (comprising strains of *Neisseria meningitidis* and *Neisseria gonorrhoeae),* **FIG. 27** (comprising strains of *Haemophilus influenza),* **FIG**. **28** (comprising strains of *Mannheimia haemolytica* and *Bibersteinia trehalosi)* and **FIG**. **29** (comprising strains of *Moraxella catharrhalis).*

[0090] In further preferred aspects of the disclosure, at least two C-lobe domains obtainable or obtained from a TbpB polypeptide are used, wherein both of the two C-lobe domains are obtainable or obtained from *Actinobacillus pleuropneumoniae, Actinobacillus suis* and *Haemophilus parasuis.* Referring to the phylogenetic tree set forth in **FIG**. **4,** in preferred aspects, at least two C-lobe domains are used, wherein a first C-lobe domain is obtained from any one of the C-lobe domains selected from a *Actinobacillus pleuropneumoniae, Actinobacillus suis* or *Haemophilus parasuis* bacterial strain belonging to phylogenetic Group 1, phylogenetic Group 2 or phylogenetic Group 3, set forth in **FIG**. **4,** and wherein the second C-lobe domain is obtained from any one of the C-lobe domains selected from a *Actinobacillus pleuropneumoniae, Actinobacillus suis* or *Haemophilus parasuis* strain belonging to a phylogenetic Group set forth in **FIG**. **4,** other than the phylogenetic Group the first C-lobe domain is selected from. In further preferred aspects, at least three C-lobe domains are used, wherein a first C-lobe domain belonging to a *Actinobacillus pleuropneumoniae, Actinobacillus suis* or *Haemophilus parasuis* bacterial strain belonging to phylogenetic Group 1 set forth in **FIG**. **4** is used, a second C-lobe domain belonging to *Actinobacillus pleuropneumoniae, Actinobacillus suis* or *Haemophilus parasuis* bacterial strain belonging to phylogenetic Group 2

set forth in **FIG**. **4** is used, and a third C-lobe domain belonging to a *Actinobacillus pleuropneumoniae, Actinobacillus suis* or *Haemophilus parasuis* bacterial strain belonging to phylogenetic Group 3 set forth in **FIG**. **4** is used. Thus by way of specific example, a C-lobe domain from *Actinobacillus suis* H57 (phylogenetic Group 1; **FIG**. **4** black arrow)) may be combined with a C-lobe domain from *Actinobacillus pleuropneumonaie* H87 (phylogenetic Group 2; **FIG. 4** black arrow) and a C-lobe domain from *Actinobacillus pleuropneumonaie* H49 (phylogenetic Group 3; **FIG. 4** black arrow).

[0091] In further preferred aspects of the disclosure, at least two C-lobe domains obtainable or obtained from a TbpB protein are used, wherein both of the two C-lobe domains are obtainable or obtained from *Neisseria meningitidis.* Referring to the phylogenetic tree set forth in **FIG. 10A,** in preferred aspects, at least two C-lobe domains are used, wherein a first C-lobe domain is obtained from any one of the C-lobe domains selected from a *Neisseria meningitidis* bacterial strain belonging to phylogenetic Group 1, phylogenetic Group 2, phylogenetic Group 3 or phylogenetic Group 4 set forth in **FIG. 10A,** and wherein the second C-lobe domain is obtained from any one of the *Neisseria meningitidis* strains belonging to a phylogenetic Group set forth in **FIG. 10A** other than the phylogenetic Group the first C-lobe domain is selected from. Thus by way of example only, a TbpB C-lobe domain obtained from *Neisseria meningitidis* strain B16B6 (phylogenetic Group 1; **FIG 10A,** black arrow) may be combined with a TbpB C-lobe domain from strain M982 (phylogenetic Group 4; **FIG 10A,** black arrow). In further preferred aspects, at least three C-lobe domains are used wherein the C-lobe domains are selected from strains belonging to three different Groups set forth in **FIG. 10A** (e.g. a C-lobe domain selected from each phylogenetic Group 1, phylogenetic Group 2 and phylogenetic Group 3). In further preferred aspects, at least four C-lobe domains are used, wherein a first C-lobe domain belonging to a *Neisseria meningitidis* bacterial strain belonging to Group 1 set forth in **FIG. 10A** is used, a second C-lobe domain belonging to *Neisseria meningitidis* bacterial strain belonging to Group 2 set forth in **FIG. 10A** is used, and a third C-lobe domain belonging to a *Neisseria meningitidis* bacterial strain belonging to phylogenetic Group 3 set forth in **FIG. 10A** is used and a fourth C-lobe domain belonging to a *Neisseria meningitidis* bacterial strain belonging to phylogenetic Group 4 set forth in **FIG. 10A** is used. Thus by way of specific example only, a TbpB C-lobe domain from a *Neisseria meningitidis* strains B16B6 (phylogenetic Group 1; **FIG 10A,** black arrow), BZ169 (phylogenetic Group 2; **FIG 10A,** black arrow), S3131 (phylogenetic Group 3; **FIG 10A,** black arrow) and M982 (phylogenetic Group 4; **FIG 10A,** black arrow) may be selected.

[0092] In further preferred aspects of the disclosure, at least two C-lobe domains obtainable or obtained from a TbpB polypeptide are used, wherein one of the two C-lobe domains is obtainable or obtained from *Neisseria meningitidis* and the other of the C-lobes is obtainable or obtained from *Neisseria gonorrhoeae.* Referring to the phylogenetic tree set forth in **FIG. 26B,** in preferred aspects, at least two C-lobe domains are used, wherein a first C-lobe domain is obtained from any one of the C-lobe domains selected from a *Neisseria gonorrhoeae* bacterial strain belonging to phylogenetic Group 3, set forth in **FIG. 26B,** and wherein the second C-lobe domain is obtained from any one of the C-lobe domains selected from a *Neisseria meningitidis* strain belonging to phylogenetic Group 1 or Group 2, set forth in **FIG. 26B.** More preferably, at

least three C-lobe domains obtainable or obtained from a TbpB polypeptide are used, wherein two C-lobe domains are obtainable or obtained from *Neisseria meningitidis* and the other C-lobe is obtainable or obtained from *Neisseria gonorrhoeae.* Preferably a C-lobe domain is selected from a *Neisseria gonorrhoeae* bacterial strain belonging to phylogenetic Group 3, set forth in **FIG**. **26B,** a the second C-lobe domain is obtained from any one of the C-lobe domains selected from a *Neisseria meningitidis* strain belonging to a phylogenetic Group 2, set forth in **FIG. 26B,** and the third C-lobe domain is obtained from any one of the C-lobe domains selected from a *Neisseria meningitidis* strain belonging to a phylogenetic Group 1, set forth in **FIG. 26B.** In further preferred aspects, at least four C-lobe domains obtainable or obtained from a TbpB polypeptide are used, wherein three C-lobe domains are obtainable or obtained from *Neisseria meningitidis* and the other C-lobe domain is obtainable or obtained from *Neisseria gonorrhoeae.* Preferably a C-lobe domain is selected from a *Neisseria gonorrhoeae* bacterial strain belonging to phylogenetic Group 3, set forth in **FIG. 26B,** the second, and third, C-lobe domain are obtained from any of the C-lobe domains selected from a *Neisseria meningitidis* strain belonging to two different Subgroups of phylogenetic Group 2 (e.g. phylogenetic Subgroup 2.1 and phylogenetic Subgroup 2.2) set forth in **FIG. 26B,** and the fourth C-lobe domain is obtained from any one of the C-lobe domains selected from a *Neisseria meningitidis* strain belonging to a phylogenetic Group 1, set forth in **FIG. 26B.** In further preferred aspects, at least four C-lobe domains obtainable or obtained from a TbpB polypeptide are used, wherein two C-lobe domains are obtainable or obtained from *Neisseria meningitidis* and the other two C-lobes are obtainable or obtained from *Neisseria gonorrhoeae.* Preferably the two C-lobe domains selected from a *Neisseria gonorrhoeae* bacterial strain belong to two different phylogenetic Subgroups of phylogenetic Group 3 (e.g. Subgroup 3.1 and Subgroup 3.2), set forth in **FIG. 26B,** the third and fourth C-lobe domains are obtained from a *Neisseria meningitidis* strain belonging to phylogenetic Group 1 and phylogenetic Group 2, respectively. In a further aspect, at least five C-lobe domains obtainable or obtained from a TbpB polypeptide are used, wherein three C-lobe domains are obtainable or obtained from *Neisseria meningitidis* and the other two C-lobes are obtainable or obtained from *Neisseria gonorrhoeae.* Preferably the two C-lobe domains selected from a *Neisseria gonorrhoeae* bacterial strain belong to two different phylogenetic Subgroups of phylogenetic Group 3 (e.g. Subgroup 3.1 and Subgroup 3.2), set forth in **FIG. 26B,** the third and fourth C-lobe domains are obtained from a *Neisseria meningitidis* strain belonging to two different phylogenetic Subgroups of phylogenetic Group 2 (e.g. Subgroup 2.1 and Subgroup 2.2), set forth in **FIG. 26B,** and the fifth C-lobe domain belongs to a *Neisseria meningitidis* strain belonging to phylogenetic Group 1 set forth in **FIG. 26B.** In a yet further preferred aspect, at least six C-lobe domains obtainable or obtained from a TbpB polypeptide are used. In this aspect, at least one C-lobe domain is obtained or obtainable from *Neisseria meningitidis* and at least one C-lobe domain is obtained or obtainable from *Neisseria gonorrhoeae,* the other C-lobes are obtained or obtainable from strains that are antigenically divergent in accordance with **FIG.** 26B. In preferred aspects, three C-lobe domains are obtainable or obtained from *Neisseria meningitidis* and the other three C-lobes are obtainable or obtained from *Neisseria gonorrhoeae.* Referring to **FIG. 26B** preferably the three C-lobe domains obtained from the *Neisseria gonorrhoeae* strains belong to three antigentically divergent groups, and the three C-lobe domains obtained from *Neisseria meningitidis* belong to three antigenically divergent

strains.

[0093] In further preferred aspects of the disclosure, at least two C-lobe domains obtainable or obtained from a TbpB polypeptide are used, wherein one of the two C-lobe domains is obtainable or obtained from *Neisseria meningitidis* and the other of the C-lobes is obtainable or obtained from *Neisseria gonorrhoeae.* Referring to the phylogenetic tree set forth in **FIG. 26A,** in preferred aspects, at least two C-lobe domains are used, wherein a first C-lobe domain is obtained from any one of the C-lobe domains selected from a *Neisseria gonorrhoeae* bacterial strain belonging to phylogenetic Group 3 or phylogenetic Group 1, set forth in **FIG. 26A,** and wherein the second C-lobe domain is obtained from any one of the C-lobe domains selected from a *Neisseria meningitidis* strain belonging to a phylogenetic Group 2, Group 4 or Group 5, set forth in **FIG. 26A.**

[0094] In further preferred aspects of the disclosure, at least two C-lobe domains obtainable or obtained from a TbpB protein are used, wherein both of the two C-lobe domains are obtainable or obtained from *Haemophilus influenzae.* Referring to the phylogenetic tree set forth in **FIG. 27A** and **FIG. 27B,** in preferred aspects, at least two C-lobe domains are used, wherein a first C-lobe domain is obtained from any one of the C-lobe domains selected from a *Haemophilus influenzae* bacterial strain belonging to phylogenetic Group 1, phylogenetic Group 2, or phylogenetic Group 3 set forth in **FIG. 27A** or **FIG. 27B,** and wherein the second C-lobe domain is obtained from any one of the *Haemophilus influenzae* strains belonging to a phylogenetic Group set forth in **FIG. 27A** or **FIG. 27B** other than the phylogenetic Group the first C-lobe domain is selected from. Thus by way of example only, a TbpB C-lobe domain obtained from *Haemophilus influenzae* strain H216 (phylogenetic Group 3; **FIG. 27B,** black arrow) may be combined with a TbpB C-lobe domain from strain H214 (phylogenetic Group 1; **FIG. 27B,** black arrow). In further preferred aspects, at least three C-lobe domains are used wherein the C-lobe domains are selected from strains belonging to three different Groups set forth in **FIG. 27A** and **FIG. 27B** (i.e. a C-lobe domain selected from each phylogenetic Group 1, phylogenetic Group 2 and phylogenetic Group 3). Thus by way of specific example only, a TbpB C-lobe domain from *Haemophilus influenzae* strains H216 (phylogenetic Group 3; **FIG. 27B,** black arrow), H214 (phylogenetic Group 1; **FIG. 27B,** black arrow), and H011 (phylogenetic Group 2; **FIG. 27B,** black arrow) maybe selected.

[0095] In further preferred aspects of the disclosure, at least two C-lobe domains obtainable or obtained from a TbpB protein are used, wherein both of the two C-lobe domains are obtainable or obtained from *Mannheimia haemolytica.* Referring to the phylogenetic tree set forth in **FIG. 28,** in preferred aspects, at least two C-lobe domains are used, wherein a first C-lobe domain is obtained from any one of the C-lobe domains selected from a *Mannheimia haemolytica* bacterial strain belonging to phylogenetic Group 1, set forth in **FIG. 28,** and wherein the second C-lobe domain is obtained from any one of the *Mannheimia haemolytica* strains belonging to a phylogenetic Group 3.

[0096] In further preferred aspects, at least two C-lobe domains obtainable or obtained from a TbpB polypeptide are used, wherein one of the two C-lobe domains is obtainable or obtained

from *Bibersteinia trehalosi* and the other of the C-lobes is obtainable or obtained from *Mannheimia haemolytica.* Referring to **FIG. 28,** in preferred aspects, at least two C-lobe domains are used, wherein a first C-lobe domain is obtained from any one of the C-lobe domains selected from a *Bibersteinia trehalosi* bacterial strain belonging to phylogenetic Group 2, set forth in **FIG. 28,** and wherein the second C-lobe domain is obtained from any one of the C-lobe domains selected from a *Mannheimia haemolytica* strain belonging to a phylogenetic Group 1, or Group 3, set forth in **FIG. 28.**

[0097] In further preferred aspects of the disclosure, at least two C-lobe domains obtainable or obtained from a TbpB protein are used, wherein both of the two C-lobe domains are obtainable or obtained from *Moraxella catharrhalis.* Referring to the phylogenetic tree set forth in **FIG. 29,** in preferred aspects, at least two C-lobe domains are used, wherein a first C-lobe domain is obtained from any one of the C-lobe domains selected from a *Moraxella catharrhalis* bacterial strain belonging to phylogenetic Group 1, phylogenetic Group 2, or phylogenetic Group 3 set forth in **FIG. 29,** and wherein the second C-lobe domain is obtained from any one of the *Moraxella catharrhalis* strains belonging to a phylogenetic Group set forth in **FIG. 29** other than the phylogenetic Group the first C-lobe domain is selected from. Thus by way of example only, a TbpB C-lobe domain obtained from *Moraxella catharrhalis* strain AAC34279.1 (phylogenetic Group 3; **FIG 29,** black arrow) may be combined with a TbpB C-lobe domain from strain AAD12263.1 (phylogenetic Group 1; **FIG 29,** black arrow). In further preferred aspects, at least three C-lobe domains are used wherein the C-lobe domains are selected from strains belonging to three different Groups set forth in **FIG. 29** (i.e. a C-lobe domain selected from each phylogenetic Group 1, phylogenetic Group 2 and phylogenetic Group 3). Thus by way of specific example only, a TbpB C-lobe domain from a *Moraxella catharrhalis* strains AAC34279.1 (phylogenetic Group 3; **Fig.** 29, black arrow), AAD12263.1 (phylogenetic Group 1; **FIG. 29**, black arrow), and 003664398.1 (phylogenetic Group 2; **FIG. 29**, black arrow) may be selected.

[0098] In particularly preferred aspects of the disclosure, the aforementioned mixtures of polypeptides comprising or consisting of C-lobe domains are C-lobe domains obtainable or obtained from TbpB polypeptides, including, without limitation the C-lobe domains set forth in SEQ.ID NO: 5; SEQ.ID NO: 6; SEQ.ID NO: 22; SEQ.ID NO: 33; SEQ.ID NO: 34; SEQ.ID NO: 119; SEQ.ID NO: 125; SEQ.ID NO: 179 to SEQ.ID NO: 195; and SEQ.ID NO: 213 to SEQ.ID NO: 218; SEQ.ID NO: 230; SEQ.ID NO: 232; and SEQ.ID NO: 234 to SEQ.ID NO: 278.

[0099] The foregoing mixtures of C-lobe domains may be prepared by mixing preparations comprising the individual C-lobe domains or by recombinantly producing fusion polypeptides comprising two or more C-lobe domains.

[0100] As hereinbefore mentioned, the immunogenic preparations of the present disclosure are preferably cross-reactive and/or cross-protective. While, as hereinbefore mentioned, formulations comprising single C-lobe domains may be cross-reactive and/or cross-protective, mixtures of C-lobe domains are particularly preferred, in that they may be used to prepare immunogenic formulations that substantially broaden cross-reactivity and/or cross-protection

against a wider range of bacterial strains and/or species, and allow the preparation of vaccine formulations providing protection from infection or disease transmitted by a plurality of bacterial species or bacterial strains.

[0101] In accordance with other aspects of the disclosure, a polypeptide comprising a C-lobe domain and/or an N-lobe domain of an HIBP surface receptor polypeptide is prepared in such a manner that a loop domain connecting two β-strands within the C-lobe domain or the N-lobe domain is modified and the polypeptide is unable to substantially bind host iron binding protein. The term "modified" as used herein in conjunction with a loop domain refers to a loop from which at least one amino acid residue has been removed or replaced. Thus the resultant loop within the C-lobe domain or the N-lobe domain may be truncated or, in other aspects the amino acid residue, residues may be replaced with one or more alternate amino residues. **FIG. 1** and **FIG. 2** show the loop domains of exemplary HIBP surface receptor proteins. **FIG. 8** and **FIG. 14** provide examples of loop reductions in the N-lobe domain and C-lobe domain, respectively. In accordance herewith at least one of the loop domains connecting two β-strands within the C-lobe domain or the N-lobe domain of the HIBP binding membrane receptor protein is modified to remove at least one amino acid residue from the loop domains, the resulting polypeptide comprising a modified N-lobe domain or C-lobe domain and unable to substantially bind host iron binding protein. In other aspects more amino acid residues are removed e.g. at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100 amino acid residues are removed from the loop domain. In other aspects the loop domain is removed in its entirety. Any of the loop domains may be selected to be modified in accordance with the present disclosure, provided such modification results in a polypeptide that is unable to substantially bind to the host iron binding protein. Thus, referring to the exemplary porcine TbpB polypeptide of **FIG. 1**, in aspects of the present disclosure where one loop domain is modified, such loop domain may be selected to be any one of the loop domains L1-L32 (as exemplified by the *Actinobacillus pleuropneumoniae* loops L1 -L32 polypeptide sequences: SEQ.ID: NO 42; SEQ.ID: NO 44; SEQ.ID: NO 46; SEQ.ID: NO 48; SEQ.ID: NO 50; SEQ.ID: NO 52; SEQ.ID: NO 54; SEQ.ID: NO 56; SEQ.ID: NO 58; SEQ.ID: NO 60; SEQ.ID: NO 62; SEQ.ID: NO 64; SEQ.ID: NO 66; SEQ.ID: NO 68; SEQ.ID: NO 70; SEQ.ID: NO 72; SEQ.ID: NO 74; SEQ.ID: NO 76; SEQ.ID: NO 78; SEQ.ID: NO 80; SEQ.ID: NO 82; SEQ.ID: NO 84; SEQ.ID: NO 86; SEQ.ID: NO 88; SEQ.ID: NO 90; SEQ.ID: NO 92; SEQ.ID: NO 94; SEQ.ID: NO 96; SEQ.ID: NO 98; SEQ.ID: NO 100; SEQ.ID: NO 102; SEQ.ID: NO 104; and SEQ.ID: NO 106, respectively, and encoded by the nucleic acid sequences SEQ.ID: NO 41; SEQ.ID: NO 43; SEQ.ID: NO 45; SEQ.ID: NO 47; SEQ.ID: NO 49; SEQ.ID: NO 51; SEQ.ID: NO 53; SEQ.ID: NO 55; SEQ.ID: NO 57; SEQ.ID: NO 59; SEQ.ID: NO 61; SEQ.ID: NO 63; SEQ.ID: NO 65; SEQ.ID: NO 67; SEQ.ID: NO 69; SEQ.ID: NO 71; SEQ.ID: NO 73; SEQ.ID: NO 75; SEQ.ID: NO 77; SEQ.ID: NO 79; SEQ.ID: NO 81; SEQ.ID: NO 83; SEQ.ID: NO 85; SEQ.ID: NO 87; SEQ.ID: NO 89; SEQ.ID: NO 91; SEQ.ID: NO 93; SEQ.ID: NO 95; SEQ.ID: NO 97; SEQ.ID: NO 99; SEQ.ID: NO 101; SEQ.ID: NO 103; and SEQ.ID: NO 105, respectively), as further set forth in **Table 1.** In aspects of the disclosure wherein two loop domains are modified, such two loop domains may be any two loop domains selected from the loop domains L1-L32 domains (again referring to the exemplary TbpB polypeptide of **FIG. 1**), as further set forth in **Table 2**. In aspects of the disclosure wherein three loop domains are modified, such three loop domains may be any three loop domains

selected from the loop domains L1-L32 domains (again referring to the exemplary TbpB polypeptide of **FIG. 1**), as further set forth in **Table 3.** In aspects of the disclosure wherein four loop domains are modified, such four loop domains may be any three loop domains selected from the combination of loops set forth in **Table 3** plus one additional loop domain selected from the loop domains L1-L32 (again referring to the exemplary TbpB polypeptide of **FIG. 1**). In other aspects a total of 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32 loop domains may be modified. It will be clear to those of skill in the art that the exact number of modified loop domains may vary and may be selected to be any 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32 loop domains selected from the loops L1-L32, in each of these aspects of the present disclosure, in a manner similar to the selection of loop domains described with respect to the aspects in which 2 or 3 loop domains have been modified. In particularly preferred aspects, one or all of loops L18, L21, L23 and L27 (as exemplified by the *Actinobacillus pleuropneumoniae* SEQ.ID NO: 76; SEQ.ID NO: 82; SEQ.ID NO: 86; and SEQ.ID NO: 96, respectively) of the C-lobe domain are modified. In further particularly preferred aspects, one or all of loop L1, L5, L8 and L12 (as exemplified by the *Actinobacillus pleuropneumoniae* SEQ.ID NO: 42; SEQ.ID NO: 50; SEQ.ID NO: 56; SEQ.ID NO: 64, respectively) of the N-lobe domain are modified. Loop domains that may be modified are loop domains that connect two β-strands assembled within a β-barrel or handle domain β-sheet of the C-lobe domain or N-terminal lobe domain, or loop domains that connect two assembled β-strands, or a combination of the foregoing. In order to truncate a loop domain within the C-lobe domain or the N-terminal lobe domain, the polypeptide may be prepared in such a manner that the loop domain is removed in its entirety, and optionally replaced with one or more linking amino acid, thus resulting in a more or less direct connection between two β-strands, or in such a manner that a portion or portions of a loop domain are removed. In accordance herewith preferably at least half of the amino acid residues from at least one of the loop domains of the C-lobe domain or the N-lobe domain is removed. In further preferred aspects, at least one half of the total amino acid residues of the loop domain are removed. Thus in such aspects where a loop domain comprises for example 40 amino residues, at least 20 amino acid residues of the loop domain will be removed. In further aspects, the loop domain is modified in such a manner that at least 60%, 70%, 80% or 90% of the amino acid residues of the loop domain are removed. In other aspects up to 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acids of the loop domains are retained, following truncation, and in yet other aspects up to 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80% or 90% of the loop domains are retained following truncation. In aspects where the loop domain is modified in such a manner that only a portion of the loop domain is removed, the removed amino acid residues may be located at the N-terminal end of the loop domain, at the C-terminal end of the loop domain or in between the N- and C-termini. In aspects where a plurality of loop domains of the C-lobe domain or the N-lobe domain are modified, such loop reductions may involve the removal of an identical number of amino acid residues from each loop, for example 10 amino acid residues from each loop within the C-lobe domain or the N-lobe domain may be removed, or the loop reduction may involve the removal of different amounts of amino acid residues from each loop, for example 10 residues in one loop and 20 residues in another loop.

[0102] In further preferred aspects of the disclosure, amino acid residues within the loop domains of the C-lobe domain and/or N-lobe domain are replaced by others e.g. by site directed mutagenesis, the resulting polypeptide comprising a modified C-lobe domain or N-lobe domain and unable to substantially bind host iron binding protein. **FIG. 22** provides examples of residue replacements in N-lobe domain loop regions of various TbpB polypeptides and **FIG. 23** illustrates the reduction in Tf binding due to these residue replacements. Thus, for example, one or more amino acid residues may be replaced in any one of loops L1 - L32. In certain preferred aspects, one or more amino acid residues are replaced in loop domain L1, L3, L5 or L8 of the N-lobe domain (as exemplified by the *Actinobacillus pleuropneumoniae* SEQ.ID NO: 42; SEQ.ID NO: 46; SEQ.ID NO: 50; and SEQ.ID NO: 56, respectively). In preferred aspects, an aromatic amino acid (phenylalanine, tyrosine, and tryptophan) within loop domain L8 is replaced with an aliphatic amino acid (glycine, valine, leucine, isoleucine). These are surface accessible aromatic amino acid residues in an otherwise generally cationic surface region. In particularly preferred aspects, a *Haemophilus parasuis* TbpB polypeptide is selected and one or more of the following mutations is made in the TbpB polypeptide to obtain a modified TbpB polypeptide: Y93A (SEQ.ID NO: 170; SEQ.ID NO: 171); Y117A (SEQ.ID NO: 172; SEQ.ID NO: 173) or W176A (SEQ.ID NO: 176; SEQ.ID NO: 177). According to the invention, a *Haemophilus parasuis* TbpB polypeptide is selected and the following mutation is made in the TbpB polypeptide to obtain a modified TbpB polypeptide: Y167A (SEQ.ID.NO: 174; SEQ.ID NO: 175;). In further preferred aspects, an *Actinobacillus pleuropneumoniae* TbpB polypeptide is selected and one or more of the following mutations is made in the polypeptide to obtain a modified TbpB polypeptide: F171A (SEQ.ID NO: 3; SEQ.ID NO: 4); Y95A (SEQ.ID NO: 13; SEQ.ID NO: 14); Y121A (SEQ.ID NO: 15; SEQ.ID NO: 16); Y174A (SEQ.ID NO: 17; SEQ.ID NO: 18); or R179E (SEQ.ID NO: 19; SEQ.ID NO: 20), and in further preferred aspects an *Actinobacillus suis* TbpB polypeptide is selected and one or more of the following mutations is made in the polypeptide to obtain a modified TbpB polypeptide: F63A (SEQ.ID NO: 29; SEQ.ID NO: 30) or F152A (SEQ.ID NO: 31; SEQ.ID NO: 32). The present disclosure includes each of the aforementioned modified polypeptides and nucleic acid sequences encoding these polypeptides, as well as immunogenic compositions and vaccine compositions comprising these polypeptides.

[0103] The reductions in size of one or more loop domains, or modification of amino acids in the loop domain of the HIBP polypeptides in accordance with the present disclosure are preferably made in such a manner that the resultant polypeptide is conformationally stable. By the term "conformationally stable" it is meant that the conformational state or conformation of the polypeptide remains substantially the same following the modification in size of the loop or replacement of amino acid residue. The conformational state of the loop domain which is modified may be more or less altered. The determinants of conformational state or confirmation of a polypeptide include: the polypeptide's primary structure as reflected in its amino acid sequence, the polypeptide's secondary structure (e.g. α-helix, β-sheet and the like), the polypeptide's tertiary structure (i.e. the three dimensional folding of the polypeptide chain) and the quarternary structure (i.e. the interaction of the polypeptide with other protein subunits). Protein conformation can further be influenced by environmental factors, such as pH, osmolarity, ionic strength and salt concentration. The design of loop reduction may be

informed by the alignment and comparison of multiple heterologous sequences, the comparison of three-dimensional conformational structures of multiple heterologous polypeptides known to the art, and the use of conservative amino acid substitutions (e.g. combinations such as gly, ala; val, ile; leu, met; asp, glu; asn, gln; ser, thr; lys, arg; cys, met; and phe, trp, tyr). Furthermore, the conformational state of a protein may be assayed by a functional assay (e.g. binding of a host iron binding protein), or by physical methods such as X-ray crystallography or Nuclear Magnetic Resonance (NMR).

[0104] In further aspects of the disclosure, at least one loop domain of the C-lobe domain or the N-lobe domain of an HIBP-surface receptor protein comprising the longest loop, is selected to be modified. In aspects wherein such a loop is modified in its entirety, this generally will involve the removal of at least 25 amino acid residues and may result in the removal of 150 amino acid residues or more.

[0105] In preferred aspects of the disclosure, at least one loop domain of the C-lobe domain or the N-lobe domain of an HIBP-surface receptor protein comprising the longest loop (i.e. comprising the most amino acid residues) of the C-lobe domain or the N-lobe domain is modified. In a further preferred aspect, at least one loop domain of the C-lobe domain or the N-lobe domain of an HIBP-surface receptor protein comprising the longest loop of the C-lobe domain or the N-lobe domain is modified, and a second loop domain of the C-lobe domain or the N-lobe domain of an HIBP-surface receptor protein comprising the second longest loop are selected to be modified. In further preferred aspects, at least one loop domain of the C-lobe domain or the N-lobe domain of an HIBP-surface receptor protein comprising the longest loop, and a second loop domain of the C-lobe domain or the N-lobe domain of an HIBP-surface receptor protein comprising the second longest loop are selected to be modified and a third loop domain of the C-lobe domain or the N-lobe domain of an HIBP-surface receptor protein comprising the third longest loop are selected to be modified. In yet further preferred aspects, at least one loop domain of the C-lobe domain or the N-lobe domain of an HIBP-surface receptor protein comprising the longest loop, and a second loop domain of the C-lobe domain or the N-lobe domain of an HIBP-surface receptor protein comprising the second longest loop are selected to be modified and a third loop domain of the C-lobe domain or the N-lobe domain of an HIBP-surface receptor protein comprising the third longest loop are selected to be modified, and a fourth loop domain of the C-lobe domain or the N-lobe domain of an HIBP-surface receptor protein comprising the fourth longest loop are selected to be modified. The aforementioned aspects are further detailed in Examples 3 and 4 hereto.

[0106] Surprisingly, in accordance herewith, it has been found that a polypeptide substantially consisting of a C-lobe domain or an N-lobe domain of a HIBP surface receptor protein can readily be produced, for example in a microbial production system, when one or more loop domains are modified, and the modified polypeptide is substantially conformationally stable.

[0107] In accordance herewith, the modified C-lobe domain or the N-lobe domain polypeptide may be used *per se* as an immunogen, or the polypeptide may be modulated to comprise further modifications. Modifications to the modified C-lobe domain or N-lobe domain of the

polypeptide that may be made in accordance herewith include the preparation of N-terminal or C-terminal polypeptide extensions of the native or the modified C-lobe domain or N-lobe domain polypeptide. Such N-terminal and C-terminal polypeptide extensions include the addition of a second full length C-lobe domain polypeptide to the C-lobe domain, thus providing a C-lobe domain dimer, the addition of a second full length N-lobe domain polypeptide to the N-lobe domain, thus providing an N-lobe domain dimer, or an addition comprising a portion of a C-lobe domain polypeptide or a portion of an N-lobe domain polypeptide. Multimers may be assembled using the same monomeric polypeptide (i.e. homodimers, homotrimers etc.), or they may be assembled using different polypeptides, e.g. a C-lobe domain or an N-lobe domain obtained from different variants (i.e hetrodimers, heterotrimers etc.). In preferred aspects, heteromultimeric proteins representing different pathogens or pathogenic strains are assembled. Thus in one preferred aspect, a heteromultimeric polypeptide comprising C-lobe domains or N-lobe domains selected from the group consisting of *Actinobacillus pleuropneumoniae, Actinobacillus suis* and *Haemophilus parasuis* C-lobe domains or N-lobe domains is prepared. In particularly preferred aspects, the C-lobe domains or N-lobe domains are selected from the group consisting of *A. pleuropneumoniae* H49, *A. suis* H57 and *A. pleuropneumoniae* H87 C-lobe domains or N-lobe domains. In a further preferred aspect, a heteromultimeric polypeptide comprising C-lobe domains selected from at least two TbpB C-lobe domains or N-lobe domains selected from strains of *Neisseria meningitidis* is prepared. In particularly preferred aspects, the strains are selected from *N. meningitidis* M982 or *N. meningitidis* B16B6. Heteromultimeric proteins may convey immunogenicity to different pathogens. In further preferred aspects the present disclosure provides, (i) a first polypeptide, comprising an N-lobe domain or a C-lobe domain of an HIBP surface receptor protein obtainable from or obtained from a Gram-negative pathogenic bacterial species, wherein the N-lobe domain or the C-lobe domain comprise a plurality of β-strands connected by a plurality of loop domains, and wherein at least one loop domain of the plurality of loop domains of the N-lobe domain or the C-lobe domain has been modified, linked to (ii) a second polypeptide comprising an HIBP surface receptor protein, or a portion thereof, obtainable from a Gram-negative bacterial species. In preferred aspects, the portion of the HIBP surface receptor protein is an N-lobe domain or a C-lobe domain. In further preferred aspects, the portion of the HIBP surface protein is an N-lobe domain or a C-lobe domain of an HIBP surface receptor protein obtainable from or obtained from a Gram-negative pathogenic bacterial species, wherein the N-lobe domain or the C-lobe domain comprise a plurality of β-strands connected by a plurality of loop domains, and wherein at least one loop domain of the plurality of loop domains of the N-lobe domain or the C-lobe domain has been modified.

[0108] In further aspects of the disclosure, a multimeric polypeptide is prepared, such multimeric protein comprising a plurality of N- and C-terminal extensions, including the addition of a second, third, fourth, fifth, sixth or seventh full length C-lobe domain polypeptide to the C-lobe domain, thus providing a C-lobe domain multimer, or the addition of a second, third, fourth, fifth, sixth or seventh, full length N-lobe domain polypeptide to the N-lobe domain, thus providing an N-lobe domain dimer, or an addition comprising a portion of a C-lobe domain polypeptide or a portion of an N-lobe domain polypeptide. Thus for example, in one aspect, the C-lobe domains are at least two, or at least three, C-lobe domains obtainable from a TbpB

polypeptide obtainable from *A. pleuropneumoniae, A. suis* and *Haemophilus parasuis.* In accordance with such an aspect, the nucleic acid sequences encoding the TbpB C-lobe domains from *A. pleuropneumoniae* H49 (SEQ.ID NO: 5), *A. suis* H57 (SEQ.ID NO: 33) and *A. pleuropneumoniae* H87 (SEQ.ID NO: 21) may be linked to form a chimeric nucleic acid sequence (SEQ.ID NO: 39) encoding a single polypeptide (SEQ.ID NO: 40) encompassing the three C-lobes (SEQ.ID NO: 6; SEQ.ID NO: 34; SEQ.ID NO: 22). Accordingly, in yet further aspects, the present disclosure provides (i) a first polypeptide, comprising an N-lobe domain or a C-lobe domain of an HIBP surface receptor protein obtainable from or obtained from a Gram-negative pathogenic bacterial species, wherein the N-lobe domain or the C-lobe domain comprise a plurality of β-strands connected by a plurality of loop domains, and wherein at least one loop domain of the plurality of loop domains of the N-lobe domain or the C-lobe domain has been modified, linked to (ii) a plurality of polypeptides each polypeptide comprising an HIBP surface receptor protein, or a portion thereof, obtainable from a Gram-negative bacterial species. In preferred aspects the portion of the HIBP surface receptor protein is an N-lobe domain or a C-lobe domain. In further preferred aspects, the portion of the HIBP surface protein is an N-lobe domain or a C-lobe domain of an HIBP surface receptor protein obtainable from or obtained from a Gram-negative pathogenic bacterial species, wherein the N-lobe domain or the C-lobe domain comprise a plurality of β-strands connected by a plurality of loop domains, and wherein at least one loop domain of the plurality of loop domains of the N-lobe domain or the C-lobe domain has been modified.

[0109] In further aspects of the disclosure, upon removal of one or more amino acids from one or more loop domains of the C-lobe or N-lobe of an HIBP surface receptor protein, these residues are replaced with one or more alternate amino acid residues. In one aspect, the alternate amino acid residues comprise a heterologous polypeptide antigenic determinant capable of eliciting an immune response in a vertebrate host organism. In further aspects the alternate amino acid residues comprise two or more heterologous polypeptide antigenic determinants capable of eliciting an immune response in a vertebrate host organism. The heterologous antigenic determinants may be immuno-cross-reactive to the same or a different pathogenic organism. Thus it will be clear that the modified C-lobe domain or N-lobe domain of an HIBP surface receptor protein in accordance herewith may be used as a scaffold to produce and present one or more antigenic determinants. In a preferred aspect, one or more loop regions of the C-lobe domain or the N-lobe domain of TbpB is replaced with one or more polypeptide portions obtainable from or obtained from an IOM protein, including a transferrin binding protein ("TbpA") or lactoferrin binding protein A ("LbpA"). LbpA and TbpA polypeptides that may be used in accordance herewith include those set forth in SEQ.ID NO: 162 and SEQ.ID NO: 152. Portions of LbpA and TbpA polypeptides that may be used in accordance herewith include those set forth in SEQ.ID NO: 286 and SEQ.ID NO: 287. These fragments may be used to construct chimeric nucleic acid sequences and polypeptides, including those set forth in SEQ.ID. NO: 163; SEQ.ID. NO: 164; SEQ.ID. NO: 165; SEQ.ID. NO: 166, SEQ.ID. NO: 167; and SEQ.ID. NO: 168. This aspect of the disclosure is further detailed in Examples 7 and 8. hereto. In a further preferred aspect, one or more loop domains of the C-lobe or N-lobe of TbpB is replaced with a lysine rich polypeptide sequence, as further described in Example 9.

[0110] In all of the hereinbefore described aspects of the disclosure which comprise an HIBP surface receptor polypeptide comprising a N-lobe domain, it is preferable that the N-lobe domain is modified in such a manner that the N-terminal anchor polypeptide, or a substantial portion thereof, is removed from the N-lobe domain. The length of the anchor polypeptide may vary depending on the HIBP surface receptor polypeptide, but typically ranges from 40 to 75 amino acids in length, and located at the N-terminal end of the mature HIPB polypeptide. Thus referring to **FIG. 1**, the anchor polypeptide of the therein depicted mature TbpB polypeptide is 43 amino acids in length. Accordingly, in preferred aspects hereof comprising a HIBP polypeptide comprising an N-lobe domain, the anchor polypeptide is reduced in length by at least 10 amino acid residues, preferably at least 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70 or 75 residues. In aspects where a portion of the anchor polypeptide is selected for reduction in length, preferably a contiguous portion of the N-terminus of the anchor polypeptide, e.g. the 10 terminal amino acid residues of the anchor peptide, are removed, however other portions of the anchor polypeptide may also removed. In further preferred aspects, the TbpB polypeptide from which the anchoring peptide has been truncated includes SEQ.ID NO: 279 to SEQ.ID NO: 283. The inventors have found that the foregoing aspects of the present disclosure are particularly desirable, since the removal of the anchor polypeptide reduces aggregation of the modified HIBP surface receptor polypeptide, rendering the polypeptide easier to produce, without however substantially impacting the immunogenic properties of the polypeptide. Thus this modification of an HIBP polypeptide may be used in conjunction with any of the modified peptides that are substantially unable to substantially bind host iron binding protein set forth herein, including the herein described HIBP polypeptides comprising a N-lobe domain or C-lobe domain comprising a modified loop domain, and HIBP polypeptides comprising a N-lobe or C-lobe domain where a single amino acid has been replaced in a such a manner that the HIBP polypeptide is substantially unable to bind host iron binding protein.

[0111] As hereinbefore mentioned, in accordance with the present disclosure the HIBP surface receptor protein is modified in such a manner that it is unable to substantially bind host iron binding protein. The binding of host iron binding protein to the modified HIBP surface receptor protein may be evaluated using any chemical or biochemical assay capable of evaluating such binding including, for example, a solid phase binding assay, an affinity capture assay, or a biophysical assay. General methodologies to conduct these assays are known to those of skilled in the art and described in for example (12, 23-25, 50, 51). By conducting these assays the difference in binding characteristics between the native HIBP surface receptor protein and the native host iron binding protein, and the modified HIBP surface receptor protein and the native host iron binding protein, may readily be determined, and a series of modified HIBP surface receptor proteins may be evaluated in order to determine whether they are able to bind host iron binding protein. Different binding characteristics may be determined, including the binding constant (Kd). As hereinbefore mentioned, the Kd characterizing the binding between the host iron binding protein and the modified HIBP surface receptor proteins of the present disclosure is at least 2X higher than the Kd characterizing the binding between the host iron binding protein and the native HIBP surface receptor protein. One exemplary assay method to determine the binding constant using host transferrin is further described in Example 11 hereto.

[0112] The present disclosure further includes a method of identifying a modified HIBP surface receptor protein, the method comprising:

1. (i) providing a modified HIBP surface receptor protein and a native HIBP surface receptor protein;
2. (ii) determining the binding characteristics between the modified HIBP surface receptor protein and a host iron binding protein to obtain the binding characteristics of the modified HIBP surface receptor proteins;
3. (iii) determining the binding characteristics between the native HIBP surface receptor protein and a host iron binding protein to obtain the native HIBP surface receptor protein binding characteristics;
4. (iv) comparing the binding characteristics of the modified HIBP surface receptor protein characteristics with the native HIBP surface receptor protein characteristics; and
5. (v) identifying an HIBP surface receptor protein exhibiting binding characteristics that are substantially modulated relative to the binding characteristics of the native HIBP surface receptor protein.

[0113] "Substantially modulated" as used herein means that the binding interaction forces between the modified HIBP surface receptor proteins and the host iron binding protein are substantially weaker than the binding interaction forces between the native HIBP surface receptor proteins and the host iron binding protein. In preferred aspects of the disclosure, the binding characteristic that is used is the Kd relating to the binding interaction of the HIBP surface receptor protein and the host iron binding protein, wherein the value of the Kd of the binding interaction between the modified HIBP surface receptor proteins and the host iron binding protein is at least 2X larger in value than the Kd of the binding interaction between the native HIBP surface receptor proteins and the host iron binding protein. It is further noted that foregoing method may be used to screen a plurality of different candidate HIBP surface receptor proteins, simultaneously or sequentially, and identifying among the screened candidate HIBP surface receptor proteins, those exhibiting a more or less pronounced modulation in binding characteristics relative to the native HIBP surface receptor proteins.

[0114] The present disclosure further includes a method of preparing a modified HIBP surface receptor protein for use as a vaccine, the method comprising:

1. (i) providing a modified HIBP surface receptor protein and a native HIBP surface receptor protein;
2. (ii) determining the binding characteristics between the modified HIBP surface receptor protein and a host iron binding protein to obtain the modified HIBP surface receptor proteins' binding characteristics;
3. (iii) determining the binding characteristics between the native HIBP surface receptor protein and a host iron binding protein to obtain the native HIBP surface receptor protein binding characteristics;

4. (iv) comparing the binding characteristics of the modified HIBP surface receptor protein with the binding characteristics of the native HIBP surface receptor protein;
5. (v) identifying an HIBP surface receptor protein exhibiting binding characteristics that are substantially modulated relative to the binding characteristics of the native HIBP surface receptor protein; and
6. (vi) preparing the modified HIBP surface receptor protein exhibiting binding characteristics that are substantially modulated relative to the binding characteristics of the native HIBP surface receptor protein for use as a vaccine.

[0115] In accordance with the foregoing, the identified HIBP surface receptor protein exhibiting substantially modulated binding characteristics relative to the binding characteristics of the native HIBP surface receptor proteins may be used to prepare immunogenic formulations, e.g. by recombinantly producing the HIBP surface receptor protein, isolating the HIBP surface protein, and preparing a vaccine formulation comprising the HIBP surface receptor protein.

[0116] In further aspects, the present disclosure comprises methods of evaluating cross-reactivity of antisera against surface receptor protein variants. Accordingly the present disclosure further comprises a method of evaluating the cross-reactivity of antisera against surface receptor protein variants, the method comprising:

1. (i) providing a plurality of nucleic acid sequences encoding surface receptor proteins;
2. (ii) determining the nucleic acid sequence variation among the plurality of surface receptor proteins;
3. (iii) selecting a variant portion of a surface receptor protein;
4. (iv) linking a nucleic acid sequence encoding an N-terminal or C-terminal portion of the variant surface receptor protein to a nucleic acid sequence encoding a peptide susceptible to enzymatic biotinylation and a nucleic acid sequence capable of controlling expression in a host cell to form a chimeric nucleic acid sequence;
5. (v) introducing the chimeric nucleic acid sequence into host cell and expressing the chimeric nucleic acid sequence to produce a fusion polypeptide comprising the N-terminal or C-terminal portion of the variant surface receptor protein fused to the peptide susceptible to biotinylation;
6. (vi) preparing cellular lysates from the host cells;
7. (vii) applying the cellular extracts to a streptavidin coated immunoassay substrate material; and
8. (viii) applying an antiserum to the immunoassay substrate material, washing the immunoassay substrate material and applying labeled second conjugates in order to evaluate the cross-reactivity between the antiserum and the variant portion of the surface receptor protein.

[0117] The nucleic acid sequence encoding the peptide susceptible to biotinylation additionally

may comprise a nucleic acid sequence of sufficient length to permit, upon expression, a polypeptide extension for the fusion polypeptide such that the surface receptor protein is distant from the immunoassay substrate material and thereby fully accessible to binding of an antibody. The streptavidin coated immunoassay substrate material may be any substrate material, including, for example, an ELISA plate.

[0118] In further aspects, the present disclosure comprises methods of evaluating the cross-reactive or protective properties of antiserum surface receptor protein variants, the method comprising:

1. (i) providing a plurality of nucleic acid sequences encoding surface receptor proteins;
2. (ii) determining the nucleic acid sequence variation among the plurality of surface receptor proteins;
3. (iii) providing a host cell comprising a counter-selectable marker capable of replacing a nucleic acid sequence encoding a surface receptor protein;
4. (iv) PCR amplifying a plurality of variant portions of one or more nucleic acid sequences encoding a surface receptor protein to obtain a plurality of PCR products encoding surface receptor variants, wherein PCR amplification is conducted in a manner that permits integration of the PCR products into the host cell comprising a counter-selectable marker, and wherein the PCR products comprise a unique extraneous nucleic acid sequence in order permit identification of each PCR product;
5. (v) introducing and expressing the plurality of PCR products into the host cell comprising the counter-selectable marker to provide a library of antigenic HIBP variants; and
6. (vi) using all or a portion of the library in an *in-vivo* or *in-vitro* immunological assay to assess the cross-reactive or cross-protective properties of the library or portion thereof.

[0119] The *in-vivo* or *in-vitro* immune assay may be any assay including any ELISA assay, functional immunological assay or animal infection model.

[0120] In yet further aspects, the present disclosure comprises a method of evaluating the efficacy of a vaccine for the prevention of colonization of the mammalian upper respiratory tract by a Gram-negative bacterial strain expressing a surface receptor protein variant, the method comprising:

1. (i) providing (a) a transgenic mouse line expressing a mammalian CEACAM receptor from the host species of the pathogen to which the vaccine is directed and (b) a mouse line genetically identical to the transgenic mouse line but not expressing the CEACAM receptor;
2. (ii) demonstrating that the Gram-negative bacterial strain expressing the variant surface receptor protein is capable of colonizing the upper respiratory tract of the transgenic mouse line, and is not capable of colonizing the upper respiratory tract of the mouse line not expressing the CEACAM receptor;
3. (iii) determining whether immunizing with antigens derived from the surface receptor

protein result in the absence of colonization of the upper respiratory tract in transgenic mice infected with the Gram-negative bacterial strain expressing the surface receptor protein variant;

4. (iv) determining whether provision of antisera from animals immunized with antigens derived from the surface receptor protein result in the absence of colonization of the upper respiratory tract in nontransgenic immunized mice infected with the Gram-negative bacterial strain expressing the surface receptor protein variant
5. (v) preparing a library comprising portions of surface receptor protein from the Gram-negative bacterial strain and use the library in an animal upper respiratory tract colonization model to evaluate colonization of the upper respiratory tract of animals challenged with the surface receptor variants; and
6. (vi) optionally, extracting and preparing DNA obtained from the library used to challenge the animal and/or from samples obtained from the challenged animals at appropriate time periods after exposure, and determine the proportion of strains expressing different receptor variants.

[0121] In general, it will be understood by a person of ordinary skill in the art, having read the current disclosure, that in accordance with the disclosure a series of different modulated polypeptides may be prepared and obtained, all of which, are modified HIBP surface receptor proteins, wherein the modification is made in such a manner that the modified HIBP surface receptor protein is unable to substantially bind host iron binding protein. These modulated polypeptides and methods of making such modulated polypeptides are all intended to be included within the scope of the compositions and methods herein provided.

[0122] The modified C-lobe domain or N-lobe domain polypeptides are conveniently prepared by providing a nucleic acid sequence encoding an HIBP surface receptor protein, and modulating the native nucleic acid sequence in such a manner that the polypeptides comprising the modified C-lobe domain or N-lobe domain are expressed in a recombinant host organism, for example a microbial cell. Modulations to the nucleic acid sequence may be made using a variety of nucleic acid modification techniques that will be generally known to those skilled in the art, including for example site directed mutagenesis, targeted mutagenesis, random mutagenesis, the addition of organic solvents, gene shuffling or a combination of these and other techniques known to those of skill in the art, each methodology designed to target the loop domains of the C-lobe domain or N-lobe domain in such a manner that a loop domain therein is modified. Alternatively the modulated nucleic acid sequences encoding the modified in size-C-lobe domain or N-lobe domain polypeptides may be prepared *ab initio* using gene synthesis techniques. General techniques to prepare and modify nucleic acid sequences are readily available to the skilled artisan, for example in Green and Sambrook, Molecular Cloning, a Laboratory Manual, Cold Spring Harbor Laboratory Press, 2012, (33).

[0123] In other aspects of the present disclosure, methods for preparing an immunogenic composition are provided. Accordingly, the present disclosure provides a method for preparing

an immunogenic composition comprising:

1. (a) providing a chimeric nucleic acid sequence comprising as operably linked components:
    1. (i) a nucleic acid sequence encoding a polypeptide comprising a C-lobe domain or N-lobe domain of an HIBP surface receptor protein obtainable from a Gram-negative bacterial species wherein the polypeptide has been modified in such a manner that it is unable to substantially bind host iron binding protein; and
    2. (ii) a nucleic acid sequence capable of controlling expression in a recombinant host cell;
2. (b) introducing the chimeric nucleic acid sequence into a host cell and growing the host cell to produce the polypeptide comprising the C-lobe domain or N-lobe domain;
3. (c) recovering the polypeptide comprising C-lobe domain or N-lobe domain from the host cell; and
4. (d) preparing an immunogenic composition

[0124] In certain aspects of the disclosure the C-lobe domain or N-lobe domain comprises a plurality of β-strands connected by a plurality of loop domains, and wherein at least one loop domain of the plurality of loop domains has been modified, and wherein the polypeptide has been modified in such a manner that it is unable to substantially bind host iron binding protein.

[0125] In further preferred aspects the present disclosure provides a method for preparing an immunogenic composition comprising:

1. (a) providing a chimeric nucleic acid sequence comprising as operably linked components:
    1. (i) a first nucleic acid sequence encoding a polypeptide comprising a first C-lobe domain or first N-lobe domain of an HIBP surface receptor protein obtainable from a Gram-negative bacterial species;
    2. (ii) a second nucleic acid sequence encoding a polypeptide comprising a second C-lobe domain or second N-lobe domain of an HIBP surface receptor protein obtainable from a Gram-negative bacterial species; and
    3. (iii) a nucleic acid sequence capable of controlling expression in a recombinant host cell;
2. (b) introducing the chimeric nucleic acid sequence into a host cell and growing the host cell to produce the polypeptide comprising the first and second C-lobe domain or first and second N-lobe domain;
3. (c) recovering the polypeptide comprising the first and second C-lobe domain or first and second N-lobe domain from the host cell; and
4. (d) preparing an immunogenic composition.

[0126] In preferred aspects of the disclosure, the first and second nucleic acids are operably linked in such a manner that a heteromultimeric fusion polypeptide comprising a first and second C-lobe domain or a first and second N-lobe domain are produced, and wherein the heteromultimeric fusion polypeptide is unable to substantially bind host iron binding protein.

[0127] The invention provides a method for preparing an immunogenic composition comprising:

1. (a) providing a chimeric nucleic acid sequence comprising as operably linked components:
    1. (i) a nucleic acid sequence encoding a TbpB polypeptide obtainable from a Gram-negative pathogenic bacterial species, wherein the TbpB polypeptide comprises the sequence of SEQ.ID NO: 174; and
    2. (ii) a nucleic acid sequence capable of controlling expression in a recombinant host cell;
2. (b) introducing the chimeric nucleic acid sequence into a host cell and growing the host cell to produce the TbpB polypeptide;
3. (c) recovering the TbpB polypeptide from the host cell; and
4. (d) preparing an immunogenic composition.

[0128] In accordance herewith, the nucleic acid sequence encoding the HIBP surface receptor protein is linked to a nucleic acid sequence capable of controlling expression of the HIBP surface receptor protein in a host cell. Accordingly, the present disclosure also provides a nucleic acid sequence encoding the HIBP surface receptor protein linked to a promoter capable of controlling expression in a host cell. Nucleic acid sequences capable of controlling expression in host cells that may be used herein include any transcriptional promoter capable of controlling expression of polypeptides in host cells. Generally, promoters obtained from bacterial cells are used when a bacterial host is selected in accordance herewith, while a fungal promoter will be used when a fungal host is selected, a plant promoter will be used when a plant cell is selected, and so on. Further nucleic acid elements capable of controlling expression in a host cell include transcriptional terminators, enhancers and the like, all of which may be included in the chimeric nucleic acid sequences of the present disclosure.

[0129] In accordance with the present disclosure, the chimeric nucleic acid sequences comprising a promoter capable of controlling expression in a host cell linked to a nucleic acid sequence encoding a polypeptide comprising a C-lobe domain or N-lobe domain of an HIBP surface receptor protein obtainable from a Gram-negative bacterial species, wherein the C-lobe domain or N-lobe domain comprises a plurality of β-strands connected by a plurality of loop domains, and wherein at least one loop domain of the plurality of loop domains has been modified, can be integrated into a recombinant expression vector which ensures good expression in the host cell. Accordingly, the present disclosure includes a recombinant expression vector comprising as operably linked components:

1. (i) a nucleic acid sequence capable of controlling expression in a host cell; and
2. (ii) a nucleic acid sequence encoding a polypeptide comprising a C-lobe domain or N-lobe domain of an HIBP surface receptor protein obtainable from or obtained from a Gram-negative bacterial species, wherein the polypeptide has been modified in such a manner that it is unable to substantially bind host iron binding protein,

wherein the expression vector is suitable for expression in a host cell. The term "suitable for expression in a host cell" means that the recombinant expression vector comprises the chimeric nucleic acid sequence of the present disclosure linked to genetic elements required to achieve expression in a host cell.

[0130] The invention provides an expression vector comprising a nucleic acid sequence encoding a TbpB polypeptide obtainable from a Gram-negative pathogenic bacterial species, wherein the TbpB polypeptide comprises the sequence of SEQ.ID NO: 174. Genetic elements that may be included in the expression vector in this regard include a transcriptional termination region, one or more nucleic acid sequences encoding marker genes, one or more origins of replication and the like. The genetic elements are operably linked, typically as will be known to those of skill in the art, by linking e.g. a promoter in the 5' to 3' direction of transcription to a coding sequence. In preferred embodiments, the expression vector further comprises genetic elements required for the integration of the vector or a portion thereof in the host cell's genome. In further aspects of the disclosure the C-lobe domain or N-lobe domain comprises a plurality of β-strands connected by a plurality of loop domains, and wherein at least one loop domain of the plurality of loop domains has been modified.

[0131] Pursuant to the present disclosure, the expression vector may further contain a marker gene. Marker genes that may be used in accordance with the present disclosure include all genes that allow the distinction of transformed cells from non-transformed cells, including all selectable and screenable marker genes. A marker gene may be a resistance marker such as an antibiotic resistance marker against, for example, kanamycin or ampicillin. Screenable markers that may be employed to identify transformants through visual inspection include, β-galactosidase, β-glucuronidase (GUS) (U.S. Pat. Nos. 5,268,463 and 5,599,670) and green fluorescent protein (GFP) (52).

[0132] One host cell that particularly conveniently may be used is *Escherichia coli.* The preparation of the *E. coli* vectors may be accomplished using commonly known techniques such as restriction digestion, ligation, ligation independent cloning, gel electrophoresis, DNA sequencing, the Polymerase Chain Reaction (PCR), and other methodologies. A wide variety of cloning vectors are available to perform the necessary steps required to prepare a recombinant expression vector including custom vectors that the inventors have developed. Among the vectors with a replication system functional in *E. coli,* are vectors such as the pUC or pET series of vectors, etc. Typically, these cloning vectors contain a marker allowing selection of transformed cells. Nucleic acid sequences may be introduced in these vectors, and the vectors may be introduced in *E. coli* by preparing competent cells, electroporation or using other well known methodologies to a person of skill in the art. *E. coli* may be grown in an

appropriate medium, such as Luria-Broth medium and harvested. Recombinant expression vectors may readily be recovered from cells upon harvesting and lysing of the cells. Further, general guidance with respect to the preparation of recombinant vectors and growth of recombinant organisms may be found in, for example: Sambrook et al., Molecular Cloning, a Laboratory Manual, Cold Spring Harbor Laboratory Press, 2001, Third Ed (33).

[0133] The production of the recombinant proteins can occur throughout the growth of the *E. coli* strain, preferably by induction of expression after a period of growth to achieve a significant biomass. This will result in the production of the polypeptide comprising the C-lobe domain or N-lobe domain or the C-lobe domain or N-lobe domain with modified loops. The polypeptide subsequently may be recovered, isolated and separated from other host cell components by a variety of different protein purification techniques including, e.g. metal-chelate chromatography, ion-exchange chromatography, size exclusion chromatography, affinity chromatography, hydrophobic interaction chromatography, reverse phase chromatography, gel filtration, etc. Further general guidance with respect to protein purification may for example be found in: Protein Purification: Principles, High Resolution Methods, and Applications (53). The term "recovered" as used herein means that the polypeptides is obtained in more or less pure form. In preferred aspects, a substantially immunogenic polypeptide comprising a C-lobe domain of an HIBP surface receptor protein obtainable from a Gram-negative bacterial species, wherein the C-lobe domain or N-lobe domain comprises a plurality of β-strands connected by a plurality of loop domains, and wherein at least one loop domain of the plurality of loop domains has been modified, may be obtained in accordance herewith. Thus the HIBP polypeptides obtained in accordance herewith may be prepared in substantially pure form. By "substantially pure" it is meant that the immunogenic protein is separated from other host cell components. In accordance here with the immunogenic protein is at least 95% pure, and more preferably at least 96%, 97%, 98% or 99% pure. Alternatively, relatively crude fractions comprising the HIBP polypeptide may be obtained, e.g. cells containing the polypeptides, cell lysates containing the polypeptides, or cellular fractions containing the polypeptide.

[0134] In further aspects, the present disclosure provides methods for eliciting an immune response in a vertebrate subject. The immune response may be elicited by the delivery of the immunogenic protein or by the delivery of an expression vector comprising a nucleic acid sequence encoding the immunogenic protein. Accordingly, the present disclosure further provides a method for eliciting an immune response in a vertebrate subject, said method comprising administering to the subject:

1. (a) an immunogen comprising a polypeptide comprising a C-lobe domain or N-lobe domain of an HIBP surface receptor protein obtainable from a Gram-negative bacterial species, wherein polypeptide is unable to substantially bind host iron binding protein; or
2. (b) an expression vector comprising a nucleic acid sequence encoding an immunogen comprising a polypeptide comprising a C-lobe domain or N-lobe domain of an HIBP surface receptor protein obtainable from a Gram-negative bacterial species wherein the polypeptide is unable to substantially bind host iron binding protein; and

wherein the immunogen is administered in, or is expressed in, an amount sufficient to elicit an

immune response in the vertebrate subject.

[0135] The present disclosure also provides a use of:

1. (a) an immunogen comprising a polypeptide comprising a C-lobe domain or N-lobe domain of an HIBP surface receptor protein obtainable from a Gram-negative bacterial species, wherein polypeptide is unable to substantially bind host iron binding protein; or
2. (b) an expression vector comprising a nucleic acid sequence encoding an immunogen comprising a polypeptide comprising a C-lobe domain or N-lobe domain of an HIBP surface receptor protein obtainable from a Gram-negative bacterial species wherein the polypeptide is unable to substantially bind host iron binding protein;

for eliciting an immune response in a vertebrate subject.

[0136] The present disclosure further provides a use of:

1. (a) an immunogen comprising a polypeptide comprising a C-lobe domain or N-lobe domain of an HIBP surface receptor protein obtainable from a Gram-negative bacterial species, wherein polypeptide is unable to substantially bind host iron binding protein; or
2. (b) an expression vector comprising a nucleic acid sequence encoding an immunogen comprising a polypeptide comprising a C-lobe domain or N-lobe domain of an HIBP surface receptor protein obtainable from a Gram-negative bacterial species wherein the polypeptide is unable to substantially bind host iron binding protein;

in the manufacture of a medicament for eliciting an immune response in a vertebrate subject.

[0137] The present disclosure yet also provides:

1. (a) an immunogen comprising a polypeptide comprising a C-lobe domain or N-lobe domain of an HIBP surface receptor protein obtainable from a Gram-negative bacterial species, wherein polypeptide is unable to substantially bind host iron binding protein.; or
2. (b) an expression vector comprising a nucleic acid sequence encoding an immunogen comprising a polypeptide comprising a C-lobe domain or N-lobe domain of an HIBP surface receptor protein obtainable from a Gram-negative bacterial species wherein the polypeptide is unable to substantially bind host iron binding protein;

for eliciting an immune response in a vertebrate subject.

[0138] In preferred aspects of the disclosure, the polypeptide comprises at least two C-lobe domains, or at least two N-lobe domains. In further preferred aspects, the polypeptide comprises at least three C-lobe domains, or at least three N-lobe domains.

[0139] In certain aspects of the disclosure, the C-lobe domain or N-lobe domain comprises a plurality of β-strands connected by a plurality of loop domains, and wherein at least one loop domain of the plurality of loop domains has been modified in such a manner that the C-lobe domain or N-lobe domain is unable to substantially bind host iron binding protein.

[0140] The present disclosure further includes an immunogen comprising a C-lobe domain or an N-lobe domain of an HIBP surface receptor polypeptide wherein the C-lobe domain or the N-lobe domain comprises a plurality of β-strands connected by a plurality of loop domains, and wherein at least one loop domain has been modified for use as a medicament.

[0141] The present disclosure further includes an immunogen comprising a C-lobe domain or an N-lobe domain of an HIBP surface receptor polypeptide wherein the C-lobe domain or the N-lobe domain comprises a plurality of β-strands connected by a plurality of loop domains, and wherein at least one loop domain has been modified for use in the prevention of infection or disease by infectious Gram-negative bacteria, including bacteria belonging to the genus *Actinobacillus, Neisseria, Haemophilus, Mannheimia, Histophilus, Pasteurella* or *Moraxella.*

[0142] The present disclosure further includes an immunogen comprising a C-lobe domain or an N-lobe domain of an HIBP surface receptor polypeptide wherein the C-lobe domain or the N-lobe domain comprises a plurality of β-strands connected by a plurality of loop domains, and wherein at least one loop domain has been modified for use in the manufacture of a medicament for the prevention of infection or disease by infectious Gram-negative bacteria, including bacteria belonging to the genus *Actinobacillus, Neisseria, Haemophilus, Mannheimia, Histophilus, Pasteurella* or *Moraxella.*

Vaccine Preparations

[0143] The present disclosure further provides vaccine preparations. Thus, the present disclosure further provides a vaccine composition comprising an antigen derived from a HIBP surface receptor protein from a Gram-negative pathogenic bacterial species, wherein the protein derived from the HIBP surface receptor protein has been modified in such a manner that it is unable to substantially bind host iron binding protein. The vaccine compositions of the present disclosure preferably comprise a vaccine comprising a polypeptide comprising, an HIPB surface receptor protein, a C-lobe domain or N-lobe domain of an HIBP surface receptor protein obtainable from a Gram-negative pathogenic bacterial species wherein the polypeptide is modified in such a manner that it is unable to substantially bind host iron binding protein. In preferred aspects, the vaccine preparation comprises a mixture of C-lobe domains belonging to two different bacterial species or two different bacterial strains. In further preferred aspects, the polypeptide comprises at least two or at least three N-lobe domains or C-lobe domains. In further preferred aspects, said at least two or at least three N-lobe domains or C-lobe domains form a heteromultimer. In further aspects, the C-lobe domain or N-lobe domain comprises a plurality of β-strands connected by a plurality of loop domains, and wherein at least one loop domain of the plurality of loop domains has been modified.

[0144] The invention provides a vaccine composition comprising an immunogenic composition according to claim 1.

[0145] The vaccine preparations of the present disclosure comprise the immunogenic HIBP polypeptides in more or less pure form. Thus, in accordance herewith, substantially pure HIBP polypeptides may be obtained and used to prepare vaccine formulations. In other embodiments more crude HIPB polypeptide preparations may be obtained and used to prepare vaccine formulations. Thus, for example, in such embodiments cells, cell lysates or cell fractions comprising the HIBP polypeptides may be used to prepare the vaccine formulations.

[0146] In order to augment an immune response in a subject, the compositions provided herein further preferably include adjuvants, such as pharmacological agents, cytokines, or the like. Suitable adjuvants include any substance that enhances the immune response of the subject to the immunogenic polypeptides of the disclosure. Non-limiting examples of adjuvants include cytokines, e.g., IL-1, IL-2, IL-12, IL-6, and further include inorganic salts, e.g. aluminum hydroxide, aluminum phosphate, and calcium phosphate; oil emulsions, eg. mineral oil, MF59, QS-21, Montamide ISA51 and ISA-720; Isocoms, eg. ISCOMATRIX; microbial derivatives, eg. MPLA, macrophage-activating protein-2, virosomes, LT/CT, CpG; natural polymers, eg. polysaccharides; and synthetic polymers, eg. polyanhydrides and polyesters, as reviewed in Wilson-Welder *et al.(54).* Adjuvants may be administered, for example, as proteins or other macromolecules at the same time, prior to, or subsequent to, administration of the polypeptide antigens.

[0147] Doses for immunogenic proteins, generally range from about 0.1 µg to about 20 mg, preferably 10 µg to about 3 mg for human subjects. The exact amount necessary, however, will vary depending on the age and general condition of the recipient subject to be treated, the severity of the condition being treated, the particular preparation delivered, the site of administration, as well as other factors. An appropriate therapeutically effective amount can be readily determined by one of skill in the art. Thus, a "therapeutically effective amount" of the present compositions will be an amount sufficient to bring about treatment or prevention of disease or condition symptoms, or to prevent colonization by the pathogenic bacteria, and will fall in a relatively broad range that can be determined through routine trials.

[0148] Vaccine preparations comprising the immunogenic composition of the present disclosure preferably further comprise vehicles, excipients and auxiliary substances, such as wetting or emulsifying agents, pH buffering substances and the like, may be present in the excipient or vehicle. These vehicles, excipients and auxiliary substances are generally pharmaceutical agents that do not induce an immune response in the recipient subject, and may be administered without undue toxicity. Pharmaceutically acceptable excipients include, but are not limited to, liquids such as water, saline, polyethyleneglycol, hyaluronic acid, glycerol and ethanol. Pharmaceutically acceptable salts can also be included therein, for example, mineral acid salts such as hydrochlorides, phosphates, sulfates, and the like; and the salts of organic acids such as acetates, propionates, benzoates, and the like. It is also preferred, although not required, that the preparation will contain a pharmaceutically acceptable excipient that serves as a stabilizer, particularly in order to stabilize the polypeptides of the present disclosure. Examples of suitable carriers that also act as stabilizers for peptides include, without limitation, pharmaceutical grades of dextrose, sucrose, lactose, sorbitol, inositol,

dextran, and the like. Other suitable carriers include, again without limitation, starch, cellulose, sodium or calcium phosphates, citric acid, glycine, polyethylene glycols (PEGs), and combinations thereof.

[0149] The vaccine preparations of the present disclosure may be used to prevent infection or disease caused by infectious Gram-negative bacteria, including, without limitation, bacteria belonging to the genus *Actinobacillus, Neisseria, Haemophilus, Mannheimia, Histophilus, Pasteurella* or *Moraxella,* including without limitation *Actinobacillus pleuropneumoniae, Actinobacillus suis, Haemophilus parasuis, Neisseria meningitidis.* The vaccine preparations may be used to immunize any vertebrate subject including any vertebrate subject expressing host iron binding proteins and including, without limitation, any mammalian subject, including any human subject, porcine subject, bovine subject, equine subject, ovine subject, hircine subject, canine subject, feline subject, leporine subject and, further any ruminant subject, and murine subject. Other vertebrate subjects that may be immunized include any avian subject and piscine subject. The vaccine preparations of the present disclosure may exhibit an enhanced cross-reactive and/or cross-protective immunological response in the recipient host organism. It is further noted that the vaccine preparations of the present disclosure may prevent infection and/or colonization by the infectious Gram-negative bacteria, including bacterial colonization of the respiratory tract or genital tract of a vertebrate subject.

[0150] The present disclosure further includes a vaccine comprising an HIPB surface receptor protein, a C-lobe domain or an N-lobe domain of an HIBP surface receptor polypeptide wherein the C-lobe domain or the N-lobe domain comprises a plurality of β-strands connected by a plurality of loop domains, and wherein at least one loop domain has been modified for use in the prevention of infection or disease by infectious gram-negative bacteria, including bacteria belonging to the genus *Actinobacillus, Neisseria, Haemophilus, Mannheimia, Histophilus, Pasteurella* or *Moraxella.*

Testing vaccine preparations

[0151] In accordance herewith the efficacy of the vaccine preparations of the present disclosure may be evaluated, for example by determining the antibody titre present in blood serum of subjects immunized with a vaccine preparation, e.g. by the performance of an Enzyme Linked Immuno Sorbent Assay (ELISA). Accordingly the present disclosure further comprises a method for evaluating the efficacy of a vaccine preparation comprising a C-lobe domain or N-lobe domain of an HIBP surface receptor protein obtainable from a Gram-negative pathogenic bacterial species wherein the polypeptide is modified in such a manner that it is unable to substantially bind host iron binding protein, the method comprising:

1. (a) administering to a vertebrate subject a vaccine preparation comprising an HIPB surface receptor protein, or a C-lobe domain or an N-lobe domain of an HIBP surface receptor polypeptide obtainable from a Gram-negative pathogenic bacterial species wherein the polypeptide is modified in such a manner that it is unable to substantially

bind host iron binding protein;

2. (b) obtaining blood serum from the vertebrate subject; and
3. (c) assaying the blood serum for the presence of antibodies against the HIBP surface receptor polypeptides.

[0152] The vertebrate blood serum may be assayed following the administration of single or multiple (e.g. 2, 3, or 4) doses of a vaccine preparation. Assays, such as ELISA assays, may be performed using HIBP surface receptor protein isolates from a single or multiple microbial different strains or species. ELISA assays may involve linking of the HIBP surface receptor polypeptide to a carrier protein, such as a maltose binding protein. Where the reactivity of antibodies against multiple HIBP surface receptor protein isolates is assayed, it is possible to evaluate the vaccine preparation for cross-reactivity.

Vaccination Regimens

[0153] As is apparent to those skilled in the art in view of the teachings of this specification, vaccination with the above-described polypeptides or with nucleic acid sequences encoding such polypeptides (DNA vaccines) can be effected in one dose, continuously or intermittently throughout the course of treatment. Methods of determining the most effective means and dosages of administration are well known to those of skill in the art and will vary with the delivery vector, the nature of the composition, the specific prophylaxis or therapy sought, the target cells, and the subject being treated. Single and multiple administrations can be carried out with the dose level and pattern being selected by suitable medical personnel.

[0154] Administration of the above-described pharmaceutical preparations can be effected in one dose, continuously or intermittently throughout the course of treatment. Delivery will most typically be via conventional needle and syringe for the liquid compositions and for liquid suspensions containing particulate compositions. In addition, various liquid jet injectors are known in the art and may be employed to administer the present compositions. The route of vaccine delivery may vary. Thus the vaccines of the present disclosure may be delivered intravenously, subcutaneous, intramuscular, intravaginal, intraperitoneal, intranasal, oral or via other mucosal routes. Methods of determining the most effective means and dosages of administration are well known to those of skill in the art and will vary with the delivery vehicle, the composition of the therapy, the target cells, and the subject being treated. Single and multiple administrations can be carried out with the dose level and pattern being selected by the attending physician or veterinarian.

EXAMPLES

[0155] The examples below are offered for illustrative purposes only, and are not intended to

limit the scope of the present disclosure in any way.

Example 1 - Immune response with a TbpB C-lobe domain, TbpB N-lobe domain and mixture thereof.

[0156] This Example provides an illustration of the value of using subdomains of the TbpB receptor proteins to obtain a more desirable immune response. In regards to what we mean by a more desirable immune response we consider both the magnitude of the antibody response and the cross-reactivity of the antibodies with variant TbpB proteins.

[0157] FIG. 3A illustrates the results from the first experiment for this Example in which different host species (mice, rabbits and pigs) were immunized with intact TbpBs from the human pathogen *Neisseria meningitidis* (strain B16B6 - SEQ.ID NO: 117) or from the porcine pathogen *Actinobacillus pleuropneumoniae* (strain H49 - SEQ.ID NO: 2). The sera from immunized animals were tested against the immunizing antigen in our customized ELISA assay (see below). The results illustrate that the magnitude (titre) of the antibody response in the pig with the TbpB from the pig pathogen *A. pleuropneumoniae* (grey bar) was substantially lower than in the other host species compared to the TbpB from the human pathogen *N. meningitidis* (black bar) suggesting that binding of host transferrin was influencing development of the antibody response against TbpB.

[0158] The second experiment **(FIG. 3B)** involves immunization of pigs with intact TbpB from the bovine pathogen *Mannheimia haemolytica* (strain H196 - SEQ.ID NO: 206) or the intact TbpB (SEQ.ID NO: 2), TbpB N-lobe (SEQ.ID NO: 8) or TbpB C-lobe (SEQ.ID NO: 6) from the porcine pathogen *Actinobacillus pleuropneumoniae* (strain H49). **FIG. 3B** illustrates the immune response in individual pigs (cluster of bars) before immunization (white bar), after the first immunization (light grey bar), after the second immunization (dark grey bar) and after the third immunization (black bar). Note that the titres are expressed as a binary logarithm to reflect the two-fold dilutions used in evaluating titre. Most of the pigs displayed high titres of antibody (between 26,000 and 256,000) after the third immunization but several of the pigs immunized with intact TbpB or TbpB N-lobe from *A. pleuropneumoniae* displayed substantially reduced titres (between 5,300 and 8,000). The observation that two of the four pigs immunized with intact TbpB and three of the pigs immunized with TbpB N-lobe displayed substantially reduced titres suggests that binding of host transferrin influences the development of the antibody response only in a subset of the animals.

[0159] The third experiment illustrated in this example (FIG. 3C) was designed to evaluate the ability of sera against intact TbpB and its subdomains to react with different representative TbpBs from porcine pathogens in order to evaluate the cross-reactivity of the antisera. Pigs were immunized with the intact TbpB (SEQ.ID NO: 2), the TbpB C-lobe domain (SEQ.ID NO: 6), the TbpB N-lobe domain (SEQ.ID NO: 8) or a mixture of the TbpB N-lobe and TbpB C-lobe. The sera were tested against (i) the intact TbpB from *Actinobacillus pleuropneumoniae* strain H49 (SEQ.ID NO: 2), (ii) the intact TbpB from *Haemophilus parasuis* strain HP5, (SEQ.ID NO:

115) or (iii) the intact TbpB from *Actinobacillus pleuropneumoniae* strain H87 (SEQ.ID NO: 12),

[0160] The results in **FIG. 3C** illustrate that the TbpB C-lobe domain from *A. pleuropneumoniae* strain H49 induces a more cross-reactive immune response than the intact TbpB (higher titre against the heterologous TbpB from strain H87) or the TbpB N-lobe (higher titres against strain H87 and HP5). The TbpBs used in this assay were designed to represent the overall sequence and structural diversity present in clinical disease isolates of *A. pleuropneumoniae, A. suis* and *Haemophilus parasuis* from pigs around the world (SEQ.ID NO: 2; SEQ.ID NO:12; SEQ.ID NO: 28; and SEQ.ID NO: 107 to SEQ.ID NO: 115) (**FIG. 4**). Thus in this example we are not limiting our analysis to a single pig pathogen but are targeting three distinct pig pathogens that are problematic for the worldwide pig industry. The fact that these pathogens happen to share a common mechanism for acquiring iron from the host provides a unique opportunity to develop a vaccine targeting the three pathogens from a common antigen, TbpB. These results indicate that by using one or more C-lobe domains as an antigen it is feasible to produce a broadly cross-reactive response against pig pathogens worldwide and thus could consider vaccination to eliminate the presence of these pathogens globally.

[0161] Surprisingly, the enhanced cross-reactivity induced by the C-lobe domain was retained even when the C-lobe was mixed with the N-lobe in the immunizing mixture (**FIG. 3C**, "N + C lobe"). These results teach us that antigens with smaller variable loop regions (the "C-lobe" compared to the "N-lobe", **FIG. 1**) are capable of inducing a more cross-reactive antibody response, and that this enhanced ability to induce a cross-reactive immune response is retained even when the C-lobe is combined with other antigens in the immunizing mixture. More specifically, these results indicate that the tendency for the N-lobe to generate a more strain specific immune response is only capable of effectively inhibiting induction of a cross-reactive immune response by the C-lobe when it is physically linked to the N-lobe. In other words, surprisingly, the propensity of the N-lobe to generate a more specific immune response is substantially reduced when the N-lobe is mixed with the C-lobe. To the best of our knowledge this phenomenon has not been described previously.

[0162] The results also suggest that there is a reduced response against the intact TbpB and TbpB N-lobe relative to the C-lobe (**FIG. 3B, 3C**), which could indicate that binding of host transferrin, a feature only present in the intact TbpB and TbpB N-lobe, may be modulating the immune response in pigs.

[0163] It is important to mention that in contrast to previous published studies we did not use the standard ELISA method for measuring antibody levels since we identified a major deficiency in the standard ELISA method. We observed that in contrast to what is commonly assumed, purified proteins do not necessarily bind randomly to the ELISA plates, providing potentially strong biases or deficiencies in evaluating the binding of antibodies to epitopes on the surface of the protein. In particular we noted that TbpB, and particularly the N-lobe of TbpB, essentially binds to the solid surface of ELISA plates in one orientation, masking the Cap region of the N-lobe so that the binding of transferrin cannot be detected (**FIG. 5**). In contrast, the recombinant fusion protein with an N-terminal maltose binding protein (Mbp) partner that

was the precursor for the purified TbpB N-lobe was proficient in transferrin binding (**FIG. 5**). This phenomenon was observed with TbpB N-lobes from human, pig and cattle pathogens, and to a lesser extent, the intact TbpBs. Since these proteins are quite different in sequence (< 30% overall sequence identity) it indicates that this is not a unique property of a specific protein but there may be varying degrees to which nonrandom binding impacts solid-phase binding assays.

[0164] To overcome this deficiency we devised a method for binding recombinant proteins to streptavidin-coated ELISA plates by virtue of a biotin residue that was enzymatically added to the N-terminus during protein expression in the cytoplasm. As shown in **FIG. 5**, the addition of an enzymatically biotinylated N-terminal peptide restored the ability of the TbpB N-lobe to bind transferrin. This approach may be more efficient at exposing the transferrin-binding region as comparison of the results with the Tbp N-lobe fused to Mbp in the left and right side of the figure indicates. This new and novel ELISA assay format was used in all our ELISA assays for monitoring antibody reactivity since it ensured complete and equal access to all epitopes on the target protein, thus providing a true comparison in evaluating the degree of cross-reactivity.

[0165] The recombinant antigens for the immunization experiments were produced in the cytoplasm of *E. coli* using a custom T7 expression vector encoding an N-terminal polyhistidine tag, a maltose binding protein and a tobacco etch virus (TEV) protease cleavage site. The recombinant fusion proteins were isolated by Ni-NTA chromatography, the antigens released by (TEV) cleavage and purified by a combination of Ni-NTA and Q-Sepharose chromatography.

[0166] FVB mice (albino MHC *haplotype* H2q from Charles River), 3 monthold New Zealand White rabbits and 51 day-old Large White Landrace FI cross pigs were used for the immunization experiment in FIG3A. Purified recombinant proteins were mixed with phosphate buffered saline and either 33% (**FIG. 3A**) or 20% (**FIG. 3B, FIG. 3C**) Emulsigen D (MVP Technologies) to a final concentration of 25 µg in 0.1ml for mice, 50 µg in 0.5ml for rabbits and 100 µg in 2 ml for pigs. Three injections were administered sub-cutaneously for mice and rabbits and sub-cutaneously (**FIG. 3A**) or intramuscularly (**FIG. 3B, FIG. 3C**) for pigs. The animals were immunized on day 0, 21, 42 and final blood was collected on day 56.

[0167] Sera taken at week 8 were tested against representative proteins in our custom solid-phase ELISA assay. The recombinant fusion proteins used in the ELISA assay were produced in the cytoplasm of *E. coli* using a custom T7 expression vector encoding an N-terminal optimized biotinylation sequence, a polyhistidine tag, a maltose binding protein and a tobacco etch virus (TEV) protease cleavage site. These proteins were biotinylated *in vivo* at the N-terminal biotinylation sequence so that they could be applied to streptavidin coated ELISA plates.

[0168] Crude extracts from small-scale overnight protein expression experiments with the expression vector for the biotinylated fusion proteins were sufficient to saturate the ELISA plates based on prior optimization experiments. Dilutions of the antisera of interest were prepared in 2.5% skim milk in phosphate buffer saline (PBST) and applied to the plates for 1

hour at room temperature. After removal and washing the primary antibody was detected by HRP-conjugated goat anti-mouse, anti-rabbit or anti-swine IgG at a dilution of 1:100,000 (1:25,000 for anti-swine) for one hour at room temperature. The titre is expressed as the reciprocal of the last dilution with an A450 > 0.3 (greater than the mean plus three standard deviations of the background reading of wells without sera added)..

[0169] The calculation of SEM error was done via ANOVA with Tukeys HSD (honest significant difference) test done as post hoc. The statistics showed that for all the sera, H49 is significantly different from H87 and that the N lobe is significantly different from the C lobe or the N+C lobe. The stars shown in **FIG. 3C** denote specific immunization/protein pairs that differ significantly from the C lobe or N+C lobe tested against H49.

Example 2 - Production of a trimer of porcine pathogen TbpB C-lobes

[0170] In this Example we demonstrate that three recombinant engineered C-lobes that represent a wide diversity of TbpBs present in the three porcine pathogens, may be linked together and retain antigenicity. The engineered C-lobes used here are those obtained from *A. pleuropneumoniae, A. suis* and *Haemophilus parasuis* (**FIG. 4**). Thus the genes encoding the TbpB C-lobes from strains *A. pleuropneumoniae* H49 (SEQ.ID NO: 6), *A. suis* H57 (SEQ.ID NO: 35) and *A. pleuropneumoniae* H87 (SEQ.ID NO: 22) were linked to form a gene encoding a single polypeptide encompassing the three C-lobes (SEQ.ID NO: 40) **Panel A** of **FIG 6.** There are relatively short peptides connecting the secondary structural elements of the C-lobes (indicated by underline) in this C-lobe trimer. The linking peptides consist of authentic interlobe sequence from the individual C-lobe domains. **Panel B** of **FIG. 6** illustrates the production of the C-lobe trimer and is compared to preparations of recombinant engineered TbpB N-lobe and C-lobe from the human pathogen *N. meningitidis* strain M982. The results indicate that the C-lobe trimer is produced in good quantity and is stable. However the preparation illustrated in **FIG. 6** requires additional purification prior to use in immunization experiments.

[0171] Since there was no major barrier to the production of a stable C-lobe trimer, the C-lobe trimer was produced and purified for an immunization experiment to determine whether it retained immunogenicity. As illustrated in **FIG. 7**, the C-lobe trimer was able to induce an immune response against the three representative TbpBs, indicating that linking the three individual C-lobes together did not substantially alter their immunological properties. The results also suggest that a single protein antigen may be able to induce an immune response capable of reacting with most, if not all strains of the *pleuropneumoniae, A. suis* and *Haemophilus parasuis,* pig pathogens, showing potential promise for development of a broadly cross-protective pig vaccine.

Example 3 - Reduction of loop regions in the N-lobe of *A pleuropneumoniae* TbpB

[0172] In this Example, the loop regions of the N-lobe domain from three representative TbpBs from porcine pathogens were modified in order to determine their impact on induction of a cross-reactive immune response. The three representative TbpBs were from *A. suis* strain H57 (SEQ.ID NO: 28), *A. pleuropneumoniae* strain H87 (SEQ.ID NO: 12) and *A. pleuropneumoniae* strain H49 (SEQ.ID NO: 2). These particular TbpBs were selected because in addition to representing sequence diversity, there was high-resolution structural data available; *A, suis* strain H57 (3PQU.pdb), *A. pleuropneumoniae* strain H87 (3PQS.pdb) and *A. pleuropneumoniae* strain H49 (3HOL.pdb). The loop reduction process resulted in an overall loss of 74 amino acids (297-224) for the TbpB N-lobe from *A.* suis strain H57 (SEQ.ID NO: 36,38], 45 amino acids (248-203) for the TbpB N-lobe from *A. pleuropneumoniae* strain H87 (SEQ.ID NO: 24,26) and 27 amino acids (274-247) for the TbpB N-lobe from the *A. pleuropneumoniae* strain H49 (SEQ.ID NO: 8,10). The design of the loop reduction for *A. pleuropneumoniae* strain H49 is described in more detail below for illustrative purposes.

[0173] To design the loop reductions, the structure of TbpB from strain H49 (3HOL.pdb) was superimposed with the structure of TbpB from strain H87 (3PQS.pdb) while simultaneously viewing a multiple sequence alignment from a set of representative TbpBs from porcine pathogens. By examining the structure and regions of variation, several areas for potential loop reduction were identified that were predicted to not perturb the overall structure of the N-lobe, These include loops 1, 5, 8a, 8c and 12 according to the standard nomenclature (**FIG. 2**) and are illustrated in **FIG. 8** on structural models of a side view (**Panel A**) and top view (**Panel B**) of the TbpB N-lobe. Loop reductions were designed to minimize the potential perturbation to the overall folding and structure of the N-lobe by selecting appropriate amino acid replacements as needed in addition to the removal of amino acids. The amino acid sequence of the original N-lobe (top sequence) and the modified N-lobe (bottom sequence) are illustrated in the sequence alignment in **FIG. 8, Panel C** where the loop regions are highlighted in grey and labeled in grey font. The DNA sequence encoding the amino acid sequence illustrated in **Panel** C was optimized for expression in *E. coli* strain and then synthesized.

[0174] A similar strategy was adopted to generate loop reductions for the TbpB N-lobes from *A.* pleuropneumoniae strain H87 and *A. suis* strain H57 since they represent considerable sequence and structural diversity of the TbpBs from porcine pathogens (**FIG. 4**) and the relevant structures are available (3PQS.pdb and 3PQU.pdb) (12). The potential of producing engineered antigens that collectively could induce a cross-reactive response against the N-lobe regions of most if not all, clinical isolates, would have considerable potential for enhancing the effectiveness of a vaccine targeting the three porcine pathogens.

[0175] The resulting genes were cloned into a custom expression vector that encodes an N-terminal polyhistidine region, maltose binding protein and TEV (tobacco etch virus) cleavage site preceding the coding sequence for the cloned N-lobe. The expression plasmid for the engineered version of the TbpB N-lobe from *A pleuropneumoniae* strain H49 was transformed into the *E. coli* expression strain ER256 that carries a chromosomal copy of the T7 RNA polymerase gene inserted downstream of the *lacZ* promoter. A small-scale expression analysis was performed using auto-induction media (55) that capitalizes on glucose repression and

lactose induction of the *lac* promoter. Thus by using a specific ratio of glucose to lactose into the media, expression of the T7 RNA polymerase is optimally initiated at mid-log phase of growth. Cells were lysed after overnight growth with a bead beater to lyse the cells, the recombinant proteins were captured with either a Ni-NTA resin or a porcine Tf-Sepharose resin, washed and the bound proteins eluted in SDS-PAGE buffer.

[0176] As illustrated in **FIG. 9** the loop reductions in the TbpB N-lobe from *A. pleuropneumoniae* strain H49, *A.* suis strain H57 or *A. pleuropneumoniae* strain H87 resulted in the production of stable proteins, thus not interfering with the overall folding of the N-lobe, and providing material suitable for immunization. The upper panel shows recombinant proteins produced in a small-scale expression experiment captured on a Ni-NTA resin with the wild-type intact TbpB and TbpB N-lobe as controls. The results also show, that unlike that wild-type protein, the mutant proteins were no longer capable of substantially binding to porcine transferrin (Tf). Thus in the middle panel the engineered N-lobes were not captured by porcine Tf -Sepharose. In the bottom panel the material illustrated in the top panel was used in a solid-phase binding assay using HRP-conjugated porcine transferrin and, unlike the controls, the engineered N-lobes did not display any binding activity. We anticipate that there will be enhanced immunogenicity of these proteins in the native host, pigs. Thus this example shows that strategies for removal of antigenically variable regions in the N-lobe of TbpB proteins are feasible and that such removal can result in enhanced immunogenicity.

Example 4- Cross-reactivity of C-lobes of *N. meningitidis* TbpB

[0177] This example illustrates the use of engineered derivatives of TbpBs from the human pathogen *Neisseria meningitidis* in accordance with the present disclosure. As a first step we examined the diversity of TbpBs from *N. meningitidis* and ensured that we would have a representative set of TbpBs for our evaluation of cross-reactivity. **FIG. 10** illustrates the overall diversity of TbpBs in strains of *N. meningitidis* that were collected globally over a long time period plus additional sequences from the Neisseria Bacterial Isolate Genome Sequence Database (BIGSDB http://pubmlst.org/neisseria/)(56) (41). The sequences for a representative set of TbpBs (SEQ ID NO: 117; SEQ.ID NO: 123; SEQ.ID NO: 132 to SEQ.ID NO: 147; SEQ,ID NO: 177; and SEQ.ID NO: 178) from strains indicated by arrows, double arrows or lines in **FIG. 10A** are included in this application to define the sequence diversity in each group. There were four major phylogenetic groupings of the *N. meningitidis* TbpBs. Group 1 includes strains that possess isotype I TbpBs. Isotype I TbpBs characteristically have smaller TbpBs (approximately 65-70 kDa) compared to the isotype II TbpBs (80 -85kDa). Comparison of the sequences by multiple sequence alignments revealed that difference in size is largely attributed to the C-lobe being larger in isotype II TbpBs. The isotype II TbpBs clustered into three major phylogenetic groups (Groups 2 -4, **FIG. 10A**).

[0178] A phylogenetic tree illustrating the sequence diversity of the TbpB C-lobes (**FIG. 10B**) supports the *conclusion* that the C-lobe sequences are largely responsible for the identification of the two TbpB isotypes. The members of Group 2 in **FIG. 10A** do not cluster together in the

C-lobe phylogenetic tree but are distributed throughout the tree in **FIG. 10B,** indicating that Group 2 was largely defined by the N-lobe sequences. This indicates that if immunological cross-reactivity is going to be determined by reactivity against the C-lobe, specific representatives of group 2 would not be required. In contrast, the arrows and lines that were used to identify a set of TbpB sequences to represent the overall TbpB diversity did not adequately represent the overall C-lobe diversity, thus two additional strains were selected to provide a more comprehensive representation of the C-lobe diversity. The C-lobe sequences from strains identified by the arrows, double arrows or lines are included in this application to provide a representative sample of the sequence diversity (SEQ ID NO: 87; SEQ.ID NO: 93; and SEQ.ID NO: 147 to SEQ.ID NO: 163).

[0179] In order to address the question as to whether a vaccine targeting the TbpB from *N. meningitidis* might *induce* an immune response directed against *N. gonorrhoeae* we performed an analysis of the sequence diversity of the TbpB and TbpB C-lobes from *N. gonorrhoeae.* The sequences of the representative TbpBs and TbpB C-lobes from the *N. meningitidis* study (**FIG. 10**; SEQ .D NO: 119; SEQ.ID NO: 125; SEQ.ID NO: 179 to SEQ.ID NO: 195; SEQ.ID NO: 117; SEQ.ID NO: 123; SEQ.ID NO: 132 to SEQ.ID NO: 147; SEQ.ID NO: 177; and SEQ.ID NO: 178) were included in the analysis. As illustrated in **FIG. 26A,** the *N. gonorrhoeae* TbpBs are most closely related to the isotype 2 TbpBs and form two subgroups within the *N. meningitidis* isotype 2 cluster. This suggests that with strategies using site-directed mutants of recombinant TbpB as preferred vaccine antigens, it might be possible to achieve broad cross-protection primarily with antigens derived from meningococcal TbpBs. **FIG. 26B** illustrates that, in contrast to the situation with the intact TbpBs, the *N. gonorrhoeae* TbpB C-lobes are a distinct subgroup from the *N. meningitidis* C-lobes. Thus with strategies using C-lobes to provide broad cross-protection, C-lobes from *N. gonorrhoease* strains would be required.

[0180] In order to compare *the* ability of the truncated TbpB and the TbpB C-lobe to induce a cross-reactive antibody response, a recombinant truncated TbpB and a TbpB C-lobe derived from *N. meningitidis* strain, B16B6 (marked by black arrow in **FIG. 10**), were selected for the immunological analysis. A recombinant truncated TbpB and a TbpB C-lobe from strain B16B6 were used to immunize rabbits and the sera was tested for cross-reactivity using our novel ELISA assay (**FIG. 5**). It is important to recognize that many of the sequences of the C-lobes included in this application start just after the end of the last beta-strand of the barrel domain on the N-lobe, thus include the linker region between the N-lobe and C-lobe (L15, **FIG. 2**). Thus it would be possible to prepare stable, functional C-lobes with N-terminal truncations that remove the L15 region (14 amino acids in the B16B6 C-lobe) for immunization experiments.

[0181] A representative set of TbpBs derived from strains distributed throughout the phylogenetic tree (black and *grey* arrows, **FIG. 10**) were selected to evaluate the cross-reactivity of the sera. Two additional TbpBs indicated by the two double-headed arrows would have been included in the analysis to provide more complete coverage, but were not available at the time of the analysis.

[0182] The proteins were expressed in our custom expression vector with an N-terminal

biotinylation *sequence,* and were applied to streptavidin coated ELISA plates. The sera from rabbits immunized with the engineered C-lobe and truncated TbpB derived from strain B16B6 were tested for their ability to recognize the panel of TbpB variants. The antiserum against the truncated TbpB had higher titres against the homologous TbpB (B16B6) than the anti-C-lobe antiserum, and slightly higher or equivalent titres against the TbpB from one of the heterologous strains (H44/76). However, the anti-C-lobe antiserum had higher titres of antibody against TbpBs from all of the other heterologous strains than that anti-TbpB antiserum. Thus the C-lobe is superior in its ability to induce cross-reactive antibodies than the intact TbpB.

[0183] In this immunization experiment the recombinant antigens were produced as described above and used to immunize rabbits (New Zealand White, 3 months old, female) sub-cutaneously in the hind region using 50 µg of of purified antigen in 20% Emulsigen D (VSA) adjuvant. The rabbits were immunized at 0, 3 and 6 weeks.

[0184] Sera taken at week 8 were tested against representative proteins in our custom solid-phase ELISA assay. The recombinant fusion proteins used in the ELISA assay were produced as described above. The recombinant proteins tested in the custom ELISA assay were truncated versions of the intact TbpBs (missing the first 19-36 amino acids) from *N. meningitidis* strains; (i) B16B6 (SEQ.ID NO: 117), (ii) H44/76 (SEQ.ID NO: 133), (iii) S3131 (SEQ.ID NO:132), (iv) M990 (SEQ.ID NO:134), (v) M978 (SEQ.ID NO:135), (vi) M992 (SEQ.ID NO:138), (vii) P3006 (SEQ.ID NO:139), (viii) 120M (SEQ.ID NO:137), (ix) MC58 (SEQ.ID NO:136) and (x) M982 (SEQ.ID NO: 123).

[0185] Crude extracts from small-scale overnight protein expression experiments with the expression vector for the biotinylated fusion proteins were sufficient to saturate the ELISA plates based on prior optimization experiments. Dilutions of the antisera of interest were prepared in 2.5% skim milk in phosphate buffer saline (PBST) and applied to the plates for 1 hour at room temperature. The primary antibody was detected by HRP-conjugated goat anti-rabbit IgG at a dilution of 1:100,000 for one hour at room temperature and the titre is expressed as the reciprocal of the last dilution with an A450 > 0.3.

Example 5 - Production of a dimer *of N. meningitidis* TbpB C-lobes

[0186] The result in **FIG. 11** illustrates that the TbpB C-lobe domain from the human pathogen *N.* meningitidis is capable of inducing an enhanced cross-reactive response relative to the intact TbpB. In this example we demonstrate that it is possible to generate a single polypeptide encompassing the two C-lobes that is stable and immunogenic. The two C-lobes are from strains with antigenically divergent TbpBs, strain B16B6 and M982, that represent the two isotypes of TbpB (**FIG. 10**). **Panel A** of **FIG. 12** illustrates a single gene that was constructed to encode the two representative TbpB C-lobes (SEQ.ID NO: 150) used in the immunization experiments described in **Example 4. Panel B** of **FIG .12** illustrates the production of the C-lobe dimer compared to preparations of the individual constituent TbpB C-lobes. There are

reasonable levels of production of the C-lobe dimer that appears to be relatively stable but additional purification would be required prior to use in immunization experiments.

[0187] FIG. 13 illustrates that the dimer consisting of the TbpB C-lobes from *N. meningitidis* strains M982 and B16B6 is capable of inducing an effective immune response against intact TbpBs from both species.

Example 6 - Reduction of loop regions from the C-lobe of *N. meningitidis.*

[0188] In this Example we demonstrate it is possible to substantially reduce the loop regions from the C-lobe *of N. meningitidis.* Such reduction is useful in that it provides a derivative lacking the large loop regions which may be used as a convenient 'scaffold' for displaying epitopes from other antigens or other pathogens, and further may display desirable immunological properties.

[0189] In this example the loop regions of the C-lobe domain from N. *meningitidis* strain M982 were modified to remove a total of 82 amino acids from the large, flexible loop regions. Structural models of the native C-lobe and the engineered C-lobe with substantial reduction of four of the large flexible loops are illustrated in **Panel A** of **FIG. 14.** The four loops targeted for reduction were not resolved in the protein crystallography based structure (3VE2.pdb), indicating that there was variation in the conformation of the loops, which is why the loops are represented by dotted lines in model on the left in **Panel A**.

[0190] The strategy for loop removal was developed by examination of the detailed structure (3VE2.pdb) while evaluating the sequence variability in sequence alignments of selected C-lobes. However, providing the most effective bridge between the loops without potentially disrupting the structure was a dominant criteria for the selection of bridging amino acids. The alignment of sequences of the native C-lobe (SEQ.ID NO: 125), engineered derivatives lacking each of the targeted loops and a 'loopless' C-lobe with all four loops removed [SEQ.ID NO: 129) is illustrated in **Panel B** of **FIG. 14.**

[0191] Using the splicing by overlap extension approach (SOEing) (57) genes encoding the individual loop deletions and the 'loopless' C-lobe with all four loops removed were prepared. The SOEing approach was performed on the expression plasmid used for production of the recombinant C-lobe from *N. meningitidis* M982, so that the stability of the resulting engineered proteins could readily be evaluated. The vector encodes an N-terminal polyhistidine tag, the gene encoding maltose binding protein and a TEV (tobacco etch virus) cleavage site preceding the inserted gene encoding the TbpB C-lobe. The expression plasmid was transformed into the *E. coli* expression strain ER2566 that carries a chromosomal copy of the T7 RNA polymerase gene inserted into the *lacZ* gene, and thus is under the control of the lac promoter. A small-scale expression analysis was performed using auto-induction media (55). After overnight growth the cells were collected and lysed and the supernatant fraction after centrifugation was applied to a Ni-NTA resin, washed and the bound proteins eluted in SDS-PAGE buffer.

[0192] As illustrated in **FIG. 15**, the yields of the recombinant C-lobes with substantial reductions in loop 18, loop 21, loop 23 or loop 27 were comparable to the native C-lobe protein (WT), indicating that the removal of the individual loops did not adversely effect protein stability. **FIG. 15** also shows that the removal of 81 amino acids in all four loops did not impact the level of protein produced, indicating that the removal of all four loops did not interfere with the overall folding of the C-lobe. It is salient to mention that the 'loopless' C-lobe was readily produced and purified in good quantity, and that the crystal structure has been obtained from the purified 'loopless' C-lobe. This indicates that the engineered antigens can readily be produced in a substantially stable form at levels of production that are suitable for commercial applications. Thus this example not only shows that strategies for removal of antigenically variable regions are feasible, but that the resulting protein may be suitable as an epitope display scaffold since the folding of the core structure is not influenced by variations in the size and nature of the loops.

[0193] Finally, as illustrated in **FIG. 16**, the 'loopless' C-lobe (SEQ.ID NO: 129, last two bars) is immunogenic and capable of inducing a strong antibody response against the intact (native) TbpB antigen (SEQ.ID NO: 123). This figure illustrates that the loopless C-lobe actually induced higher titers of antibody against the TbpB from *N. meningitidis* strain M982 in mice than the original TbpB C-lobe (SEQ ID NO: 125) antigen (compare 3rd and 1st bars in the figure). Just as surprising is the observation that the 'loopless' C-lobe induced similar levels of antibodies against the heterologous TbpB from strain B16B6 as the native TbpB C-lobe from B16B6, in spite of the fact that it is quite divergent in sequence (**FIG. 10**). Comparison of the 2nd and 4th bars in **FIG. 16** illustrate that these two proteins induce a similar level of antibodies against intact TbpB from strain B16B6.

[0194] In these experiments FvB female mice were immunized with 25ug of purified protein antigen with 20% emulisgen D on day 0, 21 and 42 and sera taken at day 56 were assessed for endpoint titre using our custom ELISA assay. The B16B6 TbpB C lobe, M982 TbpB C lobe, or modified M982 TbpB ('loopless') were used to immunize four mice each. Endpoint titres were assessed against biotinylated intact M982 or B16B6 TbpB protein. Titres were determined with 1:100,000 of goat anti-mouse IgG H+L peroxidase conjugated antibody. Endpoint titres were determined as the inverse of the last dilution at which a positive signal could be confidently detected. Each serum was run in triplicate and results are shown as the average of all mice with that treatment +/- SEM.

Example 7 - Insertion of portions of TbpA into an engineered C-lobe of a TbpB.

[0195] In this example, the DNA encoding segments of the extracellular surface loops of the integral outer membrane protein transferrin binding protein A, TbpA, were spliced into the gene encoding the modified or 'loopless' TbpB C-lobe from *N. meningitidis* strain M982, resulting in genes encoding various hybrid TbpA-TbpB proteins. The reason for splicing selected regions

of TbpA onto the TbpB C-lobe scaffold is that it provides a more efficient means of production than the intact TbpA protein, and provides the ability to specifically target surface regions of TbpA for induction of antibody.

[0196] The gene encoding the modified C-lobe of the TbpB polypeptide (SEQ ID NO: 129) prepared in Example **6** was used as a starting point (see further: **Panel A** of **FIG. 14** (middle model)). The DNA encoding segments from different surface loops of TbpA (**FIG. 17, Panel A**) were spliced into the sites where the larger loops had been removed from the TbpB C-lobe polypeptide (**FIG. 17, Panel B**). Portions from the beta-barrel extracellular loops 3, 10, and 11 of TbpA (58) (space filled and labeled regions in **Panel A**) were inserted into the modified loop regions 18, 21 and 23 of the engineered TbpB C-lobe (**Panel B**). Similarly, a segment from the N-terminal plug region that inserts between the C1 and C2 domains of human transferrin in the TbpA-transferrin structure (plug loop, **Panel A**) was inserted into the modified loop 27 of the modified TbpB C-lobe.

[0197] Assembly of the TbpA loops on the TbpB C-lobe was done using the splicing by overlap extension approach (SOEing) (57). The SOEing approach was performed on the expression plasmid used for production of the recombinant C-lobe from *N. meningitidis* M982, so that the stability of the resulting engineered proteins could readily be evaluated. The vector encodes an N-terminal polyhistidine tag, the gene encoding maltose binding protein and a TEV (tobacco etch virus) cleavage site preceding the inserted gene encoding the TbpB C-lobe. The expression plasmids were transformed into the *E. coli* expression strain ER2566 that carries a chromosomal copy of the T7 RNA polymerase gene inserted into the *lacZ* gene, and thus is under the control of the lac promoter. A small-scale expression analysis was performed using autoinduction media (55). After overnight growth the cells were collected and lysed and the supernatant fraction after centrifugation was applied to a Ni-NTA resin, washed and the bound proteins eluted in SDS-PAGE buffer.

[0198] As illustrated in **Panel A** of **FIG. 18,** insertion of the foreign TbpA segments into the loops of the modified TbpB C-lobe resulted in the production of stable recombinant protein. The recombinant proteins illustrated in **Panel A** of **FIG. 18** contained an N-terminal polyhistidine tag, a maltose-binding protein fusion partner and a TEV (tobacco etch virus) protease cleavage site. **Panel B** of **FIG. 18** illustrates the release of the wild-type and mutant C-lobes from the recombinant protein fusion partner by cleavage with TEV protease. The results demonstrate that insertion of the foreign protein segments did not substantially affect the stability of the engineered C-lobe, suggesting that the foreign segments did not interfere with the normal folding of the core structural elements of the C-lobe. The implication of these results is that the C-lobe appears to be a stable and versatile protein scaffold for the display of foreign epitopes that could ultimately be used for display of epitopes from a variety of antigens and antigenic variants, providing an additional strategy for generating engineered antigens with the ability to generate a broadly cross-protective immune response.

[0199] Finally, as illustrated in **FIG. 19**, modified TbpB C-lobes containing regions of TbpA spliced into the regions where large loops were reduced or removed are immunogenic. This

figure illustrates that hybrid TbpA-TbpB C-lobe proteins induced antibody titres equal to or higher than the parent modified ('loopless') C-lobe. Notably the proteins displaying regions from loop 10 and loop 11 from TbpA had the highest titres (2nd and 3rd bars in **FIG. 19**).

[0200] In this experiment, FvB female mice were immunized with 25 µg of purified protein antigen with 20% emulisgen D on day 0, 21 and 42 and sera taken at day 56 was assessed for endpoint titre using our custom ELISA assay. Three mice were immunized with the 'loopless' C-lobe with all four loops removed (SEQ.ID NO: 97). Five mice were used for immunization with the each of the four other hybrid antigens; (i) the 'loopless' C-lobe with TbpA loop 10 inserted into the TbpB C-lobe loop 21(SEQ.ID NO: 154), (ii) the 'loopless' C-lobe with TbpA loop 11 inserted into the TbpB C-lobe loop 23 (SEQ.ID NO: 156), (iii) the 'loopless' C-lobe with TbpA loop 3 helix inserted into the TbpB C-lobe loop 27 (SEQ.ID NO: 158), or (iv) the 'loopless' C-lobe with TbpA plug loop inserted into the TbpB C-lobe loop 18 (SEQ.ID NO: 160). The sera were tested against the biotinylated recombinant form of the modified M982 C-lobe displaying all four of the TbpA loops inserted (SEQ.ID NO: 131). Titres were determined with 1:100,000 of goat anti-mouse IgG H+L peroxidase conjugated antibody. Endpoint titres were determined as the inverse of the last dilution at which a positive signal could be confidently detected. Each serum was run in triplicate and results are shown as the average of all mice with that treatment +/- SEM.

Example 8- Insertion of portions of LbpA into a modified C-lobe of a TbpB.

[0201] In this example, segments of the extracellular surface loops of the integral outer membrane protein lactoferrin binding protein A, LbpA, from strain MC58 (SEQ.ID NO: 162), were spliced into the modified TbpB C-lobe from *N. meningitidis* strain M982 (SEQ. ID NO: 129) that was described in **Example 6.** The reason for splicing selected regions of LbpA onto the TbpB C-lobe scaffold is that it provides a more efficient means of production than the intact LbpA protein, and provides the ability to specifically target surface regions of LbpA for induction of antibody. In conjunction with **Example 7**, we are able to illustrate how the generation of hybrid proteins could provide the opportunity to induce an immune response against three different proteins present on the surface of *N. meningitidis,* providing a greater barrier to potential Vaccine escape', in which an antigenic variant of a critical target protein is able to escape the impact of the immune response generated against the vaccine antigens.

[0202] Since there were no structures available for LbpA, structural modeling of LbpA was performed using 3 web-based protein prediction servers: SWISS MODEL, I-TASSER, and PHYRE2 in an attempt to attain the most appropriate model. Initially BLAST searches were performed to find the most appropriate LbpA for modeling with the known TbpA structure (58), and revealed that the LbpA from strain MC58 (SEQ.ID NO: 130) was the most appropriate. An alignment of MC58 LbpA with K454 TbpA was generated by ClustalW and served as the input for the alignment mode in SWISS MODEL. In PHYRE2, the PDB ID for K454 TbpA structure and the FASTA sequence of MC58 LbpA were submitted as template and target, respectively.

Only the FASTA sequence of MC58 LbpA was submitted to I-TASSER. The root-mean-square deviation (RMSD) was used to evaluate the similarity of the different models generated with the template structure after superimposing them in Pymol (http://www.pymol.org/). The LbpA model generated by PHYRE2 was selected as the most appropriate model and was used to select the loop regions for generating the hybrid or chimeric protein (**FIG. 20, Panel A**).

[0203] The 'loopless' C-lobe of the TbpB polypeptide prepared in **Example 6** (SEQ.ID NO: 129) was used as a starting point. DNA encoding regions from the LbpA extracellular loop 3 and loop 2 were inserted between the DNA encoding the beta-strands flanking loops 18 and 21 of the engineered TbpB C-lobe (**FIG. 20, Panel B**). Loop regions in TbpB C-lobe and the corresponding loops in LbpA for insertion were analyzed for distances using Pymol to ensure the LbpA replacement loops were structured to fit within the distance parameters predicted by the loop. Assembly of the LbpA loops on the TbpB C-lobe was done using SOE PCR as in examples 6 and 7, and sequence analysis confirmed the insertion of the MC58 LbpA helix 3 and loop 2 in the loopless M982 TbpB C-lobe. The design of the hybrid protein involved insertion of 15 amino acids from the LbpA helix 3 region (protein sequence: 383-YGTDEAEKFRDKSGV) into the loop 18 region of M982 C-lobe (SEQ.ID NO:166), and the insertion of 11 amino acids from the LbpA loop 2 region (protein sequence: LNRWVKERIEQL) into the loop 21 region of M982 C-lobe (SEQ.ID NO:164) (**FIG 20>, Panel B**).

[0204] The methods for transformation of the recombinant plasmid and performing preliminary expression trials are as described for Example 7. The preliminary screen demonstrated that the yields of recombinant protein were high (bottom left, **Panel B**, **FIG. 20**), comparable or better than results with the native C-lobe or loopless C-lobe used as the scaffold (data not shown). Clearly the results further demonstrate that insertion of the foreign protein segments did not substantially affect the stability of the engineered C-lobe, suggesting that the foreign segments did not interfere with the normal folding of the core structural elements of the C-lobe.

Example 9 - Engineering a loop for conjugate capsular vaccine applications using the TbpB C-lobe *of H. influenzae*

[0205] The majority of the conjugate capsular vaccines that have been developed to date have used one of the toxin-based vaccine components as a carrier for conjugating the polysaccharide capsular material. There are several disadvantages to the strategy of conjugating the capsular polysaccharide to the tetanus or diphtheria toxin or toxoid. One is the potential for negatively influencing the induction of an effective immune response due to the continued exposure to the carrier proteins that are also present in vaccines used in routine immunizations; the development of immune tolerance. The second is that the carrier is not relevant to the natural exposure to the pathogen, thus will not fully take advantage of invoking the most relevant T-cell help when the pathogen is encountered.

[0206] Conjugate capsular vaccines have been very successful at preventing infection, and in fact preventing colonization, by the bacterial pathogens that express the specific capsular

polysaccharide, normally referred to as the serotype or serogroup. However, there is essentially no cross-protection for bacteria expressing other polysaccharide capsular types, which can eventually lead to disease being caused by strains expressing polysaccharides not covered by the vaccine. The resulting need to expand the spectrum of polysaccharide capsular types covered by the conjugate capsular vaccines has led to the prospect of continual development of expanded spectrum vaccines and to the view that the ultimate solution lies with protein-based vaccines that are capable of providing substantial cross-protection. However, if a protein-based vaccine capable of inducing broad cross-protection was developed it is unlikely that it would be accepted to replace the existing conjugate capsular vaccines. The addition of yet another vaccine to the already crowded routine immunization schedule could be viewed as potential barrier to introduction of protein-based vaccines.

[0207] In this example we have engineered a conjugation loop into a TbpB C-lobe from *H. influenzae* that contains 42 lysine residues, substantially exceeding the total number of lysines in the remainder of the TbpB C-lobe, lysine residues, which would be predicted to minimize modification of lysines in critical epitopes since only those lysines reacting with the activated carbohydrate moieties would be modified and the ratio of carbohydrate to protein can be controlled during the conjugation process.

[0208] The sequence of the gene encoding the engineered *H. influenzae* TbpB C-lobe from strain H36 is illustrated **Panel A** of **FIG. 21** with the DNA region encoding the conjugation loop indicated by an increased font size (14 vs 12) (SEQ.ID NO: 167). The site of insertion and the sequence of the conjugation loop was designed using the large negatively charged loop in LbpB from *N. meningitidis* strain MC58 as a model (59). Essentially the sequence of the LbpB loop was used as a template and lysines were used to replace the aspartic or glutamic acid residues in the loop. The conjugation loop was engineered onto the handle domain of the TbpB C-lobe in between beta-strands 22 and 23, in the position of loop 23 (**FIG. 2**). The location of the loop is illustrated in **Panel B** of **FIG. 21** using a structural model for the *H. influenzae* C-lobe generated with a much smaller loop (comprised of 11 amino acids) replacing loop 23. The inserted residues are illustrated as space filled spheres. The engineered loop is actually comprised of 91 amino acids that constitute over ¼ of the size of the overall C-lobe (352 amino acid residues) and the loop is set forth as highlighted residues in the entire C-lobe with the engineered loop is set forth in SEQ.ID NO: 205. This shows that the loop domain can accommodate a large number of additional amino acids.

[0209] The inclusion of a conjugation region would not be restricted to insertion into the loop regions of the N-lobe or C-lobe but for instance could be provided by including a cluster of lysine residues at the N-terminus of the intact TbpB or TbpB lobes.

Example 10 - Producing amino acid substitutions in surface binding loops of TbpB and evaluating their Tf binding properties

[0210] A series of site-directed mutants in the surface loops of the TbpB protein were

constructed to explore their impact on functional and immunological properties. In order to target surface exposed amino acids for modification, site-directed mutations were made in TbpBs for which we had the x-ray crystallography derived structures (12, 13). A splicing by overlap extension polymerase chain reaction (SOE PCR) approach was used to introduce mutations into genes encoding truncated TbpB proteins derived from the porcine pathogens *A pleuropneumoniae, A suis* and *H. parasuis.* They included *A. pleuropneumoniae* $TbpB^{20-528}$ (amino acid 20-528) derived from strain H49 (ApH49 TbpB, SEQ.ID NO: 2), and a F171A mutant of ApH49 $TbpB^{20-528}$ (SEQ ID.NO: 4). Also included were *A. pleuropneumoniae* $TbpB^{26-528}$ (amino acid 26-528) derived from strain H87 (ApH87 TbpB, SEQ.ID NO:12) and a Y95A mutant (SEQ.ID NO: 14), a Y121A mutant (SEQ.ID NO: 16), a Y174A mutant (SEQ.ID NO: 18) and a R179E mutant (SEQ.ID NO: 20). *A. suis* $TbpB^{27-577}$ (amino acid 27-577) derived from strain H57 (AsH57 TbpB, SEQ.ID NO: 28), a F63A mutant (SEQ.ID NO: 30) and a F152A mutant (SEQ ID NO:32) were also produced. Finally, *H.parasuis* $TbpB^{27-177}$ (amino acid 27-577) derived from the Nagasaki strain Hp5 (Hp5 TbpB, SEQ.ID NO: 115), a Y93A mutant (SEQ.ID NO: 170), a Y117A mutant (SEQ.ID NO: 172), a Y167A mutant (SEQ.ID NO: 174), and a W176A mutant (SEQ.ID NO: 176) were also prepared.

[0211] The recombinant proteins were initially produced with an N-terminal fusion partner containing a poly-histidine tag, a maltose binding protein and a TEV protease cleavage site. This enabled us to isolate recombinant protein suitable for a solid-phase binding assay using a nitrocellulose membrane and enzymatically labeled porcine transferrin or by capturing recombinant fusion protein from crude extracts with a porcine-Sepharose affinity resin (13). Using these assays, strong binding to by the native TbpBs was readily observed, whereas there was reduced binding by many of the site-directed mutants.

[0212] Although it is possible to derive semi-quantitative binding constants for binding of porcine Tf from these experiments we opted to utilize a variety of different biophysical and biochemical approaches to obtain more accurate and quantitative measures of the binding affinity. As shown **in FIG. 22**, using isothermal calorimetry , surface plasmon resonance or biolayer interferometry (23-25) the affinity constant (Kd) for native TbpBs were generally in the 20 to 60 nM range, with the exception of the TbpB from *Actinobacillus suis* for which the binding kinetics were somewhat unique and had an estimated Kd of 120 nM (12).

[0213] Several of the mutations resulted in a ≥ 100 fold increase in the affinity constant (Kd), such as the F171A mutation in the TbpB from *A. pleuropneumoniae* strain H49, the Y174A mutation in the TbpB from *A. pleuropneumoniae* strain H49 or the Y167A or W176A mutations in the TbpB from *H. parasuis* strain HP5. It is interesting to note that these mutants all map to loop 8.

Example 11 - Evaluating the immunological properties of derivatives of TbpB with amino acid substitutions in surface binding loops

[0214] In order to test the immunological properties of the mutant proteins derived from TbpB that were defective in binding Tf it was important to test them in the native host, and preferably directly test their ability to protect the host from infection by the targeted pathogen. Thus experiments were initiated in a well-established infection model for *Haemophilus parasuis* in which colostrum-deprived piglets were immunized starting at 28 days after birth and challenged with *Haemophilus parasuis* at day 63 (37, 60). In this infection model a commercial vaccine derived from the challenge strain (Porcillis Glasser) provided complete protection from death and recombinant forms of transferrin receptors had previously provided 20-30% survival 15 days post-challenge.

[0215] Groups of five or six pigs were immunized with recombinant intact TbpB from the Hp5 challenge strain, the site-directed Y167A TbpB protein, the Porcillis Glasser vaccine or adjuvant alone. The pigs were challenged with the standard 10^8 challenge dose of *H. parasuis* Hp5 (Nagasaki) strain and monitored for a 15 day period. As illustrated in **FIG. 23**, only 1 out of five pigs immunized with the control Porcilis Glasser vaccine survived the challenge suggesting that a more virulent variant of the Hp5 strain was used in this experiment. Follow up experiments with isolates of the strain from infected pigs had lower survival rates, supporting this conclusion. In spite of the enhanced virulence of the challenge strain, all six pigs immunized with the Y167A TbpB survived 15 days, and 5 out of the 6 pigs had little or no symptoms and there was little or no pathology observed on necropsy. This level of protection was contrasted with the six pigs immunized with the wild-type protein, in which only 3 pigs survived the challenge. The 3 surviving pigs had significant clinical symptoms after challenge and showed marked pathology upon necropsy. In summary, this experiment illustrated that the Y167A TbpB mutant protein induced a superior protective immunological response compared to the wild-type protein, and since the two proteins are virtually identical except for the transferrin binding properties (**FIG. 22),** the suboptimal immune response by the native protein can be attributed to binding of host transferrin.

[0216] To provide further evidence of the impact that the mutation had on the immune response the B-cell and T-cell responses were evaluated. Blood samples taken immediately prior to challenge (after two immunizations) and at 96 hours after challenge were analyzed for the adaptive immune response. The samples were evaluated by FACS analysis for mature B cell (αIgM^+CD21^+) and T helper cell ($CD4+CD8\alpha^-$) subsets. The results in **FIG 24** demonstrate that prior to challenge the Y167A mutant TbpB antigen had induced a stronger B-cell response (Panel A) and T helper cell response (Panel B) than the native TbpB antigen or the commercial Porcilis Glasser vaccine. At 96 hours after challenge the response to the mutant TbpB (51.48% ± 1.18%) was significantly higher than the response to the native TbpB (45.65% ± 1.20%) or PG vaccine (44.83% ± 1.59%) (**FIG. 24, Panel C**). A similar tendency was observed in the T helper cell response, however, the difference in the percentage between the three groups was less evident (**FIG. 24, Panel D**). However there were only 3/6 and 2/5 surviving pigs left in the groups immunized with native TbpB or the Porcilis Glasser vaccine after 96 hours, and since the low responders were the ones tending to die earlier, the observed differences between the groups at the 96 hr time point are actually an underestimate.

Example 12 - An immune response directed against derivatives of TbpB is capable of preventing colonization

[0217] Although infection models do provide the opportunity to evaluate the potential efficacy of vaccines, they rarely emulate the natural infectious process, in which transmission of the pathogen normally leads to colonization of the host upper respiratory tract prior to establishment of infection. The conjugate capsular vaccines designed to prevent meningitis, pneumonia and invasive infection have been shown to eliminate the targeted bacteria from the upper respiratory tract (17), providing the additional advantage of herd immunity protecting non-immunized individuals. The ability to prevent colonization has since become an important feature for making decisions on vaccine implementation (18). Thus it may be prudent to design vaccines that prevent colonization so that along with preventing infection they can eliminate the reservoir of disease-causing pathogens.

[0218] Taking advantage of prior studies characterizing the interaction of *N. meningitidis* and human CEACAM receptors (61), we developed a transgenic humanized mouse model capable of supporting colonization by *Neisseria meningitidis* (62). This model is based on a specific interaction of *Neisseria meningitidis* Opa proteins with the human CEACAM1 receptor, and could potentially be extended to other pathogens that naturally or artificially exploit this interaction. Immunization of the transgenic mice with a meningococcal group C conjugate capsular vaccine resulted in sterilizing mucosal immunity in the colonization model, or in other words, prevented colonization by group C *Neisseria meningitidis* but not strains with other capsular types.

[0219] This model was used to test the ability of TbpB and its derivatives to prevent colonization by *N. meningitidis.* Since there is no human transferrin present in these mice during the immunization stage, it was not necessary to use an engineered non-binding TbpB as was described in **Example 11.** As illustrated in **FIG. 25A,** 8 out of 9 mice immunized with recombinant truncated TbpB did not have detectable levels of *N. meningitidis* three days after an intranasal challenge with 1×10^7 CFU of *N. meningitidis* strain M982. In the control mice treated with adjuvant alone, 6 out of 8 mice had detectable levels of *N. meningitidis* present. It is salient to mention that this is first protein antigen shown to be capable of preventing colonization and this feature cannot be assumed to be common to surface protein antigens due to our limited understanding of the mechanisms involved.

[0220] In a follow up experiment we compared TbpB to another surface lipoprotein, factor H binding protein, which is a key component in two vaccines, and to the individual TbpB subdomains. As illustrated in **FIG. 25B** the C-lobe was capable of preventing colonization as well as or better than the intact TbpB or TbpB N-lobe, which in turn were as effective or more effective than factor H binding protein at inducing sterilizing immunity in this experiment. The ability of the TbpB C-lobe to induce sterilizing mucosal immunity with systemic immunization is a particularly encouraging finding as its lack of Tf binding means that it will be equally effective

in the native host, and its enhanced ability to induce a cross-reactive immune response (**FIG. 3, FIG. 11**) will facilitate the development of broadly cross-protective vaccines.

[0221] The colonization studies were performed as described previously (62). Groups of 8 or more C57/Bl6 expressing the human CEACAM-1 transgene (bred in-house) received 100 ul of designated immunizations subcutaneously on days 0 and 21. Groups received either the designated protein (25 ug) or no protein control adjuvanted with 20% Emulsigen D (MVP Laboratories) diluted in sterile phosphate buffered saline (PBS) (Gibco) to a volume of 100 ul per injection.

[0222] On day 35, mice were anesthetized with Isofluran (Baxter) and inoculated via intranasal instillation with the twice animal passaged *N. meningitidis* strain M982. To prepare inoculums, bacterial strains for infection were grown overnight on GC agar (Beckton Dickinson); the overnight lawn of growth was harvested into 1 ml of PBS containing 1 mM of MgCl2 (PBS/Mg) and OD600 was measured to adjust the number of bacteria. Cultures were adjusted such that each final 10 µl inoculum contained approximately 1×10^7 colony forming units. Density of colonization dose was confirmed via serial dilution plating on GC agar.

[0223] Three days after infection (day 38), mice were euthanized by carbon dioxide asphyxiation. Burden of colonization was assessed by tracheal lavage with 250 ul PBS/Mg followed by direct swabbing of the nasal passages with a polyester tipped applicator (Puritan Medical Products) resuspended in 500 ul PBS/Mg. Samples were enumerated after overnight growth on GC agar supplemented with VCNT inhibitor (Becton Dickinson) to prevent growth of nasal flora. Animal experiments were conducted in accordance with the Animal Ethics Review Committee of the University of Toronto.

Example 13 - Vaccine formulation comprising mixtures of TbpBs or portions thereof

[0224] Since the pathogens that possess TbpB reside exclusively in their specific host (humans, pigs, cattle and/or related ruminants) and since TbpB is capable of preventing colonization (**FIG. 25**), a broadly cross-protective vaccine based on engineered antigens targeting TbpB has the potential of eliminating the pathogen.

[0225] In order to broaden the efficacy of a vaccine formulation against a spectrum of Gram-negative pathogens, TbpBs, or portions thereof, e.g. a C-lobe domain, obtained from different bacterial species or strains may be combined. In this Example we provide preferred combinations of TbpB polypeptides or combinations thereof for use in the preparation of vaccine formulations.

[0226] One important consideration in identifying efficacious combinations of TbpB polypeptides is the extent to which different strains, species and genera are capable of readily exchanging the *tbpB* genes, thus acting as a potential reservoir for TbpB variants not covered

by the vaccine. One of the important factors influencing the horizontal exchange of *tbpB* genes is the nature of the uptake signal sequence (USS) that is inherently present in these naturally transformable species (63, 64). These bacteria preferentially take up DNA containing the specific USS and incorporate it into their genome, providing a very efficient mechanism for incorporating antigenic variants of their surface antigens.

[0227] In the case of *Neisseria meningitidis* we have an extensive strain collection that adequately represented the overall scqucncc diversity (**FIG. 10A**). There is a particularly large collection of sequences from around the world available on public databases for this pathogen that represents a very comprehensive appreciation of sequence diversity. Since the other human pathogens that possess TbpBs and normally reside in the human upper respiratory tract (*Haemophilus influenzae, Moraxella catarrhalis*) do not contain the USS specific to *Neisseria* in their genomic DNA, they do not constitute a ready reservoir for antigen variants. Thus the present example includes a vaccine formulation comprising a combination of engineered TbpB antigens, comprising at least two TbpB polypeptides, or a portion thereof (e.g. the C-lobe domain) obtained from *Neisseria meningitidis* strains selected from two different phylogenetic clusters set forth in **FIG. 10A.** Such vaccine formulation is potentially capable of inducing a cross-reactive (**FIG. 11**) and cross-protective antibody response, could potentially be used to eliminate *N. meningitidis* from the human population.

[0228] The related pathogen, *N. gonorrhoeae,* that normally resides in the human genitourinary tract shares the same USS thus could potentially serve as a reserve for antigenic variation due to the occasional presence of these two species on the same mucosal surface. However, analysis of the sequence diversity of the gonococcal TbpBs relative to diversity in *N. meningitidis* (**FIG. 26A**) indicates that they are largely a subset of the sequence diversity present in *N. meningitidis* leading to the prospect that by a slight extension of our approach a set of engineered antigens could be used for a vaccine potentially capable of eliminating colonization by either pathogen. For engineered C-lobes **(FIG. 26B)** it would involve inclusion of C-lobes specifically targeting *N. gonorrhoeae* TbpB variants. The presence of TbpB in some of the commensal *Neisseria* isolates represents another potential reservoir for antigenic variants, thus extension of our approach to include representative variants from commensal *Neisseria* might be necessary to effectively eliminate TbpB expressing *Neisseria* capable of causing disease. Thus the present example includes a vaccine formulation comprising a combination of engineered TbpB antigens, comprising a *Neisseria meningitidis* TbpB polypeptide, or a portion thereof (e.g. a C-lobe domain), and a *Neisseria gonorrhoeae* TbpB polypeptide or a portion thereof (e.g. a C-lobe domain).

[0229] The porcine pathogens *A. pleuropneumoniae, A. suis* and *H. parasuis* share the same USS and, as a consequence, the TbpB sequence diversity is distributed amongst the three species (**FIG. 4**) such that the main phylogenetic clusters have representatives from at least two species. Thus it is important to consider the overall TbpB sequence variation in all three species when developing TbpB-based vaccines against these pathogens. This is the foundation for our rather unconventional approach of developing engineered antigens capable of inducing an immune response against antigens from more that one species (**FIG. 6, FIG. 7**),

and since TbpB is capable of preventing colonization, are using an approach that could be used to eliminate all three pathogens from their porcine host. Thus the present example includes a vaccine formulation comprising a combination of engineered TbpB antigens, comprising at least two TbpB polypeptides, or a portion thereof (e.g. a C-lobe domain) obtained from *Actinobacillus pleuropneumoniae, Actinobacillus suis* and *Haemophilus parasuis.*

[0230] In regards to *Haemophilus influenzae,* the distinctly different spectrum of disease caused by the strains possessing the type b polysaccharide capsule and the non-typeable strains that lack a polysaccharide capsule have prompted focus on vaccines that target each group separately. Recent increases in invasive disease due to strains expressing the group A polysaccharide capsule has prompted consideration for development of vaccines targeting group A strains (65). An evaluation of TbpB diversity in strains of *H. influenzae* indicates that there are three major phylogenetic clusters (**FIG. 27A**) with the non-typeable strains distributed amongst all three groups. Since all strains of *H. influenzae* share the same USS, it is likely that the distribution of TbpB diversity will not be impacted by capsular type, and the development of a cross-protective vaccine derived from TbpB-based engineered antigens will effectively target type b strains, non-typeable strains and strains expressing other capsular types. Thus our approach should facilitate the development of a broadly-protective TbpB-based vaccine for *H. influenzae* as a stand-alone vaccine, or as a carrier for a conjugate capsular vaccines (**FIG. 21**). Thus the present example includes a vaccine formulation comprising a combination of engineered TbpB antigens, comprising at least two TbpB polypeptides, obtained from *H. influenzae* strains selected from two different phylogenetic clusters set forth in **FIG. 27A**.

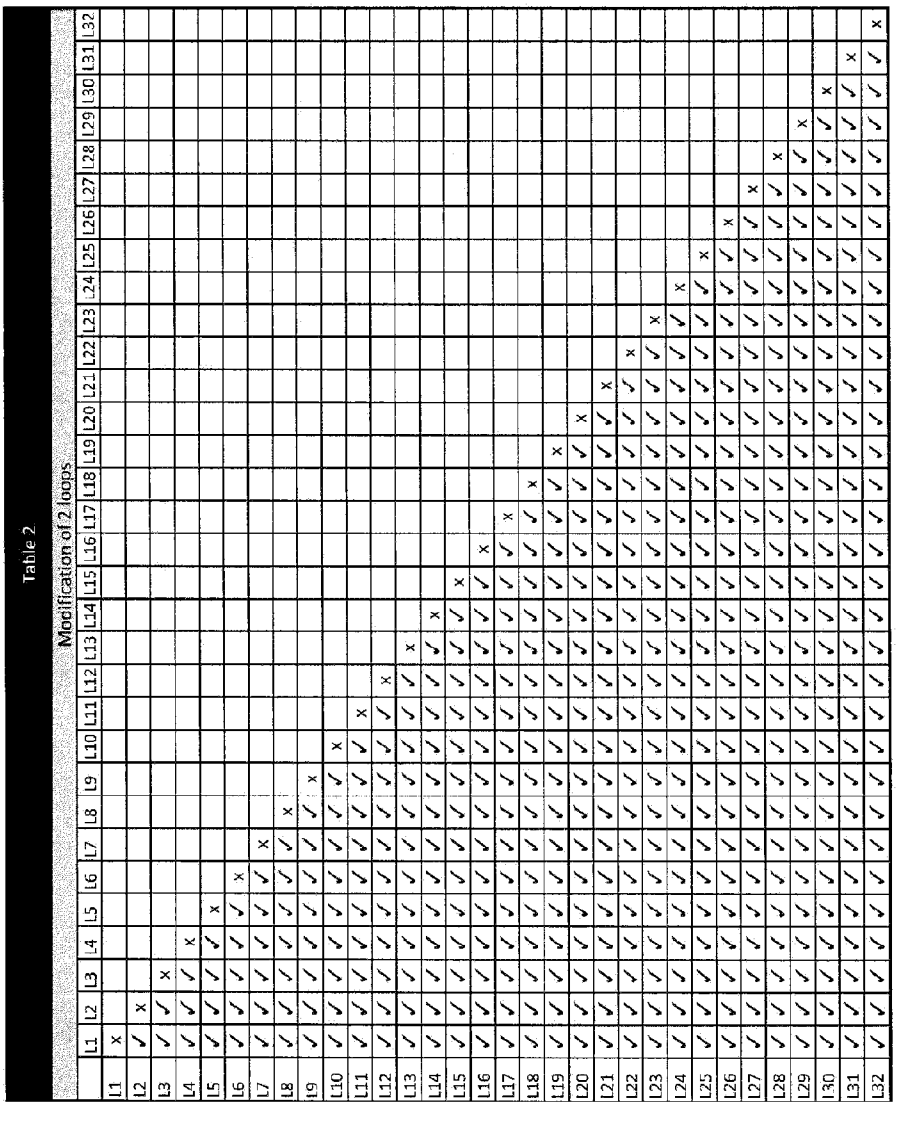
[0231] Unlike *Neisseria meningitidis* and *Haemophilus influenzae,* there are no obvious USSs present in the genomes of *Moraxella catarrhalis* strains, yet they are naturally transformable with a strong preference for *M. catarrhalis* DNA. Thus development of a broadly cross-protective vaccine against *M. catarrhalis* with engineered antigens targeting TbpB need only consider the diversity of TbpBs from *M. catarrhalis* (**FIG. 29**). Antigens derived from strains constituting the three major groups should be sufficient to induce a broadly cross-protective vaccine capable of preventing colonization by *M. catarrhalis.* Thus the present example includes a vaccine formulation comprising a combination of engineered TbpB antigens, comprising at least two TbpB polypeptides, obtained from *M. catharrhalis* strains selected from two different phylogenetic clusters set forth in **FIG. 29**.

[0232] The bovine pathogen *Mannheimia haemolytica,* formerly known as *Pasteurella haemolytica,* is major cause of bovine respiratory disease (shipping fever) in cattle and respiratory infections in sheep. The sheep pathogen, *Pasteurella trehalosi,* that has been reclassified into two species *Mannheimia glucosida* and *Bibersteinia trehalosi,* shares USSs with *Mannheimia haemolytica.* This may be largely responsible for the finding that these species share a common gene pool (66). In contrast the bovine pathogen, *Histophilus somni,* formerly known as *Haemophilus somnus,* has a distinct USS, thus is not a reservoir of antigenic variants for *M. haemolytica.* There are three main phylogenetic lineages of TbpBs from *M. haemolytica, M. glucosida* and *B. trehalosi* that obviously encompass pathogens of sheep and cattle (66) (**FIG. 28**) with clusters of variants that are primarily restricted to cattle or

sheep. Thus it will be possible to consider development of TbpB-derived engineered antigens targeting disease in cattle, in sheep or in both ruminant species. Thus the present example includes a vaccine formulation comprising a combination of engineered TbpB antigens, or a portion thereof e.g. the C-lobe domain, comprising at least two TbpB polypeptides, obtained from *Mannheimia haemolytica, Mannheimia glucosida* and *Bibersteinia trehalosi* strains selected from two different phylogenetic clusters set forth in **FIG. 28**.

Table 1	
Modification of 1 loop	
L1	✓
L2	✓
L3	✓
L4	✓
L5	✓
L6	✓
L7	✓
L8	✓
L9	✓
L10	✓
L11	✓
L12	✓
L13	✓
L14	✓
L15	✓
L16	✓
L17	✓
L18	✓
L19	✓
L20	✓
L21	✓
L22	✓
L23	✓
L24	✓
L25	✓
L26	✓

Table 1	
Modification of 1 loop	
L27	✓
L28	✓
L29	✓
L30	✓
L31	✓
L32	✓



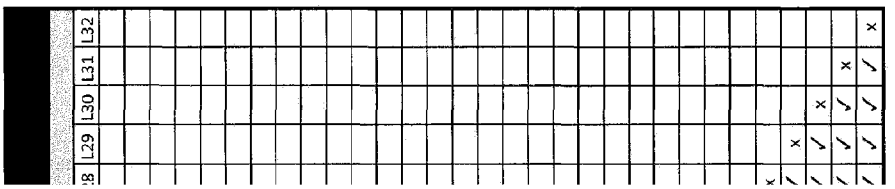


Table 3

Modification of 3 loops

	L1	L2	L3	L4	L5	L6	L7	L8	L9	L10	L11	L12	L13	L14	L15	L16	L17	L18	L19	L20	L21	L22	L23	L24	L25	L26	L27	L2
L1 +L2	x	x																										
L1 +L3	x	✓	x																									
L1 +L4	x	✓	✓	x																								
L1 +L5	x	✓	✓	✓	x																							
L1 +L6	x	✓	✓	✓	✓	x																						
L1 +L7	x	✓	✓	✓	✓	✓	x																					
L1 +L8	x	✓	✓	✓	✓	✓	✓	x																				
L1 +L9	x	✓	✓	✓	✓	✓	✓	✓	x																			
L1 +L10	x	✓	✓	✓	✓	✓	✓	✓	✓	x																		
L1 +L11	x	✓	✓	✓	✓	✓	✓	✓	✓	✓	x																	
L1 +L12	x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x																
L1 +L13	x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x															
L1 +L14	x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x														
L1 +L15	x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x													
L1 +L16	x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x												
L1 +L17	x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x											
L1 +L18	x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x										
L1 +L19	x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x									
L1 +L20	x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x								
L1 +L21	x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x							
L1 +L22	x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x						
L1 +L23	x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x					
L1 +L24	x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x				
L1 +L25	x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x			
L1 +L26	x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x		
L1 +L27	x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x	
L1 +L28	x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	
L1 +L29	x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
L1 +L30	x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
L1 +L31	x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
L1 +L32	x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓

Cont'd #1)

on of 3 loops

L16	L17	L18	L19	L20	L21	L22	L23	L24	L25	L26	L27	L28	L29	L30	L31	L32
x																
✓	x															
✓	✓	x														
✓	✓	✓	x													
✓	✓	✓	✓	x												
✓	✓	✓	✓	✓	x											
✓	✓	✓	✓	✓	✓	x										
✓	✓	✓	✓	✓	✓	✓	x									
✓	✓	✓	✓	✓	✓	✓	✓	x								
✓	✓	✓	✓	✓	✓	✓	✓	✓	x							
✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x						
✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x					
✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x				
✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x			
✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x		
✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x	
✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x

Table 3 (Cont'd #2)

Modification of 3 loops

L3	L4	L5	L6	L7	L8	L9	L10	L11	L12	L13	L14	L15	L16	L17	L18	L19	L20	L21	L22	L23	L24	L25	L26	L27	L28	L29	L30	L31	
x	x																												
x	✓	x																											
x	✓	✓	x																										
x	✓	✓	✓	x																									
x	✓	✓	✓	✓	x																								
x	✓	✓	✓	✓	✓	x																							
x	✓	✓	✓	✓	✓	✓	x																						
x	✓	✓	✓	✓	✓	✓	✓	x																					
x	✓	✓	✓	✓	✓	✓	✓	✓	x																				
x	✓	✓	✓	✓	✓	✓	✓	✓	✓	x																			
x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x																		
x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x																	
x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x																
x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x															
x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x														
x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x													
x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x												
x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x											
x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x										
x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x									
x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x								
x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x							
x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x						
x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x					
x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x				
x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x			
x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x		
x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x	
x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x

Table 3

Modificati

	L1	L2	L3	L4	L5	L6	L7	L8	L9	L10	L11	L12	L13	L14	L15
L2+L3		x	x												
L2+L4		x	✓	x											
L2+L5		x	✓	✓	x										
L2+L6		x	✓	✓	✓	x									
L2+L7		x	✓	✓	✓	✓	x								
L2+L8		x	✓	✓	✓	✓	✓	x							
L2+L9		x	✓	✓	✓	✓	✓	✓	x						
L2+L10		x	✓	✓	✓	✓	✓	✓	✓	x					
L2+L11		x	✓	✓	✓	✓	✓	✓	✓	✓	x				
L2+L12		x	✓	✓	✓	✓	✓	✓	✓	✓	✓	x			
L2+L13		x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x		
L2+L14		x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x	
L2+L15		x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x
L2+L16		x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
L2+L17		x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
L2+L18		x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
L2+L19		x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
L2+L20		x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
L2+L21		x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
L2+L22		x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
L2+L23		x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
L2+L24		x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
L2+L25		x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
L2+L26		x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
L2+L27		x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
L2+L28		x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
L2+L29		x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
L2+L30		x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
L2+L31		x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
L2+L32		x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓

L26	L27	L28	L29	L30	L31	L32
x						
✓	x					
✓	✓	x				
✓	✓	✓	x			
✓	✓	✓	✓	x		
✓	✓	✓	✓	✓	x	
✓	✓	✓	✓	✓	✓	x

Table 3 (Cont'd #3)

Modification of 3 loops

	L1	L2	L3	L4	L5	L6	L7	L8	L9	L10	L11	L12	L13	L14	L15	L16	L17	L18	L19	L20	L21	L22	L23	L24	L25	L26	L27	L28	L29	L30	L31	L32
L4+L5				x	x																											
L4+L6				x	✓	x																										
L4+L7				x	✓	✓	x																									
L4+L8				x	✓	✓	✓	x																								
L4+L9				x	✓	✓	✓	✓	x																							
L4+L10				x	✓	✓	✓	✓	✓	x																						
L4+L11				x	✓	✓	✓	✓	✓	✓	x																					
L4+L12				x	✓	✓	✓	✓	✓	✓	✓	x																				
L4+L13				x	✓	✓	✓	✓	✓	✓	✓	✓	x																			
L4+L14				x	✓	✓	✓	✓	✓	✓	✓	✓	✓	x																		
L4+L15				x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x																	
L4+L16				x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x																
L4+L17				x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x															
L4+L18				x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x														
L4+L19				x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x													
L4+L20				x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x												
L4+L21				x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x											
L4+L22				x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x										
L4+L23				x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x									
L4+L24				x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x								
L4+L25				x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x							
L4+L26				x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x						
L4+L27				x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x					
L4+L28				x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x				
L4+L29				x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x			
L4+L30				x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x		
L4+L31				x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x	
L4+L32				x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x

	L1	L2
L3+L4		
L3+L5		
L3+L6		
L3+L7		
L3+L8		
L3+L9		
L3+L10		
L3+L11		
L3+L12		
L3+L13		
L3+L14		
L3+L15		
L3+L16		
L3+L17		
L3+L18		
L3+L19		
L3+L20		
L3+L21		
L3+L22		
L3+L23		
L3+L24		
L3+L25		
L3+L26		
L3+L27		
L3+L28		
L3+L29		
L3+L30		
L3+L31		
L3+L32		

Table 3 (Cont'd #5)

Modification of 3 loops

L13	L14	L15	L16	L17	L18	L19	L20	L21	L22	L23	L24	L25	L26	L27	L28	L29	L30	L31	L32
x																			
✓	x																		
✓	✓	x																	
✓	✓	✓	x																
✓	✓	✓	✓	x															
✓	✓	✓	✓	✓	x														
✓	✓	✓	✓	✓	✓	x													
✓	✓	✓	✓	✓	✓	✓	x												
✓	✓	✓	✓	✓	✓	✓	✓	x											
✓	✓	✓	✓	✓	✓	✓	✓	✓	x										
✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x									
✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x								
✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x							
✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x						
✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x					
✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x				
✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x			
✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x		
✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x	
✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x

Table 3 (Cont'd #4)

Modification of 3 loops

	L1	L2	L3	L4	L5	L6	L7	L8	L9	L10	L11	L12	L13	L14	L15	L16	L17	L18	L19	L20	L21	L22	L23	L24	L25
L5+L6					x	x																			
L5+L7					x	✓	x																		
L5+L8					x	✓	✓	x																	
L5+L9					x	✓	✓	✓	x																
L5+L10					x	✓	✓	✓	✓	x															
L5+L11					x	✓	✓	✓	✓	✓	x														
L5+L12					x	✓	✓	✓	✓	✓	✓	x													
L5+L13					x	✓	✓	✓	✓	✓	✓	✓	x												
L5+L14					x	✓	✓	✓	✓	✓	✓	✓	✓	x											
L5+L15					x	✓	✓	✓	✓	✓	✓	✓	✓	✓	x										
L5+L16					x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x									
L5+L17					x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x								
L5+L18					x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x							
L5+L19					x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x						
L5+L20					x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x					
L5+L21					x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x				
L5+L22					x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x			
L5+L23					x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x		
L5+L24					x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x	
L5+L25					x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x
L5+L26					x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
L5+L27					x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
L5+L28					x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
L5+L29					x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
L5+L30					x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
L5+L31					x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
L5+L32					x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓

Table 3 (Cont'd #6)

Modification of 3 loops

	L1	L2	L3	L4	L5	L6	L7	L8	L9	L10	L11	L12	L13	L14	L15	L16	L17	L18	L19	L20	L21	L22	L23	L24	L25	L26	L27	L28	L29	L30	L31	L32
							x	x																								
							x	✓	x																							
0							x	✓	✓	x																						
1							x	✓	✓	✓	x																					
2							x	✓	✓	✓	✓	x																				
3							x	✓	✓	✓	✓	✓	x																			
4							x	✓	✓	✓	✓	✓	✓	x																		
5							x	✓	✓	✓	✓	✓	✓	✓	x																	
6							x	✓	✓	✓	✓	✓	✓	✓	✓	x																
7							x	✓	✓	✓	✓	✓	✓	✓	✓	✓	x															
8							x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x														
9							x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x													
0							x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x												
1							x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x											
2							x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x										
3							x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x									
4							x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x								
5							x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x							
6							x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x						
7							x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x					
8							x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x				
9							x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x			
0							x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x		
1							x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x	
2							x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x

	L1	L2	L3	L4	L5	L6	L7	L8	L9	L10	L11	L12
L6+L7						x	x					
L6+L8						x	✓	x				
L6+L9						x	✓	✓	x			
L6+L10						x	✓	✓	✓	x		
L6+L11						x	✓	✓	✓	✓	x	
L6+L12						x	✓	✓	✓	✓	✓	x
L6+L13						x	✓	✓	✓	✓	✓	✓
L6+L14						x	✓	✓	✓	✓	✓	✓
L6+L15						x	✓	✓	✓	✓	✓	✓
L6+L16						x	✓	✓	✓	✓	✓	✓
L6+L17						x	✓	✓	✓	✓	✓	✓
L6+L18						x	✓	✓	✓	✓	✓	✓
L6+L19						x	✓	✓	✓	✓	✓	✓
L6+L20						x	✓	✓	✓	✓	✓	✓
L6+L21						x	✓	✓	✓	✓	✓	✓
L6+L22						x	✓	✓	✓	✓	✓	✓
L6+L23						x	✓	✓	✓	✓	✓	✓
L6+L24						x	✓	✓	✓	✓	✓	✓
L6+L25						x	✓	✓	✓	✓	✓	✓
L6+L26						x	✓	✓	✓	✓	✓	✓
L6+L27						x	✓	✓	✓	✓	✓	✓
L6+L28						x	✓	✓	✓	✓	✓	✓
L6+L29						x	✓	✓	✓	✓	✓	✓
L6+L30						x	✓	✓	✓	✓	✓	✓
L6+L31						x	✓	✓	✓	✓	✓	✓
L6+L32						x	✓	✓	✓	✓	✓	✓

Table 3 (Cont'd #7)

Modification of 3 loops																															
	L1	L2	L3	L4	L5	L6	L7	L8	L9	L10	L11	L12	L13	L14	L15	L16	L17	L18	L19	L20	L21	L22	L23	L24	L25	L26	L27	L28	L29	L30	L31	L32
L8+L9								x	x																						
L8+L10								x	✓	x																					
L8+L11								x	✓	✓	x																				
L8+L12								x	✓	✓	✓	x																			
L8+L13								x	✓	✓	✓	✓	x																		
L8+L14								x	✓	✓	✓	✓	✓	x																	
L8+L15								x	✓	✓	✓	✓	✓	✓	x																
L8+L16								x	✓	✓	✓	✓	✓	✓	✓	x															
L8+L17								x	✓	✓	✓	✓	✓	✓	✓	✓	x														
L8+L18								x	✓	✓	✓	✓	✓	✓	✓	✓	✓	x													
L8+L19								x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x												
L8+L20								x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x											
L8+L21								x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x										
L8+L22								x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x									
L8+L23								x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x								
L8+L24								x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x							
L8+L25								x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x						
L8+L26								x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x					
L8+L27								x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x				
L8+L28								x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x			
L8+L29								x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x		
L8+L30								x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x	
L8+L31								x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x
L8+L32								x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x

	L23	L24	L25	L26	L27	L28	L29	L30	L31	L32
L7+L8										
L7+L9										
L7+L1										
L7+L1										
L7+L1										
L7+L1										
L7+L1										
L7+L1										
L7+L1										
L7+L1										
L7+L2										
L7+L2	x									
L7+L2	✓	x								
L7+L2	✓	✓	x							
L7+L2	✓	✓	✓	x						
L7+L2	✓	✓	✓	✓	x					
L7+L2	✓	✓	✓	✓	✓	x				
L7+L2	✓	✓	✓	✓	✓	✓	x			
L7+L2	✓	✓	✓	✓	✓	✓	✓	x		
L7+L2	✓	✓	✓	✓	✓	✓	✓	✓	x	
L7+L3	✓	✓	✓	✓	✓	✓	✓	✓	✓	x

Table 3 (Cont'd #8)

	Modification of 3 loops																							
	L1	L2	L3	L4	L5	L6	L7	L8	L9	L10	L11	L12	L13	L14	L15	L16	L17	L18	L19	L20	L21	L22
L9+L10									x	x												
L9+L11									x	✓	x											
L9+L12									x	✓	✓	x										
L9+L13									x	✓	✓	✓	x									
L9+L14									x	✓	✓	✓	✓	x								
L9+L15									x	✓	✓	✓	✓	✓	x							
L9+L16									x	✓	✓	✓	✓	✓	✓	x						
L9+L17									x	✓	✓	✓	✓	✓	✓	✓	x					
L9+L18									x	✓	✓	✓	✓	✓	✓	✓	✓	x				
L9+L19									x	✓	✓	✓	✓	✓	✓	✓	✓	✓	x			
L9+L20									x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x		
L9+L21									x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x	
L9+L22									x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x
L9+L23									x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
L9+L24									x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
L9+L25									x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
L9+L26									x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
L9+L27									x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
L9+L28									x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
L9+L29									x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
L9+L30									x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
L9+L31									x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
L9+L32									x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓

Table 3 (Cont'd #9)

	Modification of 3 loops																					
1	L12	L13	L14	L15	L16	L17	L18	L19	L20	L21	L22	L23	L24	L25	L26	L27	L28	L29	L30	L31	L32	
x																						
✓	x																					
✓	✓	x																				
✓	✓	✓	x																			
✓	✓	✓	✓	x																		
✓	✓	✓	✓	✓	x																	
✓	✓	✓	✓	✓	✓	x																
✓	✓	✓	✓	✓	✓	✓	x															
✓	✓	✓	✓	✓	✓	✓	✓	x														
✓	✓	✓	✓	✓	✓	✓	✓	✓	x													
✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x												
✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x											
✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x										
✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x									
✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x								
✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x							
✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x						
✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x					
✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x				
✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x			
✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x		
✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x	

DK/EP 3077512 T3

Table 3 (Cont'd #10)

Modification of 3 loops

	L1	L2	L3	L4	L5	L6	L7	L8	L9	L10	L11	L12	L13	L14	L15	L16	L17	L18	L19	L20	L21	L22	L23	L24	L25	L26	L27	L28	L29	L30	L31	
L11+L12											x	x																				
L11+L13											x	✓	x																			
L11+L14											x	✓	✓	x																		
L11+L15											x	✓	✓	✓	x																	
L11+L16											x	✓	✓	✓	✓	x																
L11+L17											x	✓	✓	✓	✓	✓	x															
L11+L18											x	✓	✓	✓	✓	✓	✓	x														
L11+L19											x	✓	✓	✓	✓	✓	✓	✓	x													
L11+L20											x	✓	✓	✓	✓	✓	✓	✓	✓	x												
L11+L21											x	✓	✓	✓	✓	✓	✓	✓	✓	✓	x											
L11+L22											x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x										
L11+L23											x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x									
L11+L24											x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x								
L11+L25											x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x							
L11+L26											x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x						
L11+L27											x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x					
L11+L28											x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x				
L11+L29											x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x			
L11+L30											x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x		
L11+L31											x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x	
L11+L32											x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x

	L1	L2	L3	L4	L5	L6	L7	L8	L9	L10	L1
L10+L11										x	
L10+L12										x	
L10+L13										x	
L10+L14										x	
L10+L15										x	
L10+L16										x	
L10+L17										x	
L10+L18										x	
L10+L19										x	
L10+L20										x	
L10+L21										x	
L10+L22										x	
L10+L23										x	
L10+L24										x	
L10+L25										x	
L10+L26										x	
L10+L27										x	
L10+L28										x	
L10+L29										x	
L10+L30										x	
L10+L31										x	
L10+L32										x	

Table 3 (Cont'd #11)

Modification of 3 loops

	L1	L2	L3	L4	L5	L6	L7	L8	L9	L10	L11	L12	L13	L14	L15	L16	L17	L18	L19	L20	L21	L22	L23	L24	L25	L26	L27	L28	L29	L30	L31	L32
L12+L13												x	x																			
L12+L14												x	✓	x																		
L12+L15												x	✓	✓	x																	
L12+L16												x	✓	✓	✓	x																
L12+L17												x	✓	✓	✓	✓	x															
L12+L18												x	✓	✓	✓	✓	✓	x														
L12+L19												x	✓	✓	✓	✓	✓	✓	x													
L12+L20												x	✓	✓	✓	✓	✓	✓	✓	x												
L12+L21												x	✓	✓	✓	✓	✓	✓	✓	✓	x											
L12+L22												x	✓	✓	✓	✓	✓	✓	✓	✓	✓	x										
L12+L23												x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x									
L12+L24												x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x								
L12+L25												x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x							
L12+L26												x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x						
L12+L27												x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x					
L12+L28												x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x				
L12+L29												x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x			
L12+L30												x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x		
L12+L31												x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x	
L12+L32												x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x

1	L22	L23	L24	L25	L26	L27	L28	L29	L30	L31	L32
	x										
	✓	x									
	✓	✓	x								
	✓	✓	✓	x							
	✓	✓	✓	✓	x						
	✓	✓	✓	✓	✓	x					
	✓	✓	✓	✓	✓	✓	x				
	✓	✓	✓	✓	✓	✓	✓	x			
	✓	✓	✓	✓	✓	✓	✓	✓	x		
	✓	✓	✓	✓	✓	✓	✓	✓	✓	x	
	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x

Table 3 (Cont'd #12)

Modification of 3 loops

	L1	L2	L3	L4	L5	L6	L7	L8	L9	L10	L11	L12	L13	L14	L15	L16	L17	L18	L19	L20	L2
L13+L14													x	x							
L13+L15													x	✓	x						
L13+L16													x	✓	✓	x					
L13+L17													x	✓	✓	✓	x				
L13+L18													x	✓	✓	✓	✓	x			
L13+L19													x	✓	✓	✓	✓	✓	x		
L13+L20													x	✓	✓	✓	✓	✓	✓	x	
L13+L21													x	✓	✓	✓	✓	✓	✓	✓	x
L13+L22													x	✓	✓	✓	✓	✓	✓	✓	✓
L13+L23													x	✓	✓	✓	✓	✓	✓	✓	✓
L13+L24													x	✓	✓	✓	✓	✓	✓	✓	✓
L13+L25													x	✓	✓	✓	✓	✓	✓	✓	✓
L13+L26													x	✓	✓	✓	✓	✓	✓	✓	✓
L13+L27													x	✓	✓	✓	✓	✓	✓	✓	✓
L13+L28													x	✓	✓	✓	✓	✓	✓	✓	✓
L13+L29													x	✓	✓	✓	✓	✓	✓	✓	✓
L13+L30													x	✓	✓	✓	✓	✓	✓	✓	✓
L13+L31													x	✓	✓	✓	✓	✓	✓	✓	✓
L13+L32													x	✓	✓	✓	✓	✓	✓	✓	✓

Table 3 (Cont'd #13)

Modification of 3 loops

L9	L10	L11	L12	L13	L14	L15	L16	L17	L18	L19	L20	L21	L22	L23	L24	L25	L26	L27	L28	L29	L30	L31	L32
					x	x																	
					x	✓	x																
					x	✓	✓	x															
					x	✓	✓	✓	x														
					x	✓	✓	✓	✓	x													
					x	✓	✓	✓	✓	✓	x												
					x	✓	✓	✓	✓	✓	✓	x											
					x	✓	✓	✓	✓	✓	✓	✓	x										
					x	✓	✓	✓	✓	✓	✓	✓	✓	x									
					x	✓	✓	✓	✓	✓	✓	✓	✓	✓	x								
					x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x							
					x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x						
					x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x					
					x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x				
					x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x			
					x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x		
					x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x	
					x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x

·1	L32
x	
√	x

Table 3 (Cont'd #14)

Modification of 3 loops

	L1	L2	L3	L4	L5	L6	L7	L8	L9	L10	L11	L12	L13	L14	L15	L16	L17	L18	L19	L20	L21	L22	L23	L24	L25	L26	L27	L28	L29	L30	L31	L32
L15+L16															x	x																
L15+L17															x	√	x															
L15+L18															x	√	√	x														
L15+L19															x	√	√	√	x													
L15+L20															x	√	√	√	√	x												
L15+L21															x	√	√	√	√	√	x											
L15+L22															x	√	√	√	√	√	√	x										
L15+L23															x	√	√	√	√	√	√	√	x									
L15+L24															x	√	√	√	√	√	√	√	√	x								
L15+L25															x	√	√	√	√	√	√	√	√	√	x							
L15+L26															x	√	√	√	√	√	√	√	√	√	√	x						
L15+L27															x	√	√	√	√	√	√	√	√	√	√	√	x					
L15+L28															x	√	√	√	√	√	√	√	√	√	√	√	√	x				
L15+L29															x	√	√	√	√	√	√	√	√	√	√	√	√	√	x			
L15+L30															x	√	√	√	√	√	√	√	√	√	√	√	√	√	√	x		
L15+L31															x	√	√	√	√	√	√	√	√	√	√	√	√	√	√	√	x	
L15+L32															x	√	√	√	√	√	√	√	√	√	√	√	√	√	√	√	√	x

	L1	L2	L3	L4	L5	L6	L7	L8
L14+L15								
L14+L16								
L14+L17								
L14+L18								
L14+L19								
L14+L20								
L14+L21								
L14+L22								
L14+L23								
L14+L24								
L14+L25								
L14+L26								
L14+L27								
L14+L28								
L14+L29								
L14+L30								
L14+L31								
L14+L32								

Table 3 (Cont'd #15)

Modification of 3 loops

	L1	L2	L3	L4	L5	L6	L7	L8	L9	L10	L11	L12	L13	L14	L15	L16	L17	L18	L19	L20	L21	L22	L23	L24	L25	L26	L27	L28	L29	L30	L3
L16+L17																x	x														
L16+L18																x	✓	x													
L16+L19																x	✓	✓	x												
L16+L20																x	✓	✓	✓	x											
L16+L21																x	✓	✓	✓	✓	x										
L16+L22																x	✓	✓	✓	✓	✓	x									
L16+L23																x	✓	✓	✓	✓	✓	✓	x								
L16+L24																x	✓	✓	✓	✓	✓	✓	✓	x							
L16+L25																x	✓	✓	✓	✓	✓	✓	✓	✓	x						
L16+L26																x	✓	✓	✓	✓	✓	✓	✓	✓	✓	x					
L16+L27																x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x				
L16+L28																x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x			
L16+L29																x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x		
L16+L30																x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x	
L16+L31																x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	
L16+L32																x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	

L19	L20	L21	L22	L23	L24	L25	L26	L27	L28	L29	L30	L31	L32
x													
✓	x												
✓	✓	x											
✓	✓	✓	x										
✓	✓	✓	✓	x									
✓	✓	✓	✓	✓	x								
✓	✓	✓	✓	✓	✓	x							
✓	✓	✓	✓	✓	✓	✓	x						
✓	✓	✓	✓	✓	✓	✓	✓	x					
✓	✓	✓	✓	✓	✓	✓	✓	✓	x				
✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x			
✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x		
✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x	
x													x

Table 3 (Cont'd #16)

Modification of 3 loops

	L1	L2	L3	L4	L5	L6	L7	L8	L9	L10	L11	L12	L13	L14	L15	L16	L17	L18
L17+L18																	x	x
L17+L19																	x	✓
L17+L20																	x	✓
L17+L21																	x	✓
L17+L22																	x	✓
L17+L23																	x	✓
L17+L24																	x	✓
L17+L25																	x	✓
L17+L26																	x	✓
L17+L27																	x	✓
L17+L28																	x	✓
L17+L29																	x	✓
L17+L30																	x	✓
L17+L31																	x	✓
L17+L32																	x	✓
L18+L19																		x
L18+L20																		x
L18+L21																		x
L18+L22																		x
L18+L23																		x
L18+L24																		x
L18+L25																		x
L18+L26																		x
L18+L27																		x
L18+L28																		x
L18+L29																		x
L18+L30																		x
L18+L31																		x
L18+L32																		x

Table 3 (Cont'd #17)

Modification of 3 loops

16	L7	L8	L9	L10	L11	L12	L13	L14	L15	L16	L17	L18	L19	L20	L21	L22	L23	L24	L25	L26	L27	L28	L29	L30	L31	L32
													x	x												
													x	✓	x											
													x	✓	✓	x										
													x	✓	✓	✓	x									
													x	✓	✓	✓	✓	x								
													x	✓	✓	✓	✓	✓	x							
													x	✓	✓	✓	✓	✓	✓	x						
													x	✓	✓	✓	✓	✓	✓	✓	x					
													x	✓	✓	✓	✓	✓	✓	✓	✓	x				
													x	✓	✓	✓	✓	✓	✓	✓	✓	✓	x			
													x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x		
													x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x	
														x	x											x
														x	✓	x										x
														x	✓	✓	x									x
														x	✓	✓	✓	x								x
														x	✓	✓	✓	✓	x							x
														x	✓	✓	✓	✓	✓	x						x
														x	✓	✓	✓	✓	✓	✓	x					x
														x	✓	✓	✓	✓	✓	✓	✓	x				x
														x	✓	✓	✓	✓	✓	✓	✓	✓	x			x
														x	✓	✓	✓	✓	✓	✓	✓	✓	✓	x		x
														x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x	x

	L29	L30	L31	L32
	x			
	✓	x		
	✓	✓	x	
	✓	✓	✓	x
	x			
	✓	x		
	✓	✓	x	
	✓	✓	✓	x
	x			
	✓	x		
	✓	✓	x	
	✓	✓	✓	x
	x			
	✓	x		
	✓	✓	x	
	✓	✓	✓	x

Table 3 (Cont'd #18)

Modification of 3 loops

	L1	L2	L3	L4	L5	L6	L7	L8	L9	L10	L11	L12	L13	L14	L15	L16	L17	L18	L19	L20	L21	L22	L23	L24	L25	L26	L27	L28	L29	L30	L31	L32
L21+L22																					x	x										
L21+L23																					x	✓	x									
L21+L24																					x	✓	✓	x								
L21+L25																					x	✓	✓	✓	x							
L21+L26																					x	✓	✓	✓	✓	x						
L21+L27																					x	✓	✓	✓	✓	✓	x					
L21+L28																					x	✓	✓	✓	✓	✓	✓	x				
L21+L29																					x	✓	✓	✓	✓	✓	✓	✓	x			
L21+L30																					x	✓	✓	✓	✓	✓	✓	✓	✓	x		
L21+L31																					x	✓	✓	✓	✓	✓	✓	✓	✓	✓	x	
L21+L32																					x	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	x
L22+L23																						x	x									
L22+L24																						x	✓	x								
L22+L25																						x	✓	✓	x							
L22+L26																						x	✓	✓	✓	x						
L22+L27																						x	✓	✓	✓	✓	x					
L22+L28																						x	✓	✓	✓	✓	✓	x				
L22+L29																						x	✓	✓	✓	✓	✓	✓	x			
L22+L30																						x	✓	✓	✓	✓	✓	✓	✓	x		
L22+L31																						x	✓	✓	✓	✓	✓	✓	✓	✓	x	
L22+L32																						x	✓	✓	✓	✓	✓	✓	✓	✓	✓	x
L23+L24																							x	x								
L23+L25																							x	✓	x							
L23+L26																							x	✓	✓	x						
L23+L27																							x	✓	✓	✓	x					
L23+L28																							x	✓	✓	✓	✓	x				
L23+L29																							x	✓	✓	✓	✓	✓	x			
L23+L30																							x	✓	✓	✓	✓	✓	✓	x		
L23+L31																							x	✓	✓	✓	✓	✓	✓	✓	x	
L23+L32																							x	✓	✓	✓	✓	✓	✓	✓	✓	x

	L1	L2	L3	L4	L5
L19+L20					
L19+L21					
L19+L22					
L19+L23					
L19+L24					
L19+L25					
L19+L26					
L19+L27					
L19+L28					
L19+L29					
L19+L30					
L19+L31					
L19+L32					
L20+L21					
L20+L22					
L20+L23					
L20+L24					
L20+L25					
L20+L26					
L20+L27					
L20+L28					
L20+L29					
L20+L30					
L20+L31					
L20+L32					

Table 3 (Cont'd #19)

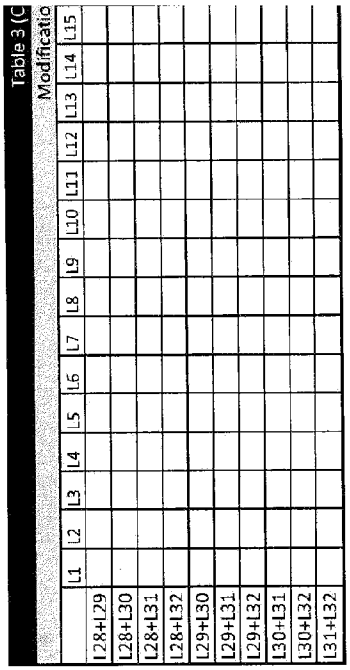
Modification of 3 loops

	L1	L2	L3	L4	L5	L6	L7	L8	L9	L10	L11	L12	L13	L14	L15	L16	L17	L18	L19	L20	L21	L22	L23	L24	L25	L26	L27	L28
L24+L25																								x	x			
L24+L26																								x	✓	x		
L24+L27																								x	✓	✓	x	
L24+L28																								x	✓	✓	✓	x
L24+L29																								x	✓	✓	✓	✓
L24+L30																								x	✓	✓	✓	✓
L24+L31																								x	✓	✓	✓	✓
L24+L32																								x	✓	✓	✓	✓
L25+L26																									x	x		
L25+L27																									x	✓	x	
L25+L28																									x	✓	✓	x
L25+L29																									x	✓	✓	✓
L25+L30																									x	✓	✓	✓
L25+L31																									x	✓	✓	✓
L25+L32																									x	✓	✓	✓
L26+L27																										x	x	
L26+L28																										x	✓	x
L26+L29																										x	✓	✓
L26+L30																										x	✓	✓
L26+L31																										x	✓	✓
L26+L32																										x	✓	✓
L27+L28																											x	x
L27+L29																											x	✓
L27+L30																											x	✓
L27+L31																											x	✓
L27+L32																											x	✓

ont'd #20)

n of 3 loops

L16	L17	L18	L19	L20	L21	L22	L23	L24	L25	L26	L27	L28	L29	L30	L31	L32
												x	x			
												x	✓	x		
												x	✓	✓	x	
												x	✓	✓	✓	x
													x	x		
													x	✓	x	
													x	✓	✓	x
														x	x	
														x	✓	x
															x	x
															✓	x
															x	x



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SEQUENCE LISTING

[0234]

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Gly Ser Asn Val Asp Thr Val Arg Ile Ile Asp Ala Ser Lys Ile Asp
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Leu Thr Asn Phe Ser Ile Ser Glu Leu Asn Asn Phe Gly Asp Ala Ser
                325                 330                 335

Val Leu Ile Ile Asp Gly Lys Lys Ile Lys Leu Ala Gly Ser Gly Phe
            340                 345                 350

Thr Asn Lys His Thr Ile Glu Ile Asn Gly Lys Thr Met Val Ala Val
        355                 360                 365

Ala Cys Cys Ser Asn Leu Glu Tyr Met Lys Phe Gly Gln Leu Trp Gln
    370                 375                 380

Gln Ala Glu Gly Gly Lys Pro Glu Asn Asn Ser Leu Phe Leu Gln Gly
385                 390                 395                 400

Glu Arg Thr Ala Thr Asp Lys Met Pro Lys Gly Gly Asn Tyr Lys Tyr
                405                 410                 415

Ile Gly Thr Trp Asp Ala Gln Val Ser Lys Glu Asn Asn Trp Val Ala
            420                 425                 430

Thr Ala Asp Asp Asp Arg Lys Ala Gly Tyr Arg Thr Glu Phe Asp Val
        435                 440                 445

Asp Phe Gly Asn Lys Asn Leu Ser Gly Lys Leu Phe Asp Lys Asn Gly
    450                 455                 460

Val Asn Pro Val Phe Thr Val Asp Ala Lys Ile Asp Gly Asn Gly Phe
465                 470                 475                 480

Thr Gly Lys Ala Lys Thr Ser Asp Ala Gly Phe Ala Leu Asp Ser Gly
                485                 490                 495

Ser Ser Arg Tyr Glu Asn Val Lys Phe Asn Asp Val Ala Val Ser Gly
            500                 505                 510

Gly Phe Tyr Gly Pro Thr Ala Ala Glu Leu Gly Gly Gln Phe His His
        515                 520                 525

Lys Ser Glu Asn Gly Ser Val Gly Ala Val Phe Gly
    530                 535                 540
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<210> 3

<211> 1640

<212> DNA

<213> Actinobacillus pleuropneumoniae

<400> 3

atgcatttta aacttaatcc ctatgcgtta gcgtttactt cgctgtttct tgtcgcttgt 60

tctggcggaa aaggaagttt tgatttagaa gatgtccggc ctaataagac aacaggcgtg 120

tctaaagagg agtacaagga tgtagaaaca gccaagaaag aaaaagaaca gttaggggaa 180

ttaatggaac ctgctttggg gtatgttgta aaagttccgg tgagttcttt tgaaaataag 240

aaagttgata tttcagatat agaagtgatt acgaacggaa atttagacga tgtgccgtac 300

aaggcaaatt catctaaata taactatcca gatataaaaa caaaagattc ttctcttcag 360

tacgttcgct caggatatgt tattgatggg gaacactctg gttctaatga aaagggatat 420

gtgtattata aaggtaattc acctgcaaaa gaattacccg ttaatcagct tttaacttat 480

acaggaagtt gggattttac ttccaatgca aatttaaata atgaagaggg aagacctaat 540

tatttaaacg acgattatta tactaaagca ataggtaaac gggtgggctt ggtttcggga 600

gatgcgaaac ctgcaaagca taaatacact agccagtttg aagttgattt tgcaactaaa 660

aaaatgacag gtaaattatc cgataaagag aaaacgattt atacagtcaa tgctgatatt 720

agaggcaatc gttttacggg ggctgctaca gcgagtgata aaaataaagg gaaaggcgaa 780

tcatataact tctttagtgc cgattctcag tctttagaag gcggcttcta tggtccaaaa 840

gcagaagaaa tggcagggaa atttgtagct aacgacaaat ctctttttgc cgtttttttca 900

gcaaaacaca atggctctaa tgttgacacc gttcgtatta ttgatgcctc aaaaattgat 960

ttaactaatt tcagcatttc agaacttaac aattttggtg atgcttccgt tttaattatt 1020

gatgggaaaa aaataaagct agctggtagc gggtttacaa ataagcacac tattgaaatc 1080

aatggcaaaa caatggtagc cgtagcctgc tgtagtaatc tggaatatat gaagtttggt 1140

caattatggc aacaagcaga gggcggaaaa cccgagaata atagtttatt cctacaaggc 1200

gaacgtaccg caacagataa gatgccaaaa ggcggaaact ataaatatat tggtacttgg 1260

gatgctcagg tttcaaaaga aaataactgg gttgctacgg cagatgatga tagaaaagct 1320

ggctatcgca cagaatttga tgttgatttt ggcaacaaaa atttaagtgg taagttattt 1380

gataaaaacg gtgtaaatcc tgtgtttacc gtagatgcaa aaattgatgg taatggtttt 1440

actggcaaag ctaaaacctc agatgctggt ttcgctctag attcaggtag ttcacgttat 1500

gagaatgtga aatttaacga tgtagcagtt agtggtggct tctatggtcc aacggcagca 1560

gagcttggcg gacaattcca ccataaatca gaaaatggca gtgtaggtgc tgtctttggt 1620

gcaaaacaac aagtaaaaaa 1640

<210> 4

<211> 540

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 4

Met His Phe Lys Leu Asn Pro Tyr Ala Leu Ala Phe Thr Ser Leu Phe
1 5 10 15

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

Arg Pro Asn Lys Thr Thr Gly Val Ser Lys Glu Glu Tyr Lys Asp Val
        35                  40                  45

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

Ala Leu Gly Tyr Val Val Lys Val Pro Val Ser Ser Phe Glu Asn Lys
65                  70                  75                  80

Lys Val Asp Ile Ser Asp Ile Glu Val Ile Thr Asn Gly Asn Leu Asp
                85                  90                  95

Asp Val Pro Tyr Lys Ala Asn Ser Ser Lys Tyr Asn Tyr Pro Asp Ile
            100                 105                 110

Lys Thr Lys Asp Ser Ser Leu Gln Tyr Val Arg Ser Gly Tyr Val Ile
        115                 120                 125

Asp Gly Glu His Ser Gly Ser Asn Glu Lys Gly Tyr Val Tyr Tyr Lys
    130                 135                 140

Gly Asn Ser Pro Ala Lys Glu Leu Pro Val Asn Gln Leu Leu Thr Tyr
145                 150                 155                 160

Thr Gly Ser Trp Asp Phe Thr Ser Asn Ala Asn Leu Asn Asn Glu Glu
                165                 170                 175

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

Lys Arg Val Gly Leu Val Ser Gly Asp Ala Lys Pro Ala Lys His Lys
        195                 200                 205

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

Lys Leu Ser Asp Lys Glu Lys Thr Ile Tyr Thr Val Asn Ala Asp Ile
225                 230                 235                 240

Arg Gly Asn Arg Phe Thr Gly Ala Ala Thr Ala Ser Asp Lys Asn Lys
                245                 250                 255

Gly Lys Gly Glu Ser Tyr Asn Phe Phe Ser Ala Asp Ser Gln Ser Leu
            260                 265                 270

Glu Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Met Ala Gly Lys Phe
        275                 280                 285

Val Ala Asn Asp Lys Ser Leu Phe Ala Val Phe Ser Ala Lys His Asn
    290                 295                 300

Gly Ser Asn Val Asp Thr Val Arg Ile Ile Asp Ala Ser Lys Ile Asp
305                 310                 315                 320
```

```
Leu Thr Asn Phe Ser Ile Ser Glu Leu Asn Asn Phe Gly Asp Ala Ser
                325                 330                 335

Val Leu Ile Ile Asp Gly Lys Lys Ile Lys Leu Ala Gly Ser Gly Phe
            340                 345                 350

Thr Asn Lys His Thr Ile Glu Ile Asn Gly Lys Thr Met Val Ala Val
        355                 360                 365

Ala Cys Cys Ser Asn Leu Glu Tyr Met Lys Phe Gly Gln Leu Trp Gln
    370                 375                 380

Gln Ala Glu Gly Gly Lys Pro Glu Asn Asn Ser Leu Phe Leu Gln Gly
385                 390                 395                 400

Glu Arg Thr Ala Thr Asp Lys Met Pro Lys Gly Gly Asn Tyr Lys Tyr
                405                 410                 415

Ile Gly Thr Trp Asp Ala Gln Val Ser Lys Glu Asn Asn Trp Val Ala
            420                 425                 430

Thr Ala Asp Asp Asp Arg Lys Ala Gly Tyr Arg Thr Glu Phe Asp Val
        435                 440                 445

Asp Phe Gly Asn Lys Asn Leu Ser Gly Lys Leu Phe Asp Lys Asn Gly
    450                 455                 460

Val Asn Pro Val Phe Thr Val Asp Ala Lys Ile Asp Gly Asn Gly Phe
465                 470                 475                 480

Thr Gly Lys Ala Lys Thr Ser Asp Ala Gly Phe Ala Leu Asp Ser Gly
                485                 490                 495

Ser Ser Arg Tyr Glu Asn Val Lys Phe Asn Asp Val Ala Val Ser Gly
            500                 505                 510

Gly Phe Tyr Gly Pro Thr Ala Ala Glu Leu Gly Gly Gln Phe His His
        515                 520                 525

Lys Ser Glu Asn Gly Ser Val Gly Ala Val Phe Gly
    530                 535                 540
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<210> 5

<211> 730

<212> DNA

<213> Actinobacillus pleuropneumoniae

<400> 5

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caatggctct aatgttgaca ccgttcgtat tattgatgcc tcaaaaattg atttaactaa       60

tttcagcatt tcagaactta acaattttgg tgatgcttcc gttttaatta ttgatgggaa      120

aaaaataaaa ctaactaata acaaatttac aaataaacac actattaaaa tcaatggcaa      180
```

aacaatggta gccgtagcct gctgtagtaa tctggaatat atgaagtttg gtcaattatg 240

gcaacaagca gagggcggaa aacccgagaa taatagttta ttcctacaag gcgaacgtac 300

cgcaacagat aagatgccaa aaggcggaaa ctataaatat attggtactt gggatgctca 360

ggtttcaaaa gaaaataact gggttgctac ggcagatgat gatagaaaag ctggctatcg 420

cacagaattt gatgttgatt ttggcaacaa aaatttaagt ggtaagttat ttgataaaaa 480

cggtgtaaat cctgtgttta ccgtagatgc aaaaattgat ggtaatggtt ttactggcaa 540

agctaaaacc tcagatgctg gtttcgctct agattcaggt agttcacgtt atgagaatgt 600

gaaatttaac gatgtagcag ttagtggtgg cttctatggt ccaacggcag cagagcttgg 660

cggacaattc caccataaat cagaaaatgg cagtgtaggt gctgtctttg gtgcaaaaca 720

acaagtaaaa 730

<210> 6

<211> 240

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 6

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His Asn Gly Ser Asn Val Asp Thr Val Arg Ile Ile Asp Ala Ser Lys
1               5                  10                  15

Ile Asp Leu Thr Asn Phe Ser Ile Ser Glu Leu Asn Asn Phe Gly Asp
            20                  25                  30

Ala Ser Val Leu Ile Ile Asp Gly Lys Lys Ile Lys Leu Ala Gly Ser
        35                  40                  45

Gly Phe Thr Asn Lys His Thr Ile Glu Ile Asn Gly Lys Thr Met Val
    50                  55                  60

Ala Val Ala Cys Cys Ser Asn Leu Glu Tyr Met Lys Phe Gly Gln Leu
65                  70                  75                  80

Trp Gln Gln Ala Glu Gly Gly Lys Pro Glu Asn Asn Ser Leu Phe Leu
                85                  90                  95

Gln Gly Glu Arg Thr Ala Thr Asp Lys Met Pro Lys Gly Gly Asn Tyr
            100                 105                 110

Lys Tyr Ile Gly Thr Trp Asp Ala Gln Val Ser Lys Glu Asn Asn Trp
        115                 120                 125

Val Ala Thr Ala Asp Asp Asp Arg Lys Ala Gly Tyr Arg Thr Glu Phe
    130                 135                 140

Asp Val Asp Phe Gly Asn Lys Asn Leu Ser Gly Lys Leu Phe Asp Lys
145                 150                 155                 160

Asn Gly Val Asn Pro Val Phe Thr Val Asp Ala Lys Ile Asp Gly Asn
                165                 170                 175
```

```
Gly Phe Thr Gly Lys Ala Lys Thr Ser Asp Ala Gly Phe Ala Leu Asp
            180                 185                 190

Ser Gly Ser Ser Arg Tyr Glu Asn Val Lys Phe Asn Asp Val Ala Val
        195                 200                 205

Ser Gly Gly Phe Tyr Gly Pro Thr Ala Ala Glu Leu Gly Gly Gln Phe
    210                 215                 220

His His Lys Ser Glu Asn Gly Ser Val Gly Ala Val Phe Gly Ala Lys
225                 230                 235                 240
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<210> 7

<211> 900

<212> DNA

<213> Actinobacillus pleuropneumoniae

<400> 7

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atgcatttta aacttaatcc ctatgcgtta gcgtttactt cgctgtttct tgtcgcttgt       60

tctggcggaa aaggaagttt tgatttagaa gatgtccggc ctaataagac aacaggcgtg      120

tctaaagagg agtacaagga tgtagaaaca gccaagaaag aaaaagaaca gttaggggaa      180

ttaatggaac ctgctttggg gtatgttgta aaagttccgg tgagttcttt tgaaaataag      240

aaagttgata tttcagatat agaagtgatt acgaacggaa atttagacga tgtgccgtac      300

aaggcaaatt catctaaata taactatcca gatataaaaa caaaagattc ttctcttcag      360

tacgttcgct caggatatgt tattgatggg gaacactctg gttctaatga aaagggatat      420

gtgtattata aaggtaattc acctgcaaaa gaattacccg ttaatcagct tttaacttat      480

acaggaagtt gggattttac ttccaatgca aatttaaata atgaagaggg aagacctaat      540

tatttaaacg acgattatta tactaaattt ataggtaaac gggtgggctt ggtttcggga      600

gatgcgaaac ctgcaaagca taaatacact agccagtttg aagttgattt tgcaactaaa      660

aaaatgacag gtaaattatc cgataaagag aaaacgattt atacagtcaa tgctgatatt      720

agaggcaatc gttttacggg ggctgctaca gcgagtgata aaaataaagg gaaaggcgaa      780

tcatataact tctttagtgc cgattctcag tctttagaag gcggcttcta tggtccaaaa      840

gcagaagaaa tggcagggaa atttgtagct aacgacaaat ctctttttgc cgttttttca      900
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<210> 8

<211> 280

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 8

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Cys Ser Gly Gly Lys Gly Ser Phe Asp Leu Glu Asp Val Arg Pro Asn
1               5                   10                  15

Lys Thr Thr Gly Val Ser Lys Glu Glu Tyr Lys Asp Val Glu Thr Ala
            20                  25                  30
```

```
Lys Lys Glu Lys Glu Gln Leu Gly Glu Leu Met Glu Pro Ala Leu Gly
        35                  40                  45

Tyr Val Val Lys Val Pro Val Ser Ser Phe Glu Asn Lys Lys Val Asp
    50                  55                  60

Ile Ser Asp Ile Glu Val Ile Thr Asn Gly Asn Leu Asp Asp Val Pro
65                  70                  75                  80

Tyr Lys Ala Asn Ser Ser Lys Tyr Asn Tyr Pro Asp Ile Lys Thr Lys
                85                  90                  95

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

His Ser Gly Ser Asn Glu Lys Gly Tyr Val Tyr Tyr Lys Gly Asn Ser
        115                 120                 125

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

Trp Asp Phe Thr Ser Asn Ala Asn Leu Asn Asn Glu Glu Gly Arg Pro
145                 150                 155                 160

Asn Tyr Leu Asn Asp Asp Tyr Tyr Thr Lys Phe Ile Gly Lys Arg Val
                165                 170                 175

Gly Leu Val Ser Gly Asp Ala Lys Pro Ala Lys His Lys Tyr Thr Ser
            180                 185                 190

Gln Phe Glu Val Asp Phe Ala Thr Lys Lys Met Thr Gly Lys Leu Ser
        195                 200                 205

Asp Lys Glu Lys Thr Ile Tyr Thr Val Asn Ala Asp Ile Arg Gly Asn

    210                 215                 220

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

Glu Ser Tyr Asn Phe Phe Ser Ala Asp Ser Gln Ser Leu Glu Gly Gly
                245                 250                 255

Phe Tyr Gly Pro Lys Ala Glu Glu Met Ala Gly Lys Phe Val Ala Asn
            260                 265                 270

Asp Lys Ser Leu Phe Ala Val Phe
        275                 280
```

<210> 9

<211> 744

<212> DNA

<213> Actinobacillus pleuropneumoniae

<400> 9

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ggatccggcg tgtcaaaaga agaatacaaa gatgtggaaa ccgctaaaaa agaaaaagaa       60

caactgggcg aactgggtga actgatggaa ccggcactgg gctatgtggt taaagtcccg      120

gtgtcagctg gtaaaaaagt cgatatttcg gacatcgaag tgattaccaa cggcaatctg      180

gatgacgtgc cgtacaaagc caatagctct aaatataact acccggatat caaaacgaaa      240

gacagttccc tgcagtatgt gcgtagcggc tacgttattt ctccggatgg cggttatgtt      300

tattacaagg gtaattctcc ggcaaaagaa ctgccggtca accaactgct gacctacacg      360

ggcagttggg attttaccag caacgctaat ctgaacgcag cacgtccggc aggtgcaggt      420

aaacgcgttg gcctggtcag cggtgatgcg aaagaacgca aatataccag ccagtttgaa      480

gtggacttcg ccaccaagaa aatgacgggt aaactgagcg ataaagaaaa aaccatctac      540

acggttaatg cggacattcg tggcaaccgc tttaccggtg cagctacggc gagcgataaa      600

aatgacccga tcctgtctgc cgattcacaa tcgctggaag gcggtttcta tggcccgaaa      660

gcagaagaaa tggctggtaa attcgtggca aatgacaaat cgctgttcgc agtcttctcc      720

gctaaacaca atggctccaa tgtc                                             744
```

<210> 10

<211> 248

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 10

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Gly Ser Gly Val Ser Lys Glu Glu Tyr Lys Asp Val Glu Thr Ala Lys
1               5                  10                  15

Lys Glu Lys Glu Gln Leu Gly Glu Leu Gly Glu Leu Met Glu Pro Ala
            20                  25                  30

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

Ile Ser Asp Ile Glu Val Ile Thr Asn Gly Asn Leu Asp Asp Val Pro
    50                  55                  60

Tyr Lys Ala Asn Ser Ser Lys Tyr Asn Tyr Pro Asp Ile Lys Thr Lys
65                  70                  75                  80

Asp Ser Ser Leu Gln Tyr Val Arg Ser Gly Tyr Val Ile Ser Pro Asp
                85                  90                  95

Gly Gly Tyr Val Tyr Tyr Lys Gly Asn Ser Pro Ala Lys Glu Leu Pro
            100                 105                 110

Val Asn Gln Leu Leu Thr Tyr Thr Gly Ser Trp Asp Phe Thr Ser Asn
        115                 120                 125

Ala Asn Leu Asn Ala Ala Arg Pro Ala Gly Ala Gly Lys Arg Val Gly
    130                 135                 140

Leu Val Ser Gly Asp Ala Lys Glu Arg Lys Tyr Thr Ser Gln Phe Glu
```

```
Leu Val Ser Gly Asp Ala Lys Glu Arg Lys Tyr Thr Ser Gln Phe Glu
145                 150                 155                 160

Val Asp Phe Ala Thr Lys Lys Met Thr Gly Lys Leu Ser Asp Lys Glu
                165                 170                 175

Lys Thr Ile Tyr Thr Val Asn Ala Asp Ile Arg Gly Asn Arg Phe Thr
            180                 185                 190

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

Ser Gln Ser Leu Glu Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Met
    210                 215                 220

Ala Gly Lys Phe Val Ala Asn Asp Lys Ser Leu Phe Ala Val Phe Ser
225                 230                 235                 240

Ala Lys His Asn Gly Ser Asn Val
                245
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<210> 11

<211> 1640

<212> DNA

<213> Actinobacillus pleuropneumoniae

<400> 11

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atgcatttta aatccgacct atatatagta gctcttacct caactttcct tgtagcttgt       60

tctggtggaa aaggtagctt tgatttggat gatgttcaac caaataaagc cgttgaacca      120

gaaaaaacaa aagtgaatta taccgacgaa gaaacacaaa aaaggaaaaa agaagagtta      180

gataagttga tggaacctgc tttgggatat gtaacaaaaa tcccagtcaa tatacctagt      240

gtaagaaaaa cagaaatttc agaaattgat acagtgactg atgaatctct ctctctcgtt      300

ccaaatgagg acaaattaag aacaatcgct aacgagaatt atgggtcggt agtaacaaaa      360

tctggaagta acactatgaa ttttgttcgt tctggatata cgattgatgt tgttcattat      420

ggtttaagag ataaaggata tgtttactac aaaggagttc atccttccaa agagctccct      480

aaaggcaata ttatcgttta tcaaggagag tgggacttta cctcaaatgc cgatctagat      540

gccaaaagac caaattacaa tcctgaattt aatggctatg gcgcagggca aagagttgga      600

gttacttctg cagatgcaaa agaaagaact tatatctcga agttcaacat agatttttca      660

aataagaaat tgaatggtca gttacttact aaaacaaaag aaaatcaaga aaaattacgc      720

tataccgttg aagctaacat tagtggcaat cgttttagag gaaaagcgac tgctactgat      780

aaaacagatc cgatattagg taaagattct gagcatcttg aaggtggctt atatggtcca      840

aaatcagaag aacttgcagg aaaatttgta gctcatgata aatctctttt tgcggtattc      900

tctggcaaaa gaggtaatga cgttcttgaa acagtcaaga tcattgatgc ctcaaaaatt      960

gatttaacta cttttgaatc atcggaactc aacaatttcg gcaacgctaa tgtgttaatt     1020

attgatggac agaaaataga tctagcaggt gcagatttta aaaatagaaa aaccgttgat     1080

atcaatggta agacaatggt agccatagct tgctgtagta atttggaata tatgaaattt     1140
```

ggtcaattat ggcaaaaaga gggcgaacaa actaaagata atagcttatt cctgcaaggt 1200

gagcgtactg ccacagataa aatacccgta ggtggaaact ataaatatgt aggaacctgg 1260

gatgcactcg tttcaaaagg aacgaactgg gtagctgagg cggataataa tcgagaatcg 1320

ggctatcgct cagaatttga tgttaatttt ggtgataaaa aagtaagcgg caagttattt 1380

gataaagggg gcatagtacc tgtctttatg atcaacgcag atattaaagg taacggcttt 1440

actgggacag ctaacactac agatacaggc tttgcgttag attcaggctc tagccaacac 1500

ggaaatgcgg tatttagtga tataaaagtc aatggtggct tctatggtcc aaccgctgga 1560

gaacttggcg gacaattcca tcataaatca gacaatggca gtgttggcgc tgtctttggt 1620

gcaaaacgac aaatagaaaa 1640

<210> 12

<211> 540

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 12

Met His Phe Lys Ser Asp Leu Tyr Ile Val Ala Leu Thr Ser Thr Phe
1 5 10 15

Leu Val Ala Cys Ser Gly Gly Lys Gly Ser Phe Asp Leu Asp Asp Val
20 25 30

Gln Pro Asn Lys Ala Val Glu Pro Glu Lys Thr Lys Val Asn Tyr Thr
35 40 45

Asp Glu Glu Thr Gln Lys Arg Lys Lys Glu Glu Leu Asp Lys Leu Met
50 55 60

Glu Pro Ala Leu Gly Tyr Val Thr Lys Ile Pro Val Asn Ile Pro Ser
65 70 75 80

Val Arg Lys Thr Glu Ile Ser Glu Ile Asp Thr Val Thr Asp Glu Ser
85 90 95

Leu Ser Leu Val Pro Asn Glu Asp Lys Leu Arg Thr Ile Ala Asn Glu
100 105 110

Asn Tyr Gly Ser Val Val Thr Lys Ser Gly Ser Asn Thr Met Asn Phe
115 120 125

Val Arg Ser Gly Tyr Thr Ile Asp Val Val His Tyr Gly Leu Arg Asp
130 135 140

Lys Gly Tyr Val Tyr Tyr Lys Gly Val His Pro Ser Lys Glu Leu Pro
145 150 155 160

Lys Gly Asn Ile Ile Val Tyr Gln Gly Glu Trp Asp Phe Thr Ser Asn
165 170 175

Ala Asp Leu Asp Ala Lys Arg Pro Asn Tyr Asn Pro Glu Phe Asn Gly
180 185 190

```
Tyr Gly Ala Gly Gln Arg Val Gly Val Thr Ser Ala Asp Ala Lys Glu
        195                 200                 205

Arg Thr Tyr Ile Ser Lys Phe Asn Ile Asp Phe Ser Asn Lys Lys Leu
    210                 215                 220

Asn Gly Gln Leu Leu Thr Lys Thr Lys Glu Asn Gln Glu Lys Leu Arg
225                 230                 235                 240

Tyr Thr Val Glu Ala Asn Ile Ser Gly Asn Arg Phe Arg Gly Lys Ala
                245                 250                 255

Thr Ala Thr Asp Lys Thr Asp Pro Ile Leu Gly Lys Asp Ser Glu His
            260                 265                 270

Leu Glu Gly Gly Leu Tyr Gly Pro Lys Ser Glu Glu Leu Ala Gly Lys
        275                 280                 285

Phe Val Ala His Asp Lys Ser Leu Phe Ala Val Phe Ser Gly Lys Arg
    290                 295                 300

Gly Asn Asp Val Leu Glu Thr Val Lys Ile Ile Asp Ala Ser Lys Ile
305                 310                 315                 320

Asp Leu Thr Thr Phe Glu Ser Ser Glu Leu Asn Asn Phe Gly Asn Ala
                325                 330                 335

Asn Val Leu Ile Ile Asp Gly Gln Lys Ile Asp Leu Ala Gly Ala Asp
            340                 345                 350

Phe Lys Asn Arg Lys Thr Val Asp Ile Asn Gly Lys Thr Met Val Ala
        355                 360                 365

Ile Ala Cys Cys Ser Asn Leu Glu Tyr Met Lys Phe Gly Gln Leu Trp
    370                 375                 380

Gln Lys Glu Gly Glu Gln Thr Lys Asp Asn Ser Leu Phe Leu Gln Gly
385                 390                 395                 400

Glu Arg Thr Ala Thr Asp Lys Ile Pro Val Gly Gly Asn Tyr Lys Tyr
                405                 410                 415

Val Gly Thr Trp Asp Ala Leu Val Ser Lys Gly Thr Asn Trp Val Ala
            420                 425                 430

Glu Ala Asp Asn Asn Arg Glu Ser Gly Tyr Arg Ser Glu Phe Asp Val
        435                 440                 445

Asn Phe Gly Asp Lys Lys Val Ser Gly Lys Leu Phe Asp Lys Gly Gly
    450                 455                 460

Ile Val Pro Val Phe Met Ile Asn Ala Asp Ile Lys Gly Asn Gly Phe
465                 470                 475                 480

Thr Gly Thr Ala Asn Thr Thr Asp Thr Gly Phe Ala Leu Asp Ser Gly
                485                 490                 495
```

```
Ser Ser Gln His Gly Asn Ala Val Phe Ser Asp Ile Lys Val Asn Gly
            500                 505                 510

Gly Phe Tyr Gly Pro Thr Ala Gly Glu Leu Gly Gly Gln Phe His His
        515                 520                 525

Lys Ser Asp Asn Gly Ser Val Gly Ala Val Phe Gly
    530                 535                 540
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<210> 13

<211> 1640

<212> DNA

<213> Actinobacillus pleuropneumoniae

<400> 13

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atgcatttta aatccgacct atatatagta gctcttacct caactttcct tgtagcttgt       60

tctggtggaa aaggtagctt tgatttggat gatgttcaac caaataaagc cgttgaacca      120

gaaaaaacaa aagtgaatta taccgacgaa gaaacacaaa aaaggaaaaa agaagagtta      180

gataagttga tggaacctgc tttgggatat gtaacaaaaa tcccagtcaa tatacctagt      240

gtaagaaaaa cagaaatttc agaaattgat acagtgactg atgaatctct ctctctcgtt      300

ccaaatgagg acaaattaag aacaatcgct aacgagaatg ctgggtcggt agtaacaaaa      360

tctggaagta acactatgaa ttttgttcgt tctggatata cgattgatgt tgttcattat      420

ggtttaagag ataaaggata tgtttactac aaaggagttc atccttccaa agagctccct      480

aaaggcaata ttatcgttta tcaaggagag tgggacttta cctcaaatgc cgatctagat      540

gccaaaagac caaattacaa tcctgaattt aatggctatg gcgcagggca aagagttgga      600

gttacttctg cagatgcaaa agaaagaact tatatctcga agttcaacat agatttttca      660

aataagaaat tgaatggtca gttacttact aaaacaaaag aaaatcaaga aaaattacgc      720

tataccgttg aagctaacat tagtggcaat cgttttagag gaaaagcgac tgctactgat      780

aaaacagatc cgatattagg taaagattct gagcatcttg aaggtggctt atatggtcca      840

aaatcagaag aacttgcagg aaaatttgta gctcatgata aatctctttt tgcggtattc      900

tctggcaaaa gaggtaatga cgttcttgaa acagtcaaga tcattgatgc ctcaaaaatt      960

gatttaacta cttttgaatc atcggaactc aacaatttcg gcaacgctaa tgtgttaatt     1020

attgatggac agaaaataga tctagcaggt gcagatttta aaaatagaaa aaccgttgat     1080

atcaatggta agacaatggt agccatagct tgctgtagta atttggaata tatgaaattt     1140

ggtcaattat ggcaaaaaga gggcgaacaa actaaagata atagcttatt cctgcaaggt     1200

gagcgtactg ccacagataa aatacccgta ggtggaaact ataaatatgt aggaacctgg     1260

gatgcactcg tttcaaaagg aacgaactgg gtagctgagg cggataataa tcgagaatcg     1320

ggctatcgct cagaatttga tgttaatttt ggtgataaaa aagtaagcgg caagttattt     1380

gataaagggg gcatagtacc tgtctttatg atcaacgcag atattaaagg taacggcttt     1440

actgggacag ctaacactac agatacaggc tttgcgttag attcaggctc tagccaacac     1500

ggaaatgcgg tatttagtga tataaaagtc aatggtggct tctatggtcc aaccgctgga     1560
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gaacttggcg gacaattcca tcataaatca gacaatggca gtgttggcgc tgtctttggt 1620

gcaaaacgac aaatagaaaa 1640

<210> 14

<211> 540

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 14

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Met His Phe Lys Ser Asp Leu Tyr Ile Val Ala Leu Thr Ser Thr Phe
1               5                  10                  15

Leu Val Ala Cys Ser Gly Gly Lys Gly Ser Phe Asp Leu Asp Asp Val
            20                  25                  30

Gln Pro Asn Lys Ala Val Glu Pro Glu Lys Thr Lys Val Asn Tyr Thr
        35                  40                  45

Asp Glu Glu Thr Gln Lys Arg Lys Lys Glu Glu Leu Asp Lys Leu Met
    50                  55                  60

Glu Pro Ala Leu Gly Tyr Val Thr Lys Ile Pro Val Asn Ile Pro Ser
65                  70                  75                  80

Val Arg Lys Thr Glu Ile Ser Glu Ile Asp Thr Val Thr Asp Glu Ser
                85                  90                  95

Leu Ser Leu Val Pro Asn Glu Asp Lys Leu Arg Thr Ile Ala Asn Glu
            100                 105                 110

Asn Ala Gly Ser Val Val Thr Lys Ser Gly Ser Asn Thr Met Asn Phe
        115                 120                 125

Val Arg Ser Gly Tyr Thr Ile Asp Val Val His Tyr Gly Leu Arg Asp
    130                 135                 140

Lys Gly Tyr Val Tyr Tyr Lys Gly Val His Pro Ser Lys Glu Leu Pro
145                 150                 155                 160

Lys Gly Asn Ile Ile Val Tyr Gln Gly Glu Trp Asp Phe Thr Ser Asn
                165                 170                 175

Ala Asp Leu Asp Ala Lys Arg Pro Asn Tyr Asn Pro Glu Phe Asn Gly
            180                 185                 190

Tyr Gly Ala Gly Gln Arg Val Gly Val Thr Ser Ala Asp Ala Lys Glu
        195                 200                 205

Arg Thr Tyr Ile Ser Lys Phe Asn Ile Asp Phe Ser Asn Lys Lys Leu
    210                 215                 220

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

Thr Ala Thr Asp Lys Thr Asp Pro Ile Leu Gly Lys Asp Ser Glu His
            260                 265                 270

Leu Glu Gly Gly Leu Tyr Gly Pro Lys Ser Glu Glu Leu Ala Gly Lys
        275                 280                 285

Phe Val Ala His Asp Lys Ser Leu Phe Ala Val Phe Ser Gly Lys Arg
    290                 295                 300

Gly Asn Asp Val Leu Glu Thr Val Lys Ile Ile Asp Ala Ser Lys Ile
305                 310                 315                 320

Asp Leu Thr Thr Phe Glu Ser Ser Glu Leu Asn Asn Phe Gly Asn Ala
                325                 330                 335

Asn Val Leu Ile Ile Asp Gly Gln Lys Ile Asp Leu Ala Gly Ala Asp
            340                 345                 350

Phe Lys Asn Arg Lys Thr Val Asp Ile Asn Gly Lys Thr Met Val Ala
        355                 360                 365

Ile Ala Cys Cys Ser Asn Leu Glu Tyr Met Lys Phe Gly Gln Leu Trp
    370                 375                 380

Gln Lys Glu Gly Glu Gln Thr Lys Asp Asn Ser Leu Phe Leu Gln Gly
385                 390                 395                 400

Glu Arg Thr Ala Thr Asp Lys Ile Pro Val Gly Gly Asn Tyr Lys Tyr
                405                 410                 415

Val Gly Thr Trp Asp Ala Leu Val Ser Lys Gly Thr Asn Trp Val Ala

            420                 425                 430

Glu Ala Asp Asn Asn Arg Glu Ser Gly Tyr Arg Ser Glu Phe Asp Val
        435                 440                 445

Asn Phe Gly Asp Lys Lys Val Ser Gly Lys Leu Phe Asp Lys Gly Gly
    450                 455                 460

Ile Val Pro Val Phe Met Ile Asn Ala Asp Ile Lys Gly Asn Gly Phe
465                 470                 475                 480

Thr Gly Thr Ala Asn Thr Thr Asp Thr Gly Phe Ala Leu Asp Ser Gly
                485                 490                 495

Ser Ser Gln His Gly Asn Ala Val Phe Ser Asp Ile Lys Val Asn Gly
            500                 505                 510

Gly Phe Tyr Gly Pro Thr Ala Gly Glu Leu Gly Gly Gln Phe His His
        515                 520                 525
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Lys Ser Asp Asn Gly Ser Val Gly Ala Val Phe Gly
    530                 535                 540
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<210> 15

<211> 1640

<212> DNA

<213> Actinobacillus pleuropneumoniae

<400> 15

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tctggtggaa aaggtagctt tgatttggat gatgttcaac caaataaagc cgttgaacca      120

gaaaaaacaa aagtgaatta taccgacgaa gaaacacaaa aaaggaaaaa agaagagtta      180

gataagttga tggaacctgc tttgggatat gtaacaaaaa tcccagtcaa tatacctagt      240

gtaagaaaaa cagaaatttc agaaattgat acagtgactg atgaatctct ctctctcgtt      300

ccaaatgagg acaaattaag aacaatcgct aacgagaatt atgggtcggt agtaacaaaa      360

tctggaagta acactatgaa ttttgttcgt tctggatata cgattgatgt tgttcatgct      420

ggtttaagag ataaaggata tgtttactac aaaggagttc atccttccaa agagctccct      480

aaaggcaata ttatcgttta tcaaggagag tgggacttta cctcaaatgc cgatctagat      540

gccaaaagac caaattacaa tcctgaattt aatggctatg gcgcagggca aagagttgga      600

gttacttctg cagatgcaaa agaaagaact tatatctcga agttcaacat agatttttca      660

aataagaaat tgaatggtca gttacttact aaaacaaaag aaaatcaaga aaaattacgc      720

tataccgttg aagctaacat tagtggcaat cgttttagag gaaaagcgac tgctactgat      780

aaaacagatc cgatattagg taaagattct gagcatcttg aaggtggctt atatggtcca      840

aaatcagaag aacttgcagg aaaatttgta gctcatgata aatctctttt tgcggtattc      900

tctggcaaaa gaggtaatga cgttcttgaa acagtcaaga tcattgatgc ctcaaaaatt      960

gatttaacta cttttgaatc atcggaactc aacaatttcg gcaacgctaa tgtgttaatt     1020

attgatggac agaaaataga tctagcaggt gcagatttta aaaatagaaa aaccgttgat     1080

atcaatggta agacaatggt agccatagct tgctgtagta atttggaata tatgaaattt     1140

ggtcaattat ggcaaaaaga gggcgaacaa actaaagata atagcttatt cctgcaaggt     1200

gagcgtactg ccacagataa aatacccgta ggtggaaact ataaatatgt aggaacctgg     1260

gatgcactcg tttcaaaagg aacgaactgg gtagctgagg cggataataa tcgagaatcg     1320

ggctatcgct cagaatttga tgttaatttt ggtgataaaa aagtaagcgg caagttattt     1380

gataaagggg gcatagtacc tgtctttatg atcaacgcag atattaaagg taacggcttt     1440

actgggacag ctaacactac agatacaggc tttgcgttag attcaggctc tagccaacac     1500

ggaaatgcgg tatttagtga tataaaagtc aatggtggct tctatggtcc aaccgctgga     1560

gaacttggcg gacaattcca tcataaatca gacaatggca gtgttggcgc tgtctttggt     1620

gcaaaacgac aaatagaaaa                                                 1640
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<210> 16

<211> 540

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 16

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Met His Phe Lys Ser Asp Leu Tyr Ile Val Ala Leu Thr Ser Thr Phe
1               5                  10                  15

Leu Val Ala Cys Ser Gly Gly Lys Gly Ser Phe Asp Leu Asp Asp Val
            20                  25                  30

Gln Pro Asn Lys Ala Val Glu Pro Glu Lys Thr Lys Val Asn Tyr Thr
        35                  40                  45

Asp Glu Glu Thr Gln Lys Arg Lys Lys Glu Glu Leu Asp Lys Leu Met
    50                  55                  60

Glu Pro Ala Leu Gly Tyr Val Thr Lys Ile Pro Val Asn Ile Pro Ser
65                  70                  75                  80

Val Arg Lys Thr Glu Ile Ser Glu Ile Asp Thr Val Thr Asp Glu Ser
                85                  90                  95

Leu Ser Leu Val Pro Asn Glu Asp Lys Leu Arg Thr Ile Ala Asn Glu

            100                 105                 110

Asn Ala Gly Ser Val Val Thr Lys Ser Gly Ser Asn Thr Met Asn Phe
        115                 120                 125

Val Arg Ser Gly Tyr Thr Ile Asp Val Val His Ala Gly Leu Arg Asp
    130                 135                 140

Lys Gly Tyr Val Tyr Tyr Lys Gly Val His Pro Ser Lys Glu Leu Pro
145                 150                 155                 160

Lys Gly Asn Ile Ile Val Tyr Gln Gly Glu Trp Asp Phe Thr Ser Asn
                165                 170                 175

Ala Asp Leu Asp Ala Lys Arg Pro Asn Tyr Asn Pro Glu Phe Asn Gly
            180                 185                 190

Tyr Gly Ala Gly Gln Arg Val Gly Val Thr Ser Ala Asp Ala Lys Glu
        195                 200                 205

Arg Thr Tyr Ile Ser Lys Phe Asn Ile Asp Phe Ser Asn Lys Lys Leu
    210                 215                 220

Asn Gly Gln Leu Leu Thr Lys Thr Lys Glu Asn Gln Glu Lys Leu Arg
225                 230                 235                 240

Tyr Thr Val Glu Ala Asn Ile Ser Gly Asn Arg Phe Arg Gly Lys Ala
                245                 250                 255

Thr Ala Thr Asp Lys Thr Asp Pro Ile Leu Gly Lys Asp Ser Glu His
            260                 265                 270
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Leu Glu Gly Gly Leu Tyr Gly Pro Lys Ser Glu Glu Leu Ala Gly Lys
        275                 280                 285

Phe Val Ala His Asp Lys Ser Leu Phe Ala Val Phe Ser Gly Lys Arg
    290                 295                 300

Gly Asn Asp Val Leu Glu Thr Val Lys Ile Ile Asp Ala Ser Lys Ile
305                 310                 315                 320

Asp Leu Thr Thr Phe Glu Ser Ser Glu Leu Asn Asn Phe Gly Asn Ala
                325                 330                 335

Asn Val Leu Ile Ile Asp Gly Gln Lys Ile Asp Leu Ala Gly Ala Asp
            340                 345                 350

Phe Lys Asn Arg Lys Thr Val Asp Ile Asn Gly Lys Thr Met Val Ala
        355                 360                 365

Ile Ala Cys Cys Ser Asn Leu Glu Tyr Met Lys Phe Gly Gln Leu Trp
    370                 375                 380

Gln Lys Glu Gly Glu Gln Thr Lys Asp Asn Ser Leu Phe Leu Gln Gly
385                 390                 395                 400

Glu Arg Thr Ala Thr Asp Lys Ile Pro Val Gly Gly Asn Tyr Lys Tyr
                405                 410                 415

Val Gly Thr Trp Asp Ala Leu Val Ser Lys Gly Thr Asn Trp Val Ala
            420                 425                 430

Glu Ala Asp Asn Asn Arg Glu Ser Gly Tyr Arg Ser Glu Phe Asp Val
        435                 440                 445

Asn Phe Gly Asp Lys Lys Val Ser Gly Lys Leu Phe Asp Lys Gly Gly
    450                 455                 460

Ile Val Pro Val Phe Met Ile Asn Ala Asp Ile Lys Gly Asn Gly Phe
465                 470                 475                 480

Thr Gly Thr Ala Asn Thr Thr Asp Thr Gly Phe Ala Leu Asp Ser Gly
                485                 490                 495

Ser Ser Gln His Gly Asn Ala Val Phe Ser Asp Ile Lys Val Asn Gly
            500                 505                 510

Gly Phe Tyr Gly Pro Thr Ala Gly Glu Leu Gly Gly Gln Phe His His
        515                 520                 525

Lys Ser Asp Asn Gly Ser Val Gly Ala Val Phe Gly
    530                 535                 540
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<210> 17

<211> 1640

<212> DNA

<213> Actinobacillus pleuropneumoniae

<400> 17

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tctggtggaa aaggtagctt tgatttggat gatgttcaac caaataaagc cgttgaacca 120

gaaaaaacaa aagtgaatta taccgacgaa gaaacacaaa aaaggaaaaa agaagagtta 180

gataagttga tggaacctgc tttgggatat gtaacaaaaa tcccagtcaa tatacctagt 240

gtaagaaaaa cagaaatttc agaaattgat acagtgactg atgaatctct ctctctcgtt 300

ccaaatgagg acaaattaag aacaatcgct aacgagaatt atgggtcggt agtaacaaaa 360

tctggaagta acactatgaa ttttgttcgt tctggatata cgattgatgt tgttcattat 420

ggtttaagag ataaaggata tgtttactac aaaggagttc atccttccaa agagctccct 480

aaaggcaata ttatcgttta tcaaggagag tgggacttta cctcaaatgc cgatctagat 540

gccaaaagac caaattacaa tcctgaattt aatggcgcag gcgcagggca aagagttgga 600

gttacttctg cagatgcaaa agaaagaact tatatctcga agttcaacat agatttttca 660

aataagaaat tgaatggtca gttacttact aaaacaaaag aaaatcaaga aaaattacgc 720

tataccgttg aagctaacat tagtggcaat cgttttagag gaaaagcgac tgctactgat 780

aaaacagatc cgatattagg taaagattct gagcatcttg aaggtggctt atatggtcca 840

aaatcagaag aacttgcagg aaaatttgta gctcatgata aatctctttt tgcggtattc 900

tctggcaaaa gaggtaatga cgttcttgaa acagtcaaga tcattgatgc ctcaaaaatt 960

gatttaacta cttttgaatc atcggaactc aacaatttcg gcaacgctaa tgtgttaatt 1020

attgatggac agaaaataga tctagcaggt gcagatttta aaaatagaaa aaccgttgat 1080

atcaatggta agacaatggt agccatagct tgctgtagta atttggaata tatgaaattt 1140

ggtcaattat ggcaaaaaga gggcgaacaa actaaagata atagcttatt cctgcaaggt 1200

gagcgtactg ccacagataa aatacccgta ggtggaaact ataaatatgt aggaacctgg 1260

gatgcactcg tttcaaaagg aacgaactgg gtagctgagg cggataataa tcgagaatcg 1320

ggctatcgct cagaatttga tgttaatttt ggtgataaaa aagtaagcgg caagttattt 1380

gataaagggg gcatagtacc tgtctttatg atcaacgcag atattaaagg taacggcttt 1440

actgggacag ctaacactac agatacaggc tttgcgttag attcaggctc tagccaacac 1500

ggaaatgcgg tatttagtga tataaaagtc aatggtggct tctatggtcc aaccgctgga 1560

gaacttggcg gacaattcca tcataaatca gacaatggca gtgttggcgc tgtctttggt 1620

gcaaaacgac aaatagaaaa 1640

<210> 18

<211> 540

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 18

Met His Phe Lys Ser Asp Leu Tyr Ile Val Ala Leu Thr Ser Thr Phe
1 5 10 15

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Leu Val Ala Cys Ser Gly Gly Lys Gly Ser Phe Asp Leu Asp Asp Val
            20                  25                  30

Gln Pro Asn Lys Ala Val Glu Pro Glu Lys Thr Lys Val Asn Tyr Thr
        35                  40                  45

Asp Glu Glu Thr Gln Lys Arg Lys Lys Glu Glu Leu Asp Lys Leu Met
    50                  55                  60

Glu Pro Ala Leu Gly Tyr Val Thr Lys Ile Pro Val Asn Ile Pro Ser
65                  70                  75                  80

Val Arg Lys Thr Glu Ile Ser Glu Ile Asp Thr Val Thr Asp Glu Ser
                85                  90                  95

Leu Ser Leu Val Pro Asn Glu Asp Lys Leu Arg Thr Ile Ala Asn Glu
            100                 105                 110

Asn Tyr Gly Ser Val Val Thr Lys Ser Gly Ser Asn Thr Met Asn Phe
        115                 120                 125

Val Arg Ser Gly Tyr Thr Ile Asp Val Val His Tyr Gly Leu Arg Asp
    130                 135                 140

Lys Gly Tyr Val Tyr Tyr Lys Gly Val His Pro Ser Lys Glu Leu Pro
145                 150                 155                 160

Lys Gly Asn Ile Ile Val Tyr Gln Gly Glu Trp Asp Phe Thr Ser Asn
                165                 170                 175

Ala Asp Leu Asp Ala Lys Arg Pro Asn Tyr Asn Pro Glu Phe Asn Gly
            180                 185                 190

Ala Gly Ala Gly Gln Arg Val Gly Val Thr Ser Ala Asp Ala Lys Glu
        195                 200                 205

Arg Thr Tyr Ile Ser Lys Phe Asn Ile Asp Phe Ser Asn Lys Lys Leu
    210                 215                 220

Asn Gly Gln Leu Leu Thr Lys Thr Lys Glu Asn Gln Glu Lys Leu Arg
225                 230                 235                 240

Tyr Thr Val Glu Ala Asn Ile Ser Gly Asn Arg Phe Arg Gly Lys Ala
                245                 250                 255

Thr Ala Thr Asp Lys Thr Asp Pro Ile Leu Gly Lys Asp Ser Glu His
            260                 265                 270

Leu Glu Gly Gly Leu Tyr Gly Pro Lys Ser Glu Glu Leu Ala Gly Lys
        275                 280                 285

Phe Val Ala His Asp Lys Ser Leu Phe Ala Val Phe Ser Gly Lys Arg
    290                 295                 300

Gly Asn Asp Val Leu Glu Thr Val Lys Ile Ile Asp Ala Ser Lys Ile
305                 310                 315                 320
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```
Asp Leu Thr Thr Phe Glu Ser Ser Glu Leu Asn Asn Phe Gly Asn Ala
                325                 330                 335

Asn Val Leu Ile Ile Asp Gly Gln Lys Ile Asp Leu Ala Gly Ala Asp
            340                 345                 350

Phe Lys Asn Arg Lys Thr Val Asp Ile Asn Gly Lys Thr Met Val Ala
        355                 360                 365

Ile Ala Cys Cys Ser Asn Leu Glu Tyr Met Lys Phe Gly Gln Leu Trp
    370                 375                 380

Gln Lys Glu Gly Glu Gln Thr Lys Asp Asn Ser Leu Phe Leu Gln Gly
385                 390                 395                 400

Glu Arg Thr Ala Thr Asp Lys Ile Pro Val Gly Gly Asn Tyr Lys Tyr
                405                 410                 415

Val Gly Thr Trp Asp Ala Leu Val Ser Lys Gly Thr Asn Trp Val Ala
            420                 425                 430

Glu Ala Asp Asn Asn Arg Glu Ser Gly Tyr Arg Ser Glu Phe Asp Val
        435                 440                 445

Asn Phe Gly Asp Lys Lys Val Ser Gly Lys Leu Phe Asp Lys Gly Gly
    450                 455                 460

Ile Val Pro Val Phe Met Ile Asn Ala Asp Ile Lys Gly Asn Gly Phe
465                 470                 475                 480

Thr Gly Thr Ala Asn Thr Thr Asp Thr Gly Phe Ala Leu Asp Ser Gly
                485                 490                 495

Ser Ser Gln His Gly Asn Ala Val Phe Ser Asp Ile Lys Val Asn Gly
            500                 505                 510

Gly Phe Tyr Gly Pro Thr Ala Gly Glu Leu Gly Gly Gln Phe His His
        515                 520                 525

Lys Ser Asp Asn Gly Ser Val Gly Ala Val Phe Gly
    530                 535                 540
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<210> 19

<211> 1640

<212> DNA

<213> Actinobacillus pleuropneumoniae

<400> 19

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tctggtggaa aaggtagctt tgatttggat gatgttcaac caaataaagc cgttgaacca      120

gaaaaaacaa aagtgaatta taccgacgaa gaaacacaaa aaaggaaaaa agaagagtta      180

gataagttga tggaacctgc tttgggatat gtaacaaaaa tcccagtcaa tatacctagt      240

gtaagaaaaa cagaaatttc agaaattgat acagtgactg atgaatctct ctctctcgtt      300

ccaaatgagg acaaattaag aacaatcgct aacgagaatt atgggtcggt agtaacaaaa      360
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tctggaagta acactatgaa ttttgttcgt tctggatata cgattgatgt tgttcattat 420

ggtttaagag ataaaggata tgtttactac aaaggagttc atccttccaa agagctccct 480

aaaggcaata ttatcgttta tcaaggagag tgggacttta cctcaaatgc cgatctagat 540

gccaaaagac caaattacaa tcctgaattt aatggctatg gcgcagggca agaggttgga 600

gttacttctg cagatgcaaa agaaagaact tatatctcga agttcaacat agatttttca 660

aataagaaat tgaatggtca gttacttact aaaacaaaag aaaatcaaga aaaattacgc 720

tataccgttg aagctaacat tagtggcaat cgttttagag gaaaagcgac tgctactgat 780

aaaacagatc cgatattagg taaagattct gagcatcttg aaggtggctt atatggtcca 840

aaatcagaag aacttgcagg aaaatttgta gctcatgata aatctctttt tgcggtattc 900

tctggcaaaa gaggtaatga cgttcttgaa acagtcaaga tcattgatgc ctcaaaaatt 960

gatttaacta cttttgaatc atcggaactc aacaatttcg gcaacgctaa tgtgttaatt 1020

attgatggac agaaaataga tctagcaggt gcagatttta aaaatagaaa aaccgttgat 1080

atcaatggta agacaatggt agccatagct tgctgtagta atttggaata tatgaaattt 1140

ggtcaattat ggcaaaaaga gggcgaacaa actaaagata atagcttatt cctgcaaggt 1200

gagcgtactg ccacagataa aatacccgta ggtggaaact ataaatatgt aggaacctgg 1260

gatgcactcg tttcaaaagg aacgaactgg gtagctgagg cggataataa tcgagaatcg 1320

ggctatcgct cagaatttga tgttaatttt ggtgataaaa aagtaagcgg caagttattt 1380

gataaagggg gcatagtacc tgtctttatg atcaacgcag atattaaagg taacggcttt 1440

actgggacag ctaacactac agatacaggc tttgcgttag attcaggctc tagccaacac 1500

ggaaatgcgg tatttagtga tataaaagtc aatggtggct tctatggtcc aaccgctgga 1560

gaacttggcg gacaattcca tcataaatca gacaatggca gtgttggcgc tgtctttggt 1620

gcaaaacgac aaatagaaaa 1640

<210> 20

<211> 540

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 20

Met His Phe Lys Ser Asp Leu Tyr Ile Val Ala Leu Thr Ser Thr Phe
1 5 10 15

Leu Val Ala Cys Ser Gly Gly Lys Gly Ser Phe Asp Leu Asp Asp Val
20 25 30

Gln Pro Asn Lys Ala Val Glu Pro Glu Lys Thr Lys Val Asn Tyr Thr
35 40 45

Asp Glu Glu Thr Gln Lys Arg Lys Lys Glu Glu Leu Asp Lys Leu Met
50 55 60

Glu Pro Ala Leu Gly Tyr Val Thr Lys Ile Pro Val Asn Ile Pro Ser
65 70 75 80

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Val Arg Lys Thr Glu Ile Ser Glu Ile Asp Thr Val Thr Asp Glu Ser
                85                  90                  95

Leu Ser Leu Val Pro Asn Glu Asp Lys Leu Arg Thr Ile Ala Asn Glu
            100                 105                 110

Asn Tyr Gly Ser Val Val Thr Lys Ser Gly Ser Asn Thr Met Asn Phe
        115                 120                 125

Val Arg Ser Gly Tyr Thr Ile Asp Val Val His Tyr Gly Leu Arg Asp
    130                 135                 140

Lys Gly Tyr Val Tyr Tyr Lys Gly Val His Pro Ser Lys Glu Leu Pro
145                 150                 155                 160

Lys Gly Asn Ile Ile Val Tyr Gln Gly Glu Trp Asp Phe Thr Ser Asn
                165                 170                 175

Ala Asp Leu Asp Ala Lys Arg Pro Asn Tyr Asn Pro Glu Phe Asn Gly
            180                 185                 190

Tyr Gly Ala Gly Gln Glu Val Gly Val Thr Ser Ala Asp Ala Lys Glu
        195                 200                 205

Arg Thr Tyr Ile Ser Lys Phe Asn Ile Asp Phe Ser Asn Lys Lys Leu
    210                 215                 220

Asn Gly Gln Leu Leu Thr Lys Thr Lys Glu Asn Gln Glu Lys Leu Arg
225                 230                 235                 240

Tyr Thr Val Glu Ala Asn Ile Ser Gly Asn Arg Phe Arg Gly Lys Ala
                245                 250                 255

Thr Ala Thr Asp Lys Thr Asp Pro Ile Leu Gly Lys Asp Ser Glu His
            260                 265                 270

Leu Glu Gly Gly Leu Tyr Gly Pro Lys Ser Glu Glu Leu Ala Gly Lys
        275                 280                 285

Phe Val Ala His Asp Lys Ser Leu Phe Ala Val Phe Ser Gly Lys Arg
    290                 295                 300

Gly Asn Asp Val Leu Glu Thr Val Lys Ile Ile Asp Ala Ser Lys Ile
305                 310                 315                 320

Asp Leu Thr Thr Phe Glu Ser Ser Glu Leu Asn Asn Phe Gly Asn Ala
                325                 330                 335

Asn Val Leu Ile Ile Asp Gly Gln Lys Ile Asp Leu Ala Gly Ala Asp
            340                 345                 350

Phe Lys Asn Arg Lys Thr Val Asp Ile Asn Gly Lys Thr Met Val Ala
        355                 360                 365

Ile Ala Cys Cys Ser Asn Leu Glu Tyr Met Lys Phe Gly Gln Leu Trp
    370                 375                 380
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Gln Lys Glu Gly Glu Gln Thr Lys Asp Asn Ser Leu Phe Leu Gln Gly
385                 390                 395                 400

Glu Arg Thr Ala Thr Asp Lys Ile Pro Val Gly Gly Asn Tyr Lys Tyr
                405                 410                 415

Val Gly Thr Trp Asp Ala Leu Val Ser Lys Gly Thr Asn Trp Val Ala
            420                 425                 430

Glu Ala Asp Asn Asn Arg Glu Ser Gly Tyr Arg Ser Glu Phe Asp Val
        435                 440                 445

Asn Phe Gly Asp Lys Lys Val Ser Gly Lys Leu Phe Asp Lys Gly Gly
    450                 455                 460

Ile Val Pro Val Phe Met Ile Asn Ala Asp Ile Lys Gly Asn Gly Phe

465                 470                 475                 480

Thr Gly Thr Ala Asn Thr Thr Asp Thr Gly Phe Ala Leu Asp Ser Gly
                485                 490                 495

Ser Ser Gln His Gly Asn Ala Val Phe Ser Asp Ile Lys Val Asn Gly
            500                 505                 510

Gly Phe Tyr Gly Pro Thr Ala Gly Glu Leu Gly Gly Gln Phe His His
        515                 520                 525

Lys Ser Asp Asn Gly Ser Val Gly Ala Val Phe Gly
    530                 535                 540
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<210> 21

<211> 730

<212> DNA

<213> Actinobacillus pleuropneumoniae

<400> 21

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aggtaatgac gttcttgaaa cagtcaagat cattgatgcc tcaaaaattg atttaactac       60

ttttgaatca tcggaactca acaatttcgg caacgctaat gtgttaatta ttgatggaca      120

gaaaatagat ctagcaggtg cagattttaa aaatagaaaa accgttgata tcaatggtaa      180

gacaatggta gccatagctt gctgtagtaa tttggaatat atgaaatttg gtcaattatg      240

gcaaaaagag ggcgaacaaa ctaaagataa tagcttattc ctgcaaggtg agcgtactgc      300

cacagataaa atacccgtag gtggaaacta taaatatgta ggaacctggg atgcactcgt      360

ttcaaaagga acgaactggg tagctgaggc ggataataat cgagaatcgg gctatcgctc      420

agaatttgat gttaattttg gtgataaaaa agtaagcggc aagttatttg ataaaggggg      480

catagtacct gtctttatga tcaacgcaga tattaaaggt aacggcttta ctgggacagc      540

taacactaca gatacaggct ttgcgttaga ttcaggctct agccaacacg gaaatgcggt      600

atttagtgat ataaaagtca atggtggctt ctatggtcca accgctggag aacttggcgg      660
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acaattccat cataaatcag acaatggcag tgttggcgct gtctttggtg caaaacgaca 720

aatagaaaaa 730

<210> 22

<211> 240

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 22

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Arg Gly Asn Asp Val Leu Glu Thr Val Lys Ile Ile Asp Ala Ser Lys
1               5                  10                  15

Ile Asp Leu Thr Thr Phe Glu Ser Ser Glu Leu Asn Asn Phe Gly Asn
            20                  25                  30

Ala Asn Val Leu Ile Ile Asp Gly Gln Lys Ile Asp Leu Ala Gly Ala
        35                  40                  45

Asp Phe Lys Asn Arg Lys Thr Val Asp Ile Asn Gly Lys Thr Met Val
    50                  55                  60

Ala Ile Ala Cys Cys Ser Asn Leu Glu Tyr Met Lys Phe Gly Gln Leu
65                  70                  75                  80

Trp Gln Lys Glu Gly Glu Gln Thr Lys Asp Asn Ser Leu Phe Leu Gln
                85                  90                  95

Gly Glu Arg Thr Ala Thr Asp Lys Ile Pro Val Gly Gly Asn Tyr Lys
            100                 105                 110

Tyr Val Gly Thr Trp Asp Ala Leu Val Ser Lys Gly Thr Asn Trp Val
        115                 120                 125

Ala Glu Ala Asp Asn Asn Arg Glu Ser Gly Tyr Arg Ser Glu Phe Asp
    130                 135                 140

Val Asn Phe Gly Asp Lys Lys Val Ser Gly Lys Leu Phe Asp Lys Gly
145                 150                 155                 160

Gly Ile Val Pro Val Phe Met Ile Asn Ala Asp Ile Lys Gly Asn Gly
                165                 170                 175

Phe Thr Gly Thr Ala Asn Thr Thr Asp Thr Gly Phe Ala Leu Asp Ser
            180                 185                 190

Gly Ser Ser Gln His Gly Asn Ala Val Phe Ser Asp Ile Lys Val Asn
        195                 200                 205

Gly Gly Phe Tyr Gly Pro Thr Ala Gly Glu Leu Gly Gly Gln Phe His
    210                 215                 220

His Lys Ser Asp Asn Gly Ser Val Gly Ala Val Phe Gly Ala Lys Arg
225                 230                 235                 240
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<210> 23
<211> 910
<212> DNA
<213> Actinobacillus pleuropneumoniae

<400> 23
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tctggtggaa aaggtagctt tgatttggat gatgttcaac caaataaagc cgttgaacca 120

gaaaaaacaa aagtgaatta taccgacgaa gaaacacaaa aaaggaaaaa agaagagtta 180

gataagttga tggaacctgc tttgggatat gtaacaaaaa tcccagtcaa tatacctagt 240

gtaagaaaaa cagaaatttc agaaattgat acagtgactg atgaatctct ctctctcgtt 300

ccaaatgagg acaaattaag aacaatcgct aacgagaatt atgggtcggt agtaacaaaa 360

tctggaagta acactatgaa ttttgttcgt tctggatata cgattgatgt tgttcattat 420

ggtttaagag ataaaggata tgtttactac aaaggagttc atccttccaa agagctccct 480

aaaggcaata ttatcgttta tcaaggagag tgggacttta cctcaaatgc cgatctagat 540

gccaaaagac caaattacaa tcctgaattt aatggctatg gcgcagggca aagagttgga 600

gttacttctg cagatgcaaa agaaagaact tatatctcga agttcaacat agatttttca 660

aataagaaat tgaatggtca gttacttact aaaacaaaag aaaatcaaga aaaattacgc 720

tataccgttg aagctaacat tagtggcaat cgttttagag gaaaagcgac tgctactgat 780

aaaacagatc cgatattagg taaagattct gagcatcttg aaggtggctt atatggtcca 840

aaatcagaag aacttgcagg aaaatttgta gctcatgata aatctctttt tgcggtattc 900

tctggcaaaa 910

<210> 24
<211> 280
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 24
Cys Ser Gly Gly Lys Gly Ser Phe Asp Leu Asp Asp Val Gln Pro Asn
1 5 10 15

Lys Ala Val Glu Pro Glu Lys Thr Lys Val Asn Tyr Thr Asp Glu Glu
20 25 30

Thr Gln Lys Arg Lys Lys Glu Glu Leu Asp Lys Leu Met Glu Pro Ala
35 40 45

Leu Gly Tyr Val Thr Lys Ile Pro Val Asn Ile Pro Ser Val Arg Lys
50 55 60

Thr Glu Ile Ser Glu Ile Asp Thr Val Thr Asp Glu Ser Leu Ser Leu
65 70 75 80

Val Pro Asn Glu Asp Lys Leu Arg Thr Ile Ala Asn Glu Asn Tyr Gly
85 90 95

```
Ser Val Val Thr Lys Ser Gly Ser Asn Thr Met Asn Phe Val Arg Ser
            100                 105                 110

Gly Tyr Thr Ile Asp Val Val His Tyr Gly Leu Arg Asp Lys Gly Tyr
        115                 120                 125

Val Tyr Tyr Lys Gly Val His Pro Ser Lys Glu Leu Pro Lys Gly Asn
    130                 135                 140

Ile Ile Val Tyr Gln Gly Glu Trp Asp Phe Thr Ser Asn Ala Asp Leu
145                 150                 155                 160

Asp Ala Lys Arg Pro Asn Tyr Asn Pro Glu Phe Asn Gly Tyr Gly Ala
                165                 170                 175

Gly Gln Arg Val Gly Val Thr Ser Ala Asp Ala Lys Glu Arg Thr Tyr
            180                 185                 190

Ile Ser Lys Phe Asn Ile Asp Phe Ser Asn Lys Lys Leu Asn Gly Gln
        195                 200                 205

Leu Leu Thr Lys Thr Lys Glu Asn Gln Glu Lys Leu Arg Tyr Thr Val
    210                 215                 220

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

Asp Lys Thr Asp Pro Ile Leu Gly Lys Asp Ser Glu His Leu Glu Gly
                245                 250                 255

Gly Leu Tyr Gly Pro Lys Ser Glu Glu Leu Ala Gly Lys Phe Val Ala
            260                 265                 270

His Asp Lys Ser Leu Phe Ala Val
        275                 280
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<210> 25

<211> 615

<212> DNA

<213> Actinobacillus pleuropneumoniae

<400> 25

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ggatccaagt tgatggaacc tgctttggga tatgtaacaa aaatcccagt cggtccgggt      60

agcgaaattt cagaaattga tacagtgact gatgaatctg tgtctggtgc gccgggtgtt     120

gttaactctg gatatacgat tgatgttgtt cattatggtt taagagataa aggttctgtg     180

tcttataaag gagttcatcc ttccaaagag ctccctaaag gcaatattat cgtttatcaa     240

ggagagtggg actttacctc aaatgccggt gcggcgggta gagttggagt tacttctgca     300

gatgcaaaag aaagaactta tatctcgaag ttcaacatag atttttcaaa taagaaattg     360

aatggtcagt tacttactaa aacaaaagaa aatcaagaaa aattacgcta taccgttgaa     420

gctaacatta gtggcaatcg ttttagagga aaagcgactg ctactgataa aacagatccg     480
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atattaggta aagattctga gcatcttgaa ggtggcttat atggtccaaa atcagaagaa 540

cttgcaggaa aatttgtagc tcatgataaa tctcttttttg cggtattctc tggcaaaaga 600

ggtaatgacg ttctt 615

<210> 26

<211> 205

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 26

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

Val Gly Pro Gly Ser Glu Ile Ser Glu Ile Asp Thr Val Thr Asp Glu
20 25 30

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

Val Val His Tyr Gly Leu Arg Asp Lys Gly Ser Val Ser Tyr Lys Gly
50 55 60

Val His Pro Ser Lys Glu Leu Pro Lys Gly Asn Ile Ile Val Tyr Gln
65 70 75 80

Gly Glu Trp Asp Phe Thr Ser Asn Ala Gly Ala Ala Gly Arg Val Gly
85 90 95

Val Thr Ser Ala Asp Ala Lys Glu Arg Thr Tyr Ile Ser Lys Phe Asn
100 105 110

Ile Asp Phe Ser Asn Lys Lys Leu Asn Gly Gln Leu Leu Thr Lys Thr
115 120 125

Lys Glu Asn Gln Glu Lys Leu Arg Tyr Thr Val Glu Ala Asn Ile Ser
130 135 140

Gly Asn Arg Phe Arg Gly Lys Ala Thr Ala Thr Asp Lys Thr Asp Pro
145 150 155 160

Ile Leu Gly Lys Asp Ser Glu His Leu Glu Gly Gly Leu Tyr Gly Pro
165 170 175

Lys Ser Glu Glu Leu Ala Gly Lys Phe Val Ala His Asp Lys Ser Leu
180 185 190

Phe Ala Val Phe Ser Gly Lys Arg Gly Asn Asp Val Leu
195 200 205

<210> 27

<211> 1790

<212> DNA

<213> Actinobacillus suis

<400> 27

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tctggcggaa aaggaggttt tgatttagaa gatgttcggc caaatcaaac tgcaaaagca 120

gaaaaagcaa caacctctta tcaagatgag gaaacgaaga aaaagacaaa ggaagaatta 180

gataagttga tggagcctac tttgggagtt gaggcaaaga tacctcgccg gaatagagct 240

ttatttgata aagaaggaaa tcgaaaagca acacctgata caactgatga attatctgaa 300

gcacaaatta tggcgatttg gaatgaaaat atagatgaaa ttcctcactt gaaagagtta 360

aacgataaaa caacgagtgg tttaatttat cactctcacg atggtaaaca ggaggacaaa 420

aaacgaaatt tacaatatgt gcgttcaggc tatgttttcg atgaatctta tagtgaaata 480

gtaaaaaata agaatggtgt accctatatt tttaaaaatg ggatcgatgg ttacatttac 540

tatttaggga caagcccgtc aaaagaactc cctaaaggaa ataaagttac ctataaaggt 600

acttgggatt tcaccagcga tgttaaaaca agctacgagt taagtggatt tagtgatgct 660

ggtaatggta aaaatgttgc agctacatct atttcggata atgtcaatcg agatcataaa 720

gttggtgaaa aactaggtga taatgaagtt aaaggggtag ctcattctag tgaatttgca 780

gtagattttg ataacaaaaa attgacaggt agtttatatc gtaatggtta tatcaacaga 840

aataaagcgc aagaagtaac gaaacgctat agcattgaag ctgatataac aggcaaccgg 900

tttacaggaa aagccaaagc agaaaaagca ggtgatccga tctttactga ttcaaattat 960

cttgaagggg gattctatgg tcctaaagct gaagaaatgg cagggaaatt tttcacaaat 1020

aataaatctc tctttgcagt atttgcagct aaaagtgaaa acggcgagac gaccacagaa 1080

cgaatcattg atgcaactaa aattgattta acccaattta atgctaaaga actcaacaat 1140

tttggtgatg cctctgtttt aattattgat ggacaaaaaa tagatctagc aggtgtcaat 1200

tttaaaaata gtaaaacggt tgaaatcaac ggcaaaacaa tggtagccgt agcttgctgt 1260

agtaatctgg aatatatgaa atttggtcaa ttgtggcaaa aagagggcaa acaacaagtt 1320

aaagataata gtttattcct acaaggtgaa cgtactgcaa cggataaaat gcccgcagga 1380

ggtaactata agtatgttgg aacttgggat gcactcgtat ctaaagggac gaactggata 1440

gcggaagcag ataataatcg agaatcgggc tatcgcactg aatttgatgt taattttagt 1500

gataaaaaag taaacggtaa gttatttgat aaaggcggtg taaatcctgt atttaccgta 1560

gatgcgacaa ttaatggtaa tggctttatc ggcagtgcga aaacctctga tagtggcttt 1620

gctttagatg caggctctag ccaacacgga aatgcggtat ttagtgatat aaaagtcaat 1680

ggtggcttct atggtccaac cgctggagaa cttggcggac aattccatca taaatcagac 1740

aatggcagtg ttggcgctgt ctttggtgca aaacgacaaa tagaaaaata 1790

<210> 28

<211> 590

<212> PRT

<213> Actinobacillus suis

<400> 28

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Met His Phe Lys Leu Asn Pro Tyr Ala Leu Ala Phe Thr Ser Leu Phe
1               5                  10                  15

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

Arg Pro Asn Gln Thr Ala Lys Ala Glu Lys Ala Thr Thr Ser Tyr Gln
        35                  40                  45

Asp Glu Glu Thr Lys Lys Lys Thr Lys Glu Glu Leu Asp Lys Leu Met
    50                  55                  60

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

Leu Phe Asp Lys Glu Gly Asn Arg Lys Ala Thr Pro Asp Thr Thr Asp
                85                  90                  95

Glu Leu Ser Glu Ala Gln Ile Met Ala Ile Trp Asn Glu Asn Ile Asp
            100                 105                 110

Glu Ile Pro His Leu Lys Glu Leu Asn Asp Lys Thr Thr Ser Gly Leu
        115                 120                 125

Ile Tyr His Ser His Asp Gly Lys Gln Glu Asp Lys Lys Arg Asn Leu
    130                 135                 140

Gln Tyr Val Arg Ser Gly Tyr Val Phe Asp Glu Ser Tyr Ser Glu Ile
145                 150                 155                 160

Val Lys Asn Lys Asn Gly Val Pro Tyr Ile Phe Lys Asn Gly Ile Asp
                165                 170                 175

Gly Tyr Ile Tyr Tyr Leu Gly Thr Ser Pro Ser Lys Glu Leu Pro Lys
            180                 185                 190

Gly Asn Lys Val Thr Tyr Lys Gly Thr Trp Asp Phe Thr Ser Asp Val
        195                 200                 205

Lys Thr Ser Tyr Glu Leu Ser Gly Phe Ser Asp Ala Gly Asn Gly Lys
    210                 215                 220

Asn Val Ala Ala Thr Ser Ile Ser Asp Asn Val Asn Arg Asp His Lys
225                 230                 235                 240

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

Ser Glu Phe Ala Val Asp Phe Asp Asn Lys Lys Leu Thr Gly Ser Leu
            260                 265                 270

Tyr Arg Asn Gly Tyr Ile Asn Arg Asn Lys Ala Gln Glu Val Thr Lys
        275                 280                 285

Arg Tyr Ser Ile Glu Ala Asp Ile Thr Gly Asn Arg Phe Thr Gly Lys
    290                 295                 300
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Ala Lys Ala Glu Lys Ala Gly Asp Pro Ile Phe Thr Asp Ser Asn Tyr
305                 310                 315                 320

Leu Glu Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Met Ala Gly Lys
                325                 330                 335

Phe Phe Thr Asn Asn Lys Ser Leu Phe Ala Val Phe Ala Ala Lys Ser
            340                 345                 350

Glu Asn Gly Glu Thr Thr Thr Glu Arg Ile Ile Asp Ala Thr Lys Ile
        355                 360                 365

Asp Leu Thr Gln Phe Asn Ala Lys Glu Leu Asn Asn Phe Gly Asp Ala
    370                 375                 380

Ser Val Leu Ile Ile Asp Gly Gln Lys Ile Asp Leu Ala Gly Val Asn
385                 390                 395                 400

Phe Lys Asn Ser Lys Thr Val Glu Ile Asn Gly Lys Thr Met Val Ala
                405                 410                 415

Val Ala Cys Cys Ser Asn Leu Glu Tyr Met Lys Phe Gly Gln Leu Trp

            420                 425                 430

Gln Lys Glu Gly Lys Gln Gln Val Lys Asp Asn Ser Leu Phe Leu Gln
        435                 440                 445

Gly Glu Arg Thr Ala Thr Asp Lys Met Pro Ala Gly Gly Asn Tyr Lys
    450                 455                 460

Tyr Val Gly Thr Trp Asp Ala Leu Val Ser Lys Gly Thr Asn Trp Ile
465                 470                 475                 480

Ala Glu Ala Asp Asn Asn Arg Glu Ser Gly Tyr Arg Thr Glu Phe Asp
                485                 490                 495

Val Asn Phe Ser Asp Lys Lys Val Asn Gly Lys Leu Phe Asp Lys Gly
            500                 505                 510

Gly Val Asn Pro Val Phe Thr Val Asp Ala Thr Ile Asn Gly Asn Gly
        515                 520                 525

Phe Ile Gly Ser Ala Lys Thr Ser Asp Ser Gly Phe Ala Leu Asp Ala
    530                 535                 540

Gly Ser Ser Gln His Gly Asn Ala Val Phe Ser Asp Ile Lys Val Asn
545                 550                 555                 560

Gly Gly Phe Tyr Gly Pro Thr Ala Gly Glu Leu Gly Gly Gln Phe His
                565                 570                 575

His Lys Ser Asp Asn Gly Ser Val Gly Ala Val Phe Gly Ala
            580                 585                 590
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<210> 29
<211> 1790
<212> DNA
<213> Actinobacillus suis

<400> 29
atgcatttta aacttaatcc ctatgcgtta gcgtttactt cgctgtttct tgtcgcttgt 60

tctggcggaa aaggaggttt tgatttagaa gatgttcggc caaatcaaac tgcaaaagca 120

gaaaaagcaa caacctctta tcaagatgag gaaacgaaga aaaagacaaa ggaagaatta 180

gataagttga tggagcctac tttgggagtt gaggcaaaga tacctcgccg gaatagagct 240

ttagcagata aagaaggaaa tcgaaaagca acacctgata caactgatga attatctgaa 300

gcacaaatta tggcgatttg gaatgaaaat atagatgaaa ttcctcactt gaaagagtta 360

aacgataaaa caacgagtgg tttaatttat cactctcacg atggtaaaca ggaggacaaa 420

aaacgaaatt tacaatatgt gcgttcaggc tatgttttcg atgaatctta tagtgaaata 480

gtaaaaaata agaatggtgt accctatatt tttaaaaatg ggatcgatgg ttacatttac 540

tatttaggga caagcccgtc aaaagaactc cctaaaggaa ataaagttac ctataaaggt 600

acttgggatt tcaccagcga tgttaaaaca agctacgagt taagtggatt tagtgatgct 660

ggtaatggta aaaatgttgc agctacatct atttcggata atgtcaatcg agatcataaa 720

gttggtgaaa aactaggtga taatgaagtt aaaggggtag ctcattctag tgaatttgca 780

gtagattttg ataacaaaaa attgacaggt agtttatatc gtaatggtta tatcaacaga 840

aataaagcgc aagaagtaac gaaacgctat agcattgaag ctgatataac aggcaaccgg 900

tttacaggaa aagccaaagc agaaaaagca ggtgatccga tctttactga ttcaaattat 960

cttgaagggg gattctatgg tcctaaagct gaagaaatgg cagggaaatt tttcacaaat 1020

aataaatctc tctttgcagt atttgcagct aaaagtgaaa acggcgagac gaccacagaa 1080

cgaatcattg atgcaactaa aattgattta acccaattta atgctaaaga actcaacaat 1140

tttggtgatg cctctgtttt aattattgat ggacaaaaaa tagatctagc aggtgtcaat 1200

tttaaaaata gtaaaacggt tgaaatcaac ggcaaaacaa tggtagccgt agcttgctgt 1260

agtaatctgg aatatatgaa atttggtcaa ttgtggcaaa aagagggcaa acaacaagtt 1320

aaagataata gtttattcct acaaggtgaa cgtactgcaa cggataaaat gcccgcagga 1380

ggtaactata agtatgttgg aacttgggat gcactcgtat ctaaagggac gaactggata 1440

gcggaagcag ataataatcg agaatcgggc tatcgcactg aatttgatgt taattttagt 1500

gataaaaaag taaacggtaa gttatttgat aaaggcggtg taaatcctgt atttaccgta 1560

gatgcgacaa ttaatggtaa tggctttatc ggcagtgcga aaacctctga tagtggcttt 1620

gctttagatg caggctctag ccaacacgga aatgcggtat ttagtgatat aaaagtcaat 1680

ggtggcttct atggtccaac cgctggagaa cttggcggac aattccatca taaatcagac 1740

aatggcagtg ttggcgctgt ctttggtgca aaacgacaaa tagaaaaata 1790

<210> 30
<211> 590

<212> PRT

<213> Actinobacillus suis

<400> 30

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Met His Phe Lys Leu Asn Pro Tyr Ala Leu Ala Phe Thr Ser Leu Phe
1               5                  10                  15

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

Arg Pro Asn Gln Thr Ala Lys Ala Glu Lys Ala Thr Thr Ser Tyr Gln

        35                  40                  45

Asp Glu Glu Thr Lys Lys Lys Thr Lys Glu Glu Leu Asp Lys Leu Met
    50                  55                  60

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

Leu Ala Asp Lys Glu Gly Asn Arg Lys Ala Thr Pro Asp Thr Thr Asp
                85                  90                  95

Glu Leu Ser Glu Ala Gln Ile Met Ala Ile Trp Asn Glu Asn Ile Asp
            100                 105                 110

Glu Ile Pro His Leu Lys Glu Leu Asn Asp Lys Thr Thr Ser Gly Leu
        115                 120                 125

Ile Tyr His Ser His Asp Gly Lys Gln Glu Asp Lys Lys Arg Asn Leu
    130                 135                 140

Gln Tyr Val Arg Ser Gly Tyr Val Phe Asp Glu Ser Tyr Ser Glu Ile
145                 150                 155                 160

Val Lys Asn Lys Asn Gly Val Pro Tyr Ile Phe Lys Asn Gly Ile Asp
                165                 170                 175

Gly Tyr Ile Tyr Tyr Leu Gly Thr Ser Pro Ser Lys Glu Leu Pro Lys
            180                 185                 190

Gly Asn Lys Val Thr Tyr Lys Gly Thr Trp Asp Phe Thr Ser Asp Val
        195                 200                 205

Lys Thr Ser Tyr Glu Leu Ser Gly Phe Ser Asp Ala Gly Asn Gly Lys
    210                 215                 220

Asn Val Ala Ala Thr Ser Ile Ser Asp Asn Val Asn Arg Asp His Lys
225                 230                 235                 240

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

Ser Glu Phe Ala Val Asp Phe Asp Asn Lys Lys Leu Thr Gly Ser Leu
            260                 265                 270
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```
Tyr Arg Asn Gly Tyr Ile Asn Arg Asn Lys Ala Gln Glu Val Thr Lys
        275                 280                 285

Arg Tyr Ser Ile Glu Ala Asp Ile Thr Gly Asn Arg Phe Thr Gly Lys
    290                 295                 300

Ala Lys Ala Glu Lys Ala Gly Asp Pro Ile Phe Thr Asp Ser Asn Tyr
305                 310                 315                 320

Leu Glu Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Met Ala Gly Lys
                325                 330                 335

Phe Phe Thr Asn Asn Lys Ser Leu Phe Ala Val Phe Ala Ala Lys Ser
            340                 345                 350

Glu Asn Gly Glu Thr Thr Thr Glu Arg Ile Ile Asp Ala Thr Lys Ile
        355                 360                 365

Asp Leu Thr Gln Phe Asn Ala Lys Glu Leu Asn Asn Phe Gly Asp Ala
    370                 375                 380

Ser Val Leu Ile Ile Asp Gly Gln Lys Ile Asp Leu Ala Gly Val Asn
385                 390                 395                 400

Phe Lys Asn Ser Lys Thr Val Glu Ile Asn Gly Lys Thr Met Val Ala
                405                 410                 415

Val Ala Cys Cys Ser Asn Leu Glu Tyr Met Lys Phe Gly Gln Leu Trp
            420                 425                 430

Gln Lys Glu Gly Lys Gln Gln Val Lys Asp Asn Ser Leu Phe Leu Gln
        435                 440                 445

Gly Glu Arg Thr Ala Thr Asp Lys Met Pro Ala Gly Gly Asn Tyr Lys
    450                 455                 460

Tyr Val Gly Thr Trp Asp Ala Leu Val Ser Lys Gly Thr Asn Trp Ile
465                 470                 475                 480

Ala Glu Ala Asp Asn Asn Arg Glu Ser Gly Tyr Arg Thr Glu Phe Asp
                485                 490                 495

Val Asn Phe Ser Asp Lys Lys Val Asn Gly Lys Leu Phe Asp Lys Gly
            500                 505                 510

Gly Val Asn Pro Val Phe Thr Val Asp Ala Thr Ile Asn Gly Asn Gly
        515                 520                 525

Phe Ile Gly Ser Ala Lys Thr Ser Asp Ser Gly Phe Ala Leu Asp Ala
    530                 535                 540

Gly Ser Ser Gln His Gly Asn Ala Val Phe Ser Asp Ile Lys Val Asn
545                 550                 555                 560

Gly Gly Phe Tyr Gly Pro Thr Ala Gly Glu Leu Gly Gly Gln Phe His
                565                 570                 575
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```
His Lys Ser Asp Asn Gly Ser Val Gly Ala Val Phe Gly Ala
            580                 585                 590
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<210> 31

<211> 1790

<212> DNA

<213> Actinobacillus suis

<400> 31

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gaaaaagcaa caacctctta tcaagatgag gaaacgaaga aaaagacaaa ggaagaatta      180

gataagttga tggagcctac tttgggagtt gaggcaaaga tacctcgccg gaatagagct      240

ttatttgata aagaaggaaa tcgaaaagca acacctgata caactgatga attatctgaa      300

gcacaaatta tggcgatttg gaatgaaaat atagatgaaa ttcctcactt gaaagagtta      360

aacgataaaa caacgagtgg tttaatttat cactctcacg atggtaaaca ggaggacaaa      420

aaacgaaatt tacaatatgt gcgttcaggc tatgttttcg atgaatctta tagtgaaata      480

gtaaaaaata agaatggtgt accctatatt gcaaaaaatg ggatcgatgg ttacatttac      540

tatttaggga caagcccgtc aaaagaactc cctaaaggaa ataaagttac ctataaaggt      600

acttgggatt tcaccagcga tgttaaaaca agctacgagt taagtggatt tagtgatgct      660

ggtaatggta aaaatgttgc agctacatct atttcggata atgtcaatcg agatcataaa      720

gttggtgaaa aactaggtga taatgaagtt aaaggggtag ctcattctag tgaatttgca      780

gtagattttg ataacaaaaa attgacaggt agtttatatc gtaatggtta tatcaacaga      840

aataaagcgc aagaagtaac gaaacgctat agcattgaag ctgatataac aggcaaccgg      900

tttacaggaa aagccaaagc agaaaaagca ggtgatccga tctttactga ttcaaattat      960

cttgaagggg gattctatgg tcctaaagct gaagaaatgg cagggaaatt tttcacaaat     1020

aataaatctc tctttgcagt atttgcagct aaaagtgaaa acggcgagac gaccacagaa     1080

cgaatcattg atgcaactaa aattgattta acccaattta atgctaaaga actcaacaat     1140

tttggtgatg cctctgtttt aattattgat ggacaaaaaa tagatctagc aggtgtcaat     1200

tttaaaaata gtaaaacggt tgaaatcaac ggcaaaacaa tggtagccgt agcttgctgt     1260

agtaatctgg aatatatgaa atttggtcaa ttgtggcaaa aagagggcaa acaacaagtt     1320

aaagataata gtttattcct acaaggtgaa cgtactgcaa cggataaaat gcccgcagga     1380

ggtaactata agtatgttgg aacttgggat gcactcgtat ctaaagggac gaactggata     1440

gcggaagcag ataataatcg agaatcgggc tatcgcactg aatttgatgt taattttagt     1500

gataaaaaag taaacggtaa gttatttgat aaaggcggtg taaatcctgt atttaccgta     1560

gatgcgacaa ttaatggtaa tggctttatc ggcagtgcga aaacctctga tagtggcttt     1620

gctttagatg caggctctag ccaacacgga aatgcggtat ttagtgatat aaaagtcaat     1680

ggtggcttct atggtccaac cgctggagaa cttggcggac aattccatca taaatcagac     1740

aatggcagtg ttggcgctgt ctttggtgca aaacgacaaa tagaaaaata                1790
```

<210> 32

<211> 590

<212> PRT

<213> Actinobacillus suis

<400> 32

```
Met His Phe Lys Leu Asn Pro Tyr Ala Leu Ala Phe Thr Ser Leu Phe
1               5                  10                  15

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

Arg Pro Asn Gln Thr Ala Lys Ala Glu Lys Ala Thr Thr Ser Tyr Gln
        35                  40                  45

Asp Glu Glu Thr Lys Lys Lys Thr Lys Glu Glu Leu Asp Lys Leu Met
    50                  55                  60

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

Leu Phe Asp Lys Glu Gly Asn Arg Lys Ala Thr Pro Asp Thr Thr Asp
                85                  90                  95

Glu Leu Ser Glu Ala Gln Ile Met Ala Ile Trp Asn Glu Asn Ile Asp
            100                 105                 110

Glu Ile Pro His Leu Lys Glu Leu Asn Asp Lys Thr Thr Ser Gly Leu
        115                 120                 125

Ile Tyr His Ser His Asp Gly Lys Gln Glu Asp Lys Lys Arg Asn Leu
    130                 135                 140

Gln Tyr Val Arg Ser Gly Tyr Val Phe Asp Glu Ser Tyr Ser Glu Ile
145                 150                 155                 160

Val Lys Asn Lys Asn Gly Val Pro Tyr Ile Ala Lys Asn Gly Ile Asp
                165                 170                 175

Gly Tyr Ile Tyr Tyr Leu Gly Thr Ser Pro Ser Lys Glu Leu Pro Lys
            180                 185                 190

Gly Asn Lys Val Thr Tyr Lys Gly Thr Trp Asp Phe Thr Ser Asp Val
        195                 200                 205

Lys Thr Ser Tyr Glu Leu Ser Gly Phe Ser Asp Ala Gly Asn Gly Lys
    210                 215                 220

Asn Val Ala Ala Thr Ser Ile Ser Asp Asn Val Asn Arg Asp His Lys
225                 230                 235                 240

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

Ser Glu Phe Ala Val Asp Phe Asp Asn Lys Lys Leu Thr Gly Ser Leu
```

```
            260                 265                 270

Tyr Arg Asn Gly Tyr Ile Asn Arg Asn Lys Ala Gln Glu Val Thr Lys
        275                 280                 285

Arg Tyr Ser Ile Glu Ala Asp Ile Thr Gly Asn Arg Phe Thr Gly Lys
    290                 295                 300

Ala Lys Ala Glu Lys Ala Gly Asp Pro Ile Phe Thr Asp Ser Asn Tyr
305                 310                 315                 320

Leu Glu Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Met Ala Gly Lys
                325                 330                 335

Phe Phe Thr Asn Asn Lys Ser Leu Phe Ala Val Phe Ala Ala Lys Ser
            340                 345                 350

Glu Asn Gly Glu Thr Thr Thr Glu Arg Ile Ile Asp Ala Thr Lys Ile
        355                 360                 365

Asp Leu Thr Gln Phe Asn Ala Lys Glu Leu Asn Asn Phe Gly Asp Ala
    370                 375                 380

Ser Val Leu Ile Ile Asp Gly Gln Lys Ile Asp Leu Ala Gly Val Asn
385                 390                 395                 400

Phe Lys Asn Ser Lys Thr Val Glu Ile Asn Gly Lys Thr Met Val Ala
                405                 410                 415

Val Ala Cys Cys Ser Asn Leu Glu Tyr Met Lys Phe Gly Gln Leu Trp
            420                 425                 430

Gln Lys Glu Gly Lys Gln Gln Val Lys Asp Asn Ser Leu Phe Leu Gln
        435                 440                 445

Gly Glu Arg Thr Ala Thr Asp Lys Met Pro Ala Gly Gly Asn Tyr Lys
    450                 455                 460

Tyr Val Gly Thr Trp Asp Ala Leu Val Ser Lys Gly Thr Asn Trp Ile
465                 470                 475                 480

Ala Glu Ala Asp Asn Asn Arg Glu Ser Gly Tyr Arg Thr Glu Phe Asp
                485                 490                 495

Val Asn Phe Ser Asp Lys Lys Val Asn Gly Lys Leu Phe Asp Lys Gly
            500                 505                 510

Gly Val Asn Pro Val Phe Thr Val Asp Ala Thr Ile Asn Gly Asn Gly
        515                 520                 525

Phe Ile Gly Ser Ala Lys Thr Ser Asp Ser Gly Phe Ala Leu Asp Ala
    530                 535                 540

Gly Ser Ser Gln His Gly Asn Ala Val Phe Ser Asp Ile Lys Val Asn
545                 550                 555                 560
```

```
Gly Gly Phe Tyr Gly Pro Thr Ala Gly Glu Leu Gly Gly Gln Phe His
                565                 570                 575

His Lys Ser Asp Asn Gly Ser Val Gly Ala Val Phe Gly Ala
            580                 585                 590
```

<210> 33

<211> 730

<212> DNA

<213> Actinobacillus suis

<400> 33

```
tgaaaacggc gagacgacca cagaacgaat cattgatgca actaaaattg atttaaccca       60

atttaatgct aaagaactca acaattttgg tgatgcctct gttttaatta ttgatggaca      120

aaaaatagat ctagcaggtg tcaattttaa aaatagtaaa acggttgaaa tcaacggcaa      180

aacaatggta gccgtagctt gctgtagtaa tctggaatat atgaaatttg gtcaattgtg      240

gcaaaaagag ggcaaacaac aagttaaaga taatagttta ttcctacaag gtgaacgtac      300

tgcaacggat aaaatgcccg caggaggtaa ctataagtat gttggaactt gggatgcact      360

cgtatctaaa gggacgaact ggatagcgga agcagataat aatcgagaat cgggctatcg      420

cactgaattt gatgttaatt ttagtgataa aaaagtaaac ggtaagttat ttgataaagg      480

cggtgtaaat cctgtattta ccgtagatgc gacaattaat ggtaatggct ttatcggcag      540

tgcgaaaacc tctgatagtg gctttgcttt agatgcaggc tctagccaac acggaaatgc      600

ggtatttagt gatataaaag tcaatggtgg cttctatggt ccaaccgctg gagaacttgg      660

cggacaattc catcataaat cagacaatgg cagtgttggc gctgtctttg gtgcaaaacg      720

acaaatagaa                                                             730
```

<210> 34

<211> 240

<212> PRT

<213> Actinobacillus suis

<400> 34

```
Ser Glu Asn Gly Glu Thr Thr Thr Glu Arg Ile Ile Asp Ala Thr Lys
1               5                   10                  15

Ile Asp Leu Thr Gln Phe Asn Ala Lys Glu Leu Asn Asn Phe Gly Asp
            20                  25                  30

Ala Ser Val Leu Ile Ile Asp Gly Gln Lys Ile Asp Leu Ala Gly Val
        35                  40                  45

Asn Phe Lys Asn Ser Lys Thr Val Glu Ile Asn Gly Lys Thr Met Val
    50                  55                  60

Ala Val Ala Cys Cys Ser Asn Leu Glu Tyr Met Lys Phe Gly Gln Leu
65                  70                  75                  80

Trp Gln Lys Glu Gly Lys Gln Gln Val Lys Asp Asn Ser Leu Phe Leu
```

```
                85                  90                  95

Gln Gly Glu Arg Thr Ala Thr Asp Lys Met Pro Ala Gly Gly Asn Tyr
            100                 105                 110

Lys Tyr Val Gly Thr Trp Asp Ala Leu Val Ser Lys Gly Thr Asn Trp
        115                 120                 125

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

Asp Val Asn Phe Ser Asp Lys Lys Val Asn Gly Lys Leu Phe Asp Lys
145                 150                 155                 160

Gly Gly Val Asn Pro Val Phe Thr Val Asp Ala Thr Ile Asn Gly Asn
                165                 170                 175

Gly Phe Ile Gly Ser Ala Lys Thr Ser Asp Ser Gly Phe Ala Leu Asp
            180                 185                 190

Ala Gly Ser Ser Gln His Gly Asn Ala Val Phe Ser Asp Ile Lys Val
        195                 200                 205

Asn Gly Gly Phe Tyr Gly Pro Thr Ala Gly Glu Leu Gly Gly Gln Phe
    210                 215                 220

His His Lys Ser Asp Asn Gly Ser Val Gly Ala Val Phe Gly Ala Lys
225                 230                 235                 240
```

<210> 35

<211> 1050

<212> DNA

<213> Actinobacillus suis

<400> 35

```
atgcatttta aacttaatcc ctatgcgtta gcgtttactt cgctgtttct tgtcgcttgt       60

tctggcggaa aaggaggttt tgatttagaa gatgttcggc caaatcaaac tgcaaaagca      120

gaaaaagcaa caacctctta tcaagatgag gaaacgaaga aaaagacaaa ggaagaatta      180

gataagttga tggagcctac tttgggagtt gaggcaaaga tacctcgccg gaatagagct      240

ttatttgata aagaaggaaa tcgaaaagca acacctgata caactgatga attatctgaa      300

gcacaaatta tggcgatttg gaatgaaaat atagatgaaa ttcctcactt gaaagagtta      360

aacgataaaa caacgagtgg tttaatttat cactctcacg atggtaaaca ggaggacaaa      420

aaacgaaatt tacaatatgt gcgttcaggc tatgttttcg atgaatctta tagtgaaata      480

gtaaaaaata agaatggtgt accctatatt tttaaaaatg ggatcgatgg ttacatttac      540

tatttaggga caagcccgtc aaaagaactc cctaaaggaa ataaagttac ctataaaggt      600

acttgggatt tcaccagcga tgttaaaaca agctacgagt taagtggatt tagtgatgct      660

ggtaatggta aaaatgttgc agctacatct atttcggata atgtcaatcg agatcataaa      720

gttggtgaaa aactaggtga taatgaagtt aaaggggtag ctcattctag tgaatttgca      780

gtagattttg ataaagaaaa attgcagagt agtttatatg gtaatggtta tatgaagaga      840
```

gtagattttg ataacaaaaa attgacaggt agtttatatc gtaatggtta tatcaacaga 840

aataaagcgc aagaagtaac gaaacgctat agcattgaag ctgatataac aggcaaccgg 900

tttacaggaa aagccaaagc agaaaaagca ggtgatccga tctttactga ttcaaattat 960

cttgaagggg gattctatgg tcctaaagct gaagaaatgg cagggaaatt tttcacaaat 1020

aataaatctc tctttgcagt atttgcagct 1050

<210> 36

<211> 330

<212> PRT

<213> Actinobacillus suis

<400> 36

```
Cys Ser Gly Gly Lys Gly Gly Phe Asp Leu Glu Asp Val Arg Pro Asn
1               5                  10                  15

Gln Thr Ala Lys Ala Glu Lys Ala Thr Thr Ser Tyr Gln Asp Glu Glu
            20                  25                  30

Thr Lys Lys Lys Thr Lys Glu Glu Leu Asp Lys Leu Met Glu Pro Thr
        35                  40                  45

Leu Gly Val Glu Ala Lys Ile Pro Arg Arg Asn Arg Ala Leu Phe Asp
    50                  55                  60

Lys Glu Gly Asn Arg Lys Ala Thr Pro Asp Thr Thr Asp Glu Leu Ser
65                  70                  75                  80

Glu Ala Gln Ile Met Ala Ile Trp Asn Glu Asn Ile Asp Glu Ile Pro
                85                  90                  95

His Leu Lys Glu Leu Asn Asp Lys Thr Thr Ser Gly Leu Ile Tyr His
            100                 105                 110

Ser His Asp Gly Lys Gln Glu Asp Lys Lys Arg Asn Leu Gln Tyr Val
        115                 120                 125

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

Lys Asn Gly Val Pro Tyr Ile Phe Lys Asn Gly Ile Asp Gly Tyr Ile
145                 150                 155                 160

Tyr Tyr Leu Gly Thr Ser Pro Ser Lys Glu Leu Pro Lys Gly Asn Lys
                165                 170                 175

Val Thr Tyr Lys Gly Thr Trp Asp Phe Thr Ser Asp Val Lys Thr Ser
            180                 185                 190

Tyr Glu Leu Ser Gly Phe Ser Asp Ala Gly Asn Gly Lys Asn Val Ala
        195                 200                 205

Ala Thr Ser Ile Ser Asp Asn Val Asn Arg Asp His Lys Val Gly Glu
    210                 215                 220
```

```
Lys Leu Gly Asp Asn Glu Val Lys Gly Val Ala His Ser Ser Glu Phe
225                 230                 235                 240

Ala Val Asp Phe Asp Asn Lys Lys Leu Thr Gly Ser Leu Tyr Arg Asn
                245                 250                 255

Gly Tyr Ile Asn Arg Asn Lys Ala Gln Glu Val Thr Lys Arg Tyr Ser
            260                 265                 270

Ile Glu Ala Asp Ile Thr Gly Asn Arg Phe Thr Gly Lys Ala Lys Ala
        275                 280                 285

Glu Lys Ala Gly Asp Pro Ile Phe Thr Asp Ser Asn Tyr Leu Glu Gly
    290                 295                 300

Gly Phe Tyr Gly Pro Lys Ala Glu Glu Met Ala Gly Lys Phe Phe Thr
305                 310                 315                 320

Asn Asn Lys Ser Leu Phe Ala Val Phe Ala
                325                 330
```

<210> 37

<211> 675

<212> DNA

<213> Actinobacillus suis

<400> 37

```
ggatccaagt tgatggagcc tactttggga gttgaggcaa agatacctcg ccggggtgca       60

gcgacaactg atgaattatc tcaaattatg gcgatttgga atgaaaatat agatgaaatt      120

cctcacttga aagagttaaa cgataaaaca acgagtggtt taatttatca ctctgcgggt      180

tctaatttac aatatgtgcg ttcaggctat gttttcgatg aatctccggg tgggatcgat      240

ggttacattt actatttagg gacaagcccg tcaaaagaac tccctaaagg aaataaagtt      300

acctataaag gtacttggga tttcaccagc gatgttaaag gtaaaaatgt tgcagctaca      360

tctatttcgg ataatgtcgg tgctggtcat tctagtgaat ttgcagtaga ttttgataac      420

aaaaaattga caggtagttt atatcgtaat ccgggtgcgg taacgaaacg ctatagcatt      480

gaagctgata taacaggcaa ccgttttaga ggaaaagcca aagcagaaaa agcaggtgat      540

ccgatcttta ctgattcaaa ttatcttgaa gggggattct atggtcctaa agctgaagaa      600

atggcaggga aatttttcac aaataataaa tctctctttg cagtatttgc agctaaaagt      660

gaaaacggcg agacg                                                       675
```

<210> 38

<211> 195

<212> PRT

<213> Actinobacillus suis

<400> 38

```
Gly Ser Lys Leu Met Glu Pro Thr Leu Gly Val Glu Ala Lys Ile Pro
1               5                   10                  15
```

```
Arg Arg Gly Ala Ala Thr Thr Asp Glu Leu Ser Gln Ile Met Ala Ile
            20                  25                  30

Trp Asn Glu Asn Ile Asp Glu Ile Pro His Leu Lys Glu Leu Asn Asp
        35                  40                  45

Lys Thr Thr Ser Gly Leu Ile Tyr His Ser Ala Gly Ser Asn Leu Gln
    50                  55                  60

Tyr Val Arg Ser Gly Tyr Val Phe Asp Glu Ser Pro Gly Gly Ile Asp
65                  70                  75                  80

Gly Tyr Ile Tyr Tyr Leu Gly Thr Ser Pro Ser Lys Glu Leu Pro Lys
                85                  90                  95

Gly Asn Lys Val Thr Tyr Lys Gly Thr Trp Asp Phe Thr Ser Asp Val
            100                 105                 110

Lys Gly Lys Asn Val Ala Ala Thr Ser Ile Ser Asp Asn Val Gly Ala
        115                 120                 125

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

Gly Ser Leu Tyr Arg Asn Pro Ile Phe Thr Asp Ser Asn Tyr Leu Glu
145                 150                 155                 160

Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Met Ala Gly Lys Phe Phe
                165                 170                 175

Thr Asn Asn Lys Ser Leu Phe Ala Val Phe Ala Ala Lys Ser Glu Asn
            180                 185                 190

Gly Glu Thr
        195
```

<210> 39

<211> 2154

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<221> misc_feature

<223> Organism: Actinobacillus suis (as well)

<400> 39

```
gacaccgttc gtattattga tgcctcaaaa attgatttaa ctaatttcag catttcagaa      60

cttaacaatt ttggtgatgc ttccgtttta attattgatg ggaaaaaaat aaagctagct     120

ggtagcgggt ttacaaataa gcacactatt gaaatcaatg gcaaaacaat ggtagccgta     180

gcctgctgta gtaatctgga atatatgaag tttggtcaat tatggcaaca agcagagggc     240

ggaaaacccg agaataatag tttattccta caaggcgaac gtaccgcaac agataagatg     300
```

ccaaaaggcg gaaactataa atatattggt acttgggatg ctcaggtttc aaaagaaaat 360

aactgggttg ctacggcaga tgatgataga aaagctggct atcgcacaga atttgatgtt 420

gattttggca acaaaaattt aagtggtaag ttatttgata aaaacggtgt aaatcctgtg 480

tttaccgtag atgcaaaaat tgatggtaat ggttttactg gcaaagctaa aacctcagat 540

gctggtttcg ctctagattc aggtagttca cgttatgaga atgtgaaatt taacgatgta 600

gcagttagtg gtggcttcta tggtccaacg gcagcagagc ttggcggaca attccaccat 660

aaatcagaaa atggcagtgt aggtgctgtc tttggtgcaa aacaacaagt aaaaaaactt 720

gaaacagtca agatcattga tgcctcaaaa attgatttaa ctacttttga atcatcggaa 780

ctcaacaatt tcggcaacgc taatgtgtta attattgatg gacagaaaat agatctagca 840

ggtgcagatt ttaaaaatag aaaaaccgtt gatatcaatg gtaagacaat ggtagccata 900

gcttgctgta gtaatttgga atatatgaaa tttggtcaat tatggcaaaa agagggcgaa 960

caaactaaag ataatagctt attcctgcaa ggtgagcgta ctgccacaga taaaataccc 1020

gtaggtggaa actataaata tgtaggaacc tgggatgcac tcgtttcaaa aggaacgaac 1080

tgggtagctg aggcggataa taatcgagaa tcgggctatc gctcagaatt tgatgttaat 1140

tttggtgata aaaaagtaag cggcaagtta tttgataaag ggggcatagt acctgtcttt 1200

atgatcaacg cagatattaa aggtaacggc tttactggga cagctaacac tacagataca 1260

ggctttgcgt tagattcagg ctctagccaa cacggaaatg cggtatttag tgatataaaa 1320

gtcaatggtg gcttctatgg tccaaccgct ggagaacttg gcggacaatt ccatcataaa 1380

tcagacaatg gcagtgttgg cgctgtcttt ggtgcaaaac gacaaataga aaaaacgacc 1440

acagaacgaa tcattgatgc aactaaaatt gatttaaccc aatttaatgc taaagaactc 1500

aacaattttg gtgatgcctc tgttttaatt attgatggac aaaaaatага tctagcaggt 1560

gtcaatttta aaaatagtaa aacggttgaa atcaacggca aaacaatggt agccgtagct 1620

tgctgtagta atctggaata tatgaaattt ggtcaattgt ggcaaaaaga gggcaaacaa 1680

caagttaaag ataatagttt attcctacaa ggtgaacgta ctgcaacgga taaaatgccc 1740

gcaggaggta actataagta tgttggaact tgggatgcac tcgtatctaa agggacgaac 1800

tggatagcgg aagcagataa taatcgagaa tcgggctatc gcactgaatt tgatgttaat 1860

tttagtgata aaaaagtaaa cggtaagtta tttgataaag gcggtgtaaa tcctgtattt 1920

accgtagatg cgacaattaa tggtaatggc tttatcggca gtgcgaaaac ctctgatagt 1980

ggctttgctt tagatgcagg ctctagccaa cacggaaatg cggtatttag tgatataaaa 2040

gtcaatggtg gcttctatgg tccaaccgct ggagaacttg gcggacaatt ccatcataaa 2100

tcagacaatg gcagtgttgg cgctgtcttt ggtgcaaaac gacaaataga aaaa 2154

<210> 40

<211> 718

<212> PRT

<213> Actinobacillus pleuropneumoniae

<220>

<221> MISC_FEATURE

<223> Organism: Actinobacillus suis (as well)

<400> 40

```
Asp Thr Val Arg Ile Ile Asp Ala Ser Lys Ile Asp Leu Thr Asn Phe
1               5                   10                  15

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

Asp Gly Lys Lys Ile Lys Leu Ala Gly Ser Gly Phe Thr Asn Lys His
        35                  40                  45

Thr Ile Glu Ile Asn Gly Lys Thr Met Val Ala Val Ala Cys Cys Ser
    50                  55                  60

Asn Leu Glu Tyr Met Lys Phe Gly Gln Leu Trp Gln Gln Ala Glu Gly
65                  70                  75                  80

Gly Lys Pro Glu Asn Asn Ser Leu Phe Leu Gln Gly Glu Arg Thr Ala
                85                  90                  95

Thr Asp Lys Met Pro Lys Gly Gly Asn Tyr Lys Tyr Ile Gly Thr Trp
            100                 105                 110

Asp Ala Gln Val Ser Lys Glu Asn Asn Trp Val Ala Thr Ala Asp Asp
        115                 120                 125

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

Lys Asn Leu Ser Gly Lys Leu Phe Asp Lys Asn Gly Val Asn Pro Val
145                 150                 155                 160

Phe Thr Val Asp Ala Lys Ile Asp Gly Asn Gly Phe Thr Gly Lys Ala
                165                 170                 175

Lys Thr Ser Asp Ala Gly Phe Ala Leu Asp Ser Gly Ser Ser Arg Tyr
            180                 185                 190

Glu Asn Val Lys Phe Asn Asp Val Ala Val Ser Gly Gly Phe Tyr Gly
        195                 200                 205

Pro Thr Ala Ala Glu Leu Gly Gly Gln Phe His His Lys Ser Glu Asn
    210                 215                 220

Gly Ser Val Gly Ala Val Phe Gly Ala Lys Gln Gln Val Lys Lys Leu
225                 230                 235                 240

Glu Thr Val Lys Ile Ile Asp Ala Ser Lys Ile Asp Leu Thr Thr Phe
                245                 250                 255

Glu Ser Ser Glu Leu Asn Asn Phe Gly Asn Ala Asn Val Leu Ile Ile
            260                 265                 270

Asp Gly Gln Lys Ile Asp Leu Ala Gly Ala Asp Phe Lys Asn Arg Lys
```

```
                275                 280                 285

Thr Val Asp Ile Asn Gly Lys Thr Met Val Ala Ile Ala Cys Cys Ser
    290                 295                 300

Asn Leu Glu Tyr Met Lys Phe Gly Gln Leu Trp Gln Lys Glu Gly Glu
305                 310                 315                 320

Gln Thr Lys Asp Asn Ser Leu Phe Leu Gln Gly Glu Arg Thr Ala Thr
                325                 330                 335

Asp Lys Ile Pro Val Gly Gly Asn Tyr Lys Tyr Val Gly Thr Trp Asp
            340                 345                 350

Ala Leu Val Ser Lys Gly Thr Asn Trp Val Ala Glu Ala Asp Asn Asn
        355                 360                 365

Arg Glu Ser Gly Tyr Arg Ser Glu Phe Asp Val Asn Phe Gly Asp Lys
    370                 375                 380

Lys Val Ser Gly Lys Leu Phe Asp Lys Gly Gly Ile Val Pro Val Phe
385                 390                 395                 400

Met Ile Asn Ala Asp Ile Lys Gly Asn Gly Phe Thr Gly Thr Ala Asn

                405                 410                 415

Thr Thr Asp Thr Gly Phe Ala Leu Asp Ser Gly Ser Ser Gln His Gly
            420                 425                 430

Asn Ala Val Phe Ser Asp Ile Lys Val Asn Gly Gly Phe Tyr Gly Pro
        435                 440                 445

Thr Ala Gly Glu Leu Gly Gly Gln Phe His His Lys Ser Asp Asn Gly
    450                 455                 460

Ser Val Gly Ala Val Phe Gly Ala Lys Arg Gln Ile Glu Lys Thr Thr
465                 470                 475                 480

Thr Glu Arg Ile Ile Asp Ala Thr Lys Ile Asp Leu Thr Gln Phe Asn
                485                 490                 495

Ala Lys Glu Leu Asn Asn Phe Gly Asp Ala Ser Val Leu Ile Ile Asp
            500                 505                 510

Gly Gln Lys Ile Asp Leu Ala Gly Val Asn Phe Lys Asn Ser Lys Thr
        515                 520                 525

Val Glu Ile Asn Gly Lys Thr Met Val Ala Val Ala Cys Cys Ser Asn
    530                 535                 540

Leu Glu Tyr Met Lys Phe Gly Gln Leu Trp Gln Lys Glu Gly Lys Gln
545                 550                 555                 560

Gln Val Lys Asp Asn Ser Leu Phe Leu Gln Gly Glu Arg Thr Ala Thr
                565                 570                 575
```

```
Asp Lys Met Pro Ala Gly Gly Asn Tyr Lys Tyr Val Gly Thr Trp Asp
            580                 585                 590

Ala Leu Val Ser Lys Gly Thr Asn Trp Ile Ala Glu Ala Asp Asn Asn
        595                 600                 605

Arg Glu Ser Gly Tyr Arg Thr Glu Phe Asp Val Asn Phe Ser Asp Lys
    610                 615                 620

Lys Val Asn Gly Lys Leu Phe Asp Lys Gly Gly Val Asn Pro Val Phe
625                 630                 635                 640

Thr Val Asp Ala Thr Ile Asn Gly Asn Gly Phe Ile Gly Ser Ala Lys
                645                 650                 655

Thr Ser Asp Ser Gly Phe Ala Leu Asp Ala Gly Ser Ser Gln His Gly
            660                 665                 670

Asn Ala Val Phe Ser Asp Ile Lys Val Asn Gly Gly Phe Tyr Gly Pro
        675                 680                 685

Thr Ala Gly Glu Leu Gly Gly Gln Phe His His Lys Ser Asp Asn Gly
    690                 695                 700

Ser Val Gly Ala Val Phe Gly Ala Lys Arg Gln Ile Glu Lys
705                 710                 715
```

<210> 41

<211> 51

<212> **DNA**

<213> Actinobacillus pleuropneumoniae

<400> 41

aaagttccgg tgagttcttt tgaaaataag aaagttgata tttcagatat a 51

<210> 42

<211> 17

<212> **PRT**

<213> Actinobacillus pleuropneumoniae

<400> 42

```
Lys Val Pro Val Ser Ser Phe Glu Asn Lys Lys Val Asp Ile Ser Asp
1               5                   10                  15

Ile
```

<210> 43

<211> 27

<212> DNA

<213> Actinobacillus pleuropneumoniae

<400> 43

acgaacggaa atttagacga tgtgccg 27

<210> 44
<211> 9
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 44
Thr Asn Gly Asn Leu Asp Asp Val Pro
1 5

<210> 45
<211> 12
<212> **DNA**
<213> Actinobacillus pleuropneumoniae

<400> 45
aaatataact at 12

<210> 46
<211> 4
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 46
Lys Tyr Asn Tyr
1

<210> 47
<211> 27
<212> DNA
<213> Actinobacillus pleuropneumoniae

<400> 47
aaaacaaaag attcttctct tcagtac 27

<210> 48
<211> 9
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 48
Lys Thr Lys Asp Ser Ser Leu Gln Tyr
1 5

<210> 49
<211> 30
<212> DNA
<213> Actinobacillus pleuropneumoniae

<400> 49
gatggggaac actctggttc taatgaaaag 30

<210> 50
<211> 10
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 50
Asp Gly Glu His Ser Gly Ser Asn Glu Lys
1 5 10

<210> 51
<211> 18
<212> **DNA**
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<400> 51
ggtaattcac ctgcaaaa 18

<210> 52
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<400> 52
Gly Asn Ser Pro Ala Lys
1 5

<210> 53
<211> 15
<212> DNA
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<400> 53
cccgttaatc agctt 15

<210> 54
<211> 5
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 54
Pro Val Asn Gln Leu
1 5

<210> 55
<211> 123
<212> **DNA**
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<400> 55

tccaatgcaa atttaaataa tgaagaggga agacctaatt atttaaacga cgattattat 60

actaaattta taggtaaacg ggtgggcttg gtttcgggag atgcgaaacc tgcaaagcat 120

aaa 123

<210> 56

<211> 41

<212> **PRT**

<213> Actinobacillus pleuropneumoniae

<400> 56

Ser Asn Ala Asn Leu Asn Asn Glu Glu Gly Arg Pro Asn Tyr Leu Asn
1 5 10 15

Asp Asp Tyr Tyr Thr Lys Phe Ile Gly Lys Arg Val Gly Leu Val Ser
20 25 30

Gly Asp Ala Lys Pro Ala Lys His Lys

35 40

<210> 57

<211> 18

<212> DNA

<213> Actinobacillus pleuropneumoniae

<400> 57

gattttgcaa ctaaaaaa 18

<210> 58

<211> 6

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 58

Asp Phe Ala Thr Lys Lys
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<210> 59

<211> 12

<212> DNA

<213> Actinobacillus pleuropneumoniae

<400> 59

gataaagaga aa 12

<210> 60

<211> 4

<212> PRT

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<400> 60
Asp Lys Glu Lys
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<210> 61
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<212> DNA
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<400> 61
agaggcaatc gt 12

<210> 62
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<213> Actinobacillus pleuropneumoniae

<400> 62
Arg Gly Asn Arg
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<210> 63
<211> 54
<212> DNA
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<400> 63
gcgagtgata aaaataaagg gaaaggcgaa tcatataact tctttagtgc cgat 54

<210> 64
<211> 18
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 64
Ala Ser Asp Lys Asn Lys Gly Lys Gly Glu Ser Tyr Asn Phe Phe Ser
1 5 10 15

Ala Asp

<210> 65
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<212> DNA
<213> Actinobacillus pleuropneumoniae

<400> 65
tatggtccaa aagcagaaga a 21

<210> 66
<211> 7
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 66
Tyr Gly Pro Lys Ala Glu Glu
1 5

<210> 67
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<212> DNA
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<400> 67
gtagctaacg acaaatctct t 21

<210> 68
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<400> 68
Val Ala Asn Asp Lys Ser Leu
1 5

<210> 69
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<212> DNA
<213> Actinobacillus pleuropneumoniae

<400> 69
cacaatggct ctaatgttga c 21

<210> 70
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<213> Actinobacillus pleuropneumoniae

<400> 70
His Asn Gly Ser Asn Val Asp
1 5

<210> 71
<211> 6
<212> DNA
<213> Actinobacillus pleuropneumoniae

<400> 71
cgtatt 6

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<400> 72
Arg Ile
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<210> 73
<211> 15
<212> DNA
<213> Actinobacillus pleuropneumoniae

<400> 73
gatttaacta atttc 15

<210> 74
<211> 5
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<400> 74
Asp Leu Thr Asn Phe
1 5

<210> 75
<211> 27
<212> DNA
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<400> 75
gaacttaaca attttggtga tgcttcc 27

<210> 76
<211> 9
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 76
Glu Leu Asn Asn Phe Gly Asp Ala Ser
1 5

<210> 77
<211> 9
<212> DNA
<213> Actinobacillus pleuropneumoniae

<400> 77
attgatggg 9

<210> 78
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<212> PRT
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<400> 78
Ile Asp Gly
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<210> 79
<211> 24
<212> DNA
<213> Actinobacillus pleuropneumoniae

<400> 79
aagctagctg gtagcgggtt taca 24

<210> 80
<211> 8
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 80
Lys Leu Ala Gly Ser Gly Phe Thr
1 5

<210> 81
<211> 12
<212> **DNA**
<213> Actinobacillus pleuropneumoniae

<400> 81
atcaatggca aa 12

<210> 82
<211> 4
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 82
Ile Asn Gly Lys
1

<210> 83
<211> 24
<212> DNA
<213> Actinobacillus pleuropneumoniae

<400> 83

tgctgtagta atctggaata tatg 24

<210> 84
<211> 8
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 84
Cys Cys Ser Asn Leu Glu Tyr Met
1 5

<210> 85
<211> 24
<212> DNA
<213> Actinobacillus pleuropneumoniae

<400> 85
caacaagcag agggcggaaa accc 24

<210> 86
<211> 8
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 86
Gln Gln Ala Glu Gly Gly Lys Pro
1 5

<210> 87
<211> 42
<212> DNA
<213> Actinobacillus pleuropneumoniae

<400> 87
ggcgaacgta ccgcaacaga taagatgcca aaaggcggaa ac 42

<210> 88
<211> 14
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 88
Gly Glu Arg Thr Ala Thr Asp Lys Met Pro Lys Gly Gly Asn
1 5 10

<210> 89
<211> 15
<212> DNA
<213> Actinobacillus pleuropneumoniae

<400> 89
tcaaaagaaa ataac 15

<210> 90
<211> 5
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 90
Ser Lys Glu Asn Asn
1 5

<210> 91
<211> 36
<212> DNA
<213> Actinobacillus pleuropneumoniae

<400> 91
gctacggcag atgatgatag aaaagctggc tatcgc 36

<210> 92
<211> 12
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 92
Ala Thr Ala Asp Asp Asp Arg Lys Ala Gly Tyr Arg
1 5 10

<210> 93
<211> 18
<212> DNA
<213> Actinobacillus pleuropneumoniae

<400> 93
gattttggca acaaaaat 18

<210> 94
<211> 6
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 94
Asp Phe Gly Asn Lys Asn
1 5

<210> 95
<211> 33
<212> DNA
<213> Actinobacillus pleuropneumoniae

<400> 95
ttatttgata aaaacggtgt aaatcctgtg ttt 33

<210> 96
<211> 11
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 96
Leu Phe Asp Lys Asn Gly Val Asn Pro Val Phe
1 5 10

<210> 97
<211> 12
<212> DNA
<213> Actinobacillus pleuropneumoniae

<400> 97
gatggtaatg gt 12

<210> 98
<211> 4
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 98
Asp Gly Asn Gly
1

<210> 99
<211> 69
<212> DNA
<213> Actinobacillus pleuropneumoniae

<400> 99
aaaacctcag atgctggttt cgctctagat tcaggtagtt cacgttatga gaatgtgaaa 60

tttaacgat 69

<210> 100
<211> 23
<212> PRT
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<400> 100
Lys Thr Ser Asp Ala Gly Phe Ala Leu Asp Ser Gly Ser Ser Arg Tyr
1 5 10 15

Glu Asn Val Lys Phe Asn Asp
20

<210> 101
<211> 12
<212> DNA
<213> Actinobacillus pleuropneumoniae

<400> 101
tatggtccaa cg 12

<210> 102
<211> 4
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 102
Tyr Gly Pro Thr
1

<210> 103
<211> 12
<212> DNA
<213> Actinobacillus pleuropneumoniae

<400> 103
tcagaaaatg gc 12

<210> 104
<211> 4
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 104
Ser Glu Asn Gly
1

<210> 105
<211> 6
<212> DNA
<213> Actinobacillus pleuropneumoniae

<400> 105
aaaaaa 6

<210> 106
<211> 2
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 106
Lys Lys
1

<210> 107

<211> 540

<212> PRT

<213> Haemophilus parasuis

<400> 107

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Met His Phe Lys Leu Asn Pro Tyr Ala Leu Ala Phe Thr Ser Leu Phe
1               5                  10                  15

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

Gln Pro Asn Lys Thr Thr Gly Met Ser Lys Glu Glu Tyr Lys Asp Val
        35                  40                  45

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

Ala Leu Gly Tyr Val Val Lys Val Pro Val Ser Gln Asn Gly Val Arg
65                  70                  75                  80

Arg Thr Glu Ile Ser Asn Leu Glu Ala Ile Thr Asp Glu Asp Leu Asn
                85                  90                  95

Lys Ile Pro Asn His Asp Ile Ile Lys Asp Val Ala Tyr Gln Asn Tyr
            100                 105                 110

Gly Glu Leu Val Asp Lys Thr Ala Ala Lys Lys Met Thr Tyr Val Arg
        115                 120                 125

Ser Gly Tyr Ala Ile Asp Val Phe His Tyr Gly Thr Arg Asp Lys Gly
    130                 135                 140

Tyr Val Phe Tyr Lys Gly Ile Thr Pro Ser Lys Glu Leu Pro Gln Gly
145                 150                 155                 160

Pro Val Leu Thr Tyr Gln Gly Glu Trp Asp Phe Thr Ser Asp Ala Asn
                165                 170                 175

Leu Asp Ala Lys Arg Pro Asn Ser Asn Pro Glu Phe Asn Gly Tyr Gly
            180                 185                 190

Pro Gly Gln Arg Ile Ala Ala Thr Ser Ala Asp Ala Lys Gly Arg Thr
        195                 200                 205

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

Lys Leu Ser Ser Lys Thr Ala Asn Ala Glu Ser Leu Glu Arg Tyr Ser
225                 230                 235                 240

Ile Glu Ala Glu Leu Lys Gly Asn Arg Phe Arg Gly Lys Ala Ile Ala
                245                 250                 255

Lys Asn Asp Ser Asp Ala Ser Leu Gly Lys Ser Ser Asp Asn Leu Glu
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            260                 265                 270

Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Ala Gly Lys Phe Ile
        275                 280                 285

Thr Asn Asp Lys Ser Leu Phe Ala Val Phe Ser Ala Lys His Asn Gly
    290                 295                 300

Ser Asn Val Asp Thr Val Arg Ile Ile Asp Ala Ser Lys Ile Asp Leu
305                 310                 315                 320

Thr Asn Phe Ser Ile Ser Glu Leu Thr Asn Phe Gly Asp Ala Ser Val
                325                 330                 335

Leu Ile Ile Asp Gly Gln Lys Met Glu Leu Ala Gly Ser Gly Phe Thr
            340                 345                 350

Asn Lys His Thr Ile Glu Ile Asn Gly Lys Thr Met Val Ala Val Ala
        355                 360                 365

Cys Cys Ser Asn Leu Glu Tyr Met Lys Phe Gly Gln Leu Trp Gln Gln
    370                 375                 380

Ala Glu Gly Glu Lys Ala Lys Asp Asn Ser Leu Phe Leu Gln Gly Glu
385                 390                 395                 400

Arg Thr Ala Thr Asp Lys Met Pro Lys Gly Gly Asn Tyr Lys Tyr Ile
                405                 410                 415

Gly Thr Trp Asp Ala Gln Val Ser Lys Glu Asn Asn Trp Val Ala Thr
            420                 425                 430

Ala Asp Asp Asp Arg Lys Ala Gly Tyr Arg Thr Glu Phe Asp Val Asp
        435                 440                 445

Phe Gly Asn Lys Asn Leu Ser Gly Lys Leu Phe Asp Lys Asn Gly Val
    450                 455                 460

Asn Pro Val Phe Thr Val Asp Ala Lys Ile Asn Gly Asn Gly Phe Thr
465                 470                 475                 480

Gly Lys Ala Lys Thr Ser Asp Ala Gly Phe Ala Leu Asp Ser Gly Ser
                485                 490                 495

Ser Arg Tyr Asp Asn Val Lys Phe Ser Asp Val Ala Val Asn Gly Gly
            500                 505                 510

Phe Tyr Gly Pro Thr Ala Ala Glu Leu Gly Gly Gln Phe Phe His Lys
        515                 520                 525

Ser Asp Asn Gly Ser Val Gly Ala Val Phe Gly Ala
    530                 535                 540
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<210> 108

<211> 590

<212> PRT

<213> Haemophilus parasuis

<400> 108

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Met His Phe Lys Leu Asn Pro Tyr Ala Leu Ala Phe Thr Ser Leu Phe
1               5                  10                  15

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

Gln Pro Asn Gln Thr Ala Lys Val Glu Lys Ala Thr Thr Ser Tyr Gln
        35                  40                  45

Asp Glu Glu Thr Lys Lys Lys Thr Lys Glu Glu Leu Asp Lys Leu Met
    50                  55                  60

Glu Pro Ala Leu Gly Tyr Glu Thr Gln Ile Leu Arg Arg Asn Arg Ala
65                  70                  75                  80

Pro Lys Thr Glu Thr Gly Glu Pro Arg Asn Glu Arg Ala Val Gly Leu
                85                  90                  95

Ser Glu Asp Gln Ile Thr Lys Leu Tyr Gln Glu Asn Ile Glu Ile Ile
            100                 105                 110

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

His Ser His Asp Gly Lys Gly Leu Asp Lys Lys Arg Asp Leu Lys Tyr
    130                 135                 140

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

Asn Glu His Gly Phe His Val Phe Lys Gln Gly Ile Asp Gly Tyr Ile
                165                 170                 175

Tyr Tyr Leu Gly Val Ile Pro Ser Lys Glu Leu Pro Lys Gly Lys Ile
            180                 185                 190

Val Thr Tyr Lys Gly Ser Trp Asp Phe Val Ser Asn Ile Asn Leu Asp
        195                 200                 205

Arg Glu Ile Asp Gly Phe Asp Thr Ser Gly Asp Gly Lys Asn Val Ser
    210                 215                 220

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

Lys Val Gly Glu Asn Glu Val Lys Gly Val Ala His Ser Ser Glu Phe
                245                 250                 255

Ala Val Asp Phe Asp Asn Lys Lys Leu Thr Gly Ser Leu Tyr Arg Asn
            260                 265                 270

Gly Tyr Ile Asn Arg Asn Lys Ala Gln Glu Val Thr Lys Arg Tyr Ser
        275                 280                 285
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Ile Glu Ala Asp Ile Ala Gly Asn Arg Phe Arg Gly Lys Ala Lys Ala
    290                 295                 300

Glu Lys Ala Asp Asp Pro Ile Phe Thr Asn Ser Asp Tyr Leu Glu Gly
305                 310                 315                 320

Gly Ile Tyr Gly Pro Lys Ala Glu Glu Met Ala Gly Lys Phe Phe Thr
                325                 330                 335

Asn Asn Lys Ser Leu Phe Ala Val Phe Ala Ala Lys Ser Glu Asn Gly
            340                 345                 350

Glu Thr Thr Thr Glu Arg Ile Ile Asp Ala Thr Lys Ile Asp Leu Thr
        355                 360                 365

Gln Phe Asn Ala Lys Glu Leu Asn Asn Phe Gly Asp Ala Ser Val Leu

    370                 375                 380

Ile Ile Asp Gly Gln Lys Met Asp Leu Ala Gly Val Asp Phe Lys Asn
385                 390                 395                 400

Ser Lys Thr Val Glu Ile Asn Gly Lys Thr Met Val Ala Val Ala Cys
                405                 410                 415

Cys Ser Asn Leu Glu Tyr Met Lys Phe Gly Gln Leu Trp Gln Lys Glu
            420                 425                 430

Gly Glu Gln Gln Val Lys Asp Asn Ser Leu Phe Leu Gln Gly Glu Arg
        435                 440                 445

Thr Ala Thr Asp Lys Met Pro Ala Gly Gly Asn Tyr Lys Tyr Val Gly
    450                 455                 460

Thr Trp Asp Ala Leu Val Ser Lys Gly Thr Asn Trp Ile Ala Glu Ala
465                 470                 475                 480

Asp Asn Asn Arg Glu Ser Gly Tyr Arg Thr Glu Phe Asp Val Asn Phe
                485                 490                 495

Ser Asp Lys Lys Val Asn Gly Lys Leu Phe Asp Lys Gly Gly Val Asn
            500                 505                 510

Pro Val Phe Thr Val Asp Ala Thr Ile Asn Gly Asn Gly Phe Ile Gly
        515                 520                 525

Ser Ala Lys Thr Ser Asp Ser Gly Phe Ala Leu Asp Ser Gly Ser Ser
    530                 535                 540

Gln His Gly Asn Ala Val Phe Ser Asn Val Asp Val Lys Gly Gly Phe
545                 550                 555                 560

Tyr Gly Pro Thr Ala Gly Glu Leu Gly Gly Gln Phe His His Lys Ser
                565                 570                 575
```

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Asp Asn Gly Ser Val Gly Ala Val Phe Gly Ala Lys Arg Gln
            580                 585                 590
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<210> 109

<211> 590

<212> PRT

<213> Haemophilus parasuis

<400> 109

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Met His Phe Lys Leu Asn Pro Tyr Ala Leu Ala Phe Thr Ser Leu Phe

1               5                   10                  15

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

Gln Pro Asn Gln Thr Ala Lys Val Glu Lys Ala Thr Thr Ser Tyr Gln
        35                  40                  45

Asp Glu Glu Thr Lys Lys Lys Thr Lys Glu Glu Leu Asp Lys Leu Met
    50                  55                  60

Glu Pro Ala Leu Gly Tyr Glu Thr Gln Ile Leu Arg Arg Asn Arg Ala
65                  70                  75                  80

Pro Lys Thr Glu Thr Gly Glu Pro Arg Asn Glu Arg Ala Val Gly Leu
                85                  90                  95

Ser Glu Asp Gln Ile Thr Lys Leu Tyr Gln Glu Asn Ile Glu Ile Ile
            100                 105                 110

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

His Ser His Asp Gly Lys Arg Leu Asp Lys Lys Arg Asp Leu Lys Tyr
    130                 135                 140

Val Arg Ser Gly Tyr Val Tyr Asp Gly Ser Phe Arg Glu Ile Gln Arg
145                 150                 155                 160

Asn Asp Thr Gly Phe Tyr Val Phe Lys Gln Gly Ile Asp Gly Tyr Val
                165                 170                 175

Tyr Tyr Leu Gly Val Ile Pro Ser Lys Glu Leu Pro Lys Gly Lys Val
            180                 185                 190

Val Ser Tyr Lys Gly Thr Trp Asp Phe Val Ser Asn Ile Asn Leu Asp
        195                 200                 205

Arg Glu Ile Asp Gly Phe Asp Thr Ala Gly Asp Gly Lys Asn Val Ser
    210                 215                 220

Ala Thr Ser Ile Thr Glu Thr Val Asn Arg Glu His Lys Ile Gly Asp
225                 230                 235                 240
```

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Lys Val Gly Glu Asn Glu Val Lys Gly Val Ala His Ser Ser Glu Phe
                245                 250                 255

Ala Val Asp Phe Asp Asn Lys Lys Leu Thr Gly Ser Leu Tyr Arg Asn
            260                 265                 270

Gly Tyr Ile Asn Arg Asn Lys Ala Gln Glu Val Thr Lys Arg Tyr Ser
        275                 280                 285

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

Glu Lys Ala Asp Asp Pro Ile Phe Thr Asn Ser Asp Tyr Leu Glu Gly
305                 310                 315                 320

Gly Phe Tyr Gly Pro Lys Ala Glu Glu Met Ala Gly Lys Phe Phe Thr
                325                 330                 335

Asn Asn Lys Ser Leu Phe Ala Val Phe Ala Ala Lys Ser Glu Asn Gly
            340                 345                 350

Glu Thr Thr Thr Glu Arg Ile Ile Asp Ala Thr Lys Ile Asp Leu Thr
        355                 360                 365

Gln Phe Asn Ala Lys Glu Leu Asn Asn Phe Gly Asp Ala Ser Val Leu
    370                 375                 380

Ile Ile Asp Gly Gln Lys Met Asp Leu Ala Gly Val Asp Phe Lys Asn
385                 390                 395                 400

Ser Lys Thr Val Glu Ile Asn Gly Lys Thr Met Val Ala Val Ala Cys
                405                 410                 415

Cys Ser Asn Leu Glu Tyr Met Lys Phe Gly Gln Leu Trp Gln Lys Glu
            420                 425                 430

Gly Glu Gln Gln Val Lys Asp Asn Ser Leu Phe Leu Gln Gly Glu Arg
        435                 440                 445

Thr Ala Thr Asp Lys Met Pro Ala Gly Gly Asn Tyr Lys Tyr Val Gly
    450                 455                 460

Thr Trp Asp Ala Leu Val Ser Lys Gly Thr Asn Trp Ile Ala Glu Ala
465                 470                 475                 480

Asp Asn Asn Arg Glu Ser Gly Tyr Arg Thr Glu Phe Asp Val Asn Phe
                485                 490                 495

Ser Asp Lys Lys Val Asn Gly Lys Leu Phe Asp Lys Gly Gly Val Asn
            500                 505                 510

Pro Val Phe Thr Val Asp Ala Thr Ile Asn Gly Asn Gly Phe Ile Gly
        515                 520                 525

Ser Ala Lys Thr Ser Asp Ser Gly Phe Ala Leu Asp Ala Gly Ser Ser
    530                 535                 540
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Gln His Gly Asn Ala Val Phe Ser Asn Val Asp Val Lys Gly Gly Phe
545                 550                 555                 560

Tyr Gly Pro Thr Ala Gly Glu Leu Gly Gly Gln Phe His His Lys Ser
                565                 570                 575

Asp Asn Gly Ser Val Gly Ala Val Phe Gly Ala Lys Arg Gln
            580                 585                 590
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<210> 110

<211> 540

<212> PRT

<213> Haemophilus parasuis

<400> 110

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Met His Phe Lys Ser Asp Leu Tyr Ile Val Ala Leu Thr Ser Thr Phe
1               5                   10                  15

Leu Val Ala Cys Ser Gly Gly Lys Gly Ser Phe Asp Leu Asp Asp Val
            20                  25                  30

Gln Pro Asn Lys Ala Val Glu Pro Glu Lys Thr Lys Val Asn Tyr Thr
        35                  40                  45

Asp Glu Glu Thr Gln Lys Arg Lys Lys Glu Glu Leu Asp Lys Leu Met
    50                  55                  60

Glu Pro Ala Leu Gly Tyr Val Thr Lys Ile Pro Val Asn Ile Pro Ser
65                  70                  75                  80

Val Arg Lys Thr Glu Ile Ser Glu Ile Asp Thr Val Thr Asp Glu Ser
                85                  90                  95

Leu Ser Leu Val Pro Asn Glu Asp Lys Leu Arg Thr Ile Ala Asn Glu
            100                 105                 110

Asn Tyr Gly Ser Val Val Thr Lys Ser Gly Ser Asn Thr Met Asn Phe
        115                 120                 125

Val Arg Ser Gly Tyr Thr Ile Asp Val Asp His Tyr Gly Leu Arg Asp
    130                 135                 140

Lys Gly Tyr Val Tyr Tyr Lys Gly Val His Pro Ser Lys Glu Leu Pro
145                 150                 155                 160

Lys Gly Asn Ile Ile Val Tyr Gln Gly Glu Trp Asp Phe Thr Ser Asn
                165                 170                 175

Ala Asp Leu Asp Ala Lys Arg Pro Asn Tyr Asn Pro Glu Phe Asn Gly
            180                 185                 190

Tyr Gly Ala Gly Gln Arg Val Gly Val Thr Ser Ala Asp Ala Lys Glu
        195                 200                 205

Arg Thr Tyr Ile Ser Lys Phe Asn Ile Asp Phe Ser Asn Lys Lys Leu
    210                 215                 220
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Asn Gly Gln Leu Leu Thr Lys Thr Lys Glu Asn Gln Glu Lys Leu Arg
225                 230                 235                 240

Tyr Thr Val Glu Ala Asn Ile Ser Gly Asn Arg Phe Arg Gly Lys Ala
                245                 250                 255

Thr Ala Thr Asp Lys Thr Asp Pro Ile Leu Gly Lys Asp Ser Glu His
            260                 265                 270

Leu Glu Gly Gly Leu Tyr Gly Pro Lys Ser Glu Glu Leu Ala Gly Lys
        275                 280                 285

Phe Val Ala His Asp Lys Ser Leu Phe Ala Val Phe Ser Gly Lys Arg
    290                 295                 300

Gly Asn Asp Val Leu Glu Thr Val Lys Ile Ile Asp Ala Ser Lys Ile
305                 310                 315                 320

Asp Leu Thr Thr Phe Glu Ser Ser Glu Leu Asn Asn Phe Gly Asn Ala
                325                 330                 335

Asn Val Leu Ile Ile Asp Gly Gln Lys Ile Asp Leu Ala Gly Ala Asp
            340                 345                 350

Phe Lys Asn Arg Lys Thr Val Asp Ile Asn Gly Lys Thr Met Val Ala
        355                 360                 365

Ile Ala Cys Cys Ser Asn Leu Glu Tyr Met Lys Phe Gly Gln Leu Trp
    370                 375                 380

Gln Lys Glu Gly Glu Gln Thr Lys Asp Asn Ser Leu Phe Leu Gln Gly
385                 390                 395                 400

Glu Arg Thr Ala Thr Asp Lys Ile Pro Val Gly Gly Asn Tyr Lys Tyr
                405                 410                 415

Val Gly Thr Trp Asp Ala Leu Val Ser Lys Gly Thr Asn Trp Val Ala
            420                 425                 430

Glu Ala Asp Asn Asn Arg Glu Ser Gly Tyr Arg Ser Glu Phe Asp Val
        435                 440                 445

Asn Phe Gly Asp Lys Lys Val Ser Gly Lys Leu Phe Asp Lys Gly Gly
    450                 455                 460

Ile Val Pro Val Phe Met Ile Asn Ala Asp Ile Lys Gly Asn Gly Phe
465                 470                 475                 480

Thr Gly Thr Ala Asn Thr Thr Asp Thr Gly Phe Ala Leu Asp Ser Gly
                485                 490                 495

Ser Ser Gln His Gly Asn Ala Val Phe Ser Asp Ile Lys Val Asn Gly
            500                 505                 510

Gly Phe Tyr Gly Pro Thr Ala Gly Glu Leu Gly Gly Gln Phe His His
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        515                 520                 525

Lys Ser Asp Asn Gly Ser Val Gly Ala Val Phe Gly
    530                 535                 540
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<210> 111

<211> 590

<212> PRT

<213> Haemophilus parasuis

<400> 111

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Met His Phe Lys Leu Asn Pro Tyr Ala Leu Ala Phe Thr Ser Leu Phe
1               5                  10                  15

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

Gln Pro Asn Gln Thr Ala Lys Val Glu Lys Ala Thr Thr Ser Tyr Gln
        35                  40                  45

Asp Glu Glu Thr Lys Lys Lys Thr Lys Glu Glu Leu Asp Lys Leu Met
    50                  55                  60

Glu Pro Ala Leu Gly Tyr Glu Thr Gln Ile Leu Arg Arg Asn Arg Ala
65                  70                  75                  80

Pro Lys Thr Glu Thr Gly Glu Pro Arg Asn Glu Arg Ala Val Gly Leu
                85                  90                  95

Ser Glu Asp Gln Ile Thr Lys Leu Tyr Gln Glu Asn Ile Glu Ile Ile
            100                 105                 110

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

His Ser His Asp Gly Lys Arg Leu Asp Lys Lys Arg Asp Leu Lys Tyr
    130                 135                 140

Val Arg Ser Gly Tyr Val Tyr Asp Gly Ser Phe Arg Glu Ile Gln Arg
145                 150                 155                 160

Asn Asp Thr Gly Phe Tyr Val Phe Lys Gln Gly Ile Asp Gly Tyr Val
                165                 170                 175

Tyr Tyr Leu Gly Val Thr Pro Ser Lys Glu Leu Pro Lys Gly Lys Val
            180                 185                 190

Val Ser Tyr Lys Gly Thr Trp Asp Phe Val Ser Asn Ile Asn Leu Asp
        195                 200                 205

Arg Glu Ile Asp Gly Phe Asp Thr Ser Gly Asp Gly Lys Asn Val Ser
    210                 215                 220

Ala Thr Ser Ile Thr Glu Thr Val Asn Arg Glu His Lys Ile Gly Asp
225                 230                 235                 240
```

```
Lys Val Gly Glu Asn Glu Val Lys Gly Val Ala His Ser Ser Glu Phe
                245                 250                 255

Ala Val Asp Phe Asp Asn Lys Lys Leu Thr Gly Ser Leu Tyr Arg Asn
            260                 265                 270

Gly Tyr Ile Asn Arg Asn Lys Ala Gln Glu Val Thr Lys Arg Tyr Ser
        275                 280                 285

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

Glu Lys Ala Asp Asp Pro Ile Phe Thr Asn Ser Asp Tyr Leu Glu Gly
305                 310                 315                 320

Gly Phe Tyr Gly Pro Lys Ala Glu Glu Met Ala Gly Lys Phe Phe Thr

                325                 330                 335

Asn Asn Lys Ser Leu Phe Ala Val Phe Ala Ala Lys Ser Glu Asn Gly
            340                 345                 350

Glu Thr Thr Thr Glu Arg Ile Ile Asp Ala Thr Lys Ile Asp Leu Thr
        355                 360                 365

Gln Phe Asn Ala Lys Glu Leu Asn Asn Phe Gly Asp Ala Ser Val Leu
    370                 375                 380

Ile Ile Asp Gly Gln Lys Met Asp Leu Ala Gly Ala Asp Phe Lys Asn
385                 390                 395                 400

Arg Lys Thr Val Asp Ile Asn Gly Lys Thr Met Val Ala Ile Ala Cys
                405                 410                 415

Cys Ser Asn Leu Glu Tyr Met Lys Phe Gly Gln Leu Trp Gln Lys Glu
            420                 425                 430

Gly Glu Gln Gln Val Lys Asp Asn Ser Leu Phe Leu Gln Gly Glu Arg
        435                 440                 445

Thr Ala Thr Asp Lys Met Pro Ala Gly Gly Asn Tyr Lys Tyr Val Gly
    450                 455                 460

Thr Trp Asp Ala Leu Val Ser Lys Gly Thr Asn Trp Ile Ala Glu Ala
465                 470                 475                 480

Asp Asn Asn Arg Glu Ser Gly Tyr Arg Thr Glu Phe Asp Val Asn Phe
                485                 490                 495

Ser Asp Lys Lys Val Asn Gly Lys Leu Phe Asp Lys Gly Gly Val Asn
            500                 505                 510

Pro Val Phe Thr Val Asp Ala Thr Ile Asn Gly Asn Gly Phe Ile Gly
        515                 520                 525
```

```
Ser Ala Lys Thr Ser Asp Ser Gly Phe Ala Leu Asp Ala Gly Ser Ser
    530                 535                 540

Gln His Gly Asn Ala Val Phe Ser Asn Val Asp Val Lys Gly Gly Phe
545                 550                 555                 560

Tyr Gly Pro Thr Ala Gly Glu Leu Gly Gly Gln Phe His His Lys Ser
                565                 570                 575

Asp Asn Gly Ser Val Gly Ala Val Phe Gly Ala Lys Arg Gln
            580                 585                 590
```

<210> 112

<211> 540

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 112

```
Met His Phe Lys Leu Asn Pro Tyr Ala Leu Ala Phe Thr Ser Leu Phe
1               5                   10                  15

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

Arg Pro Asn Lys Thr Thr Gly Val Ser Lys Glu Glu Tyr Lys Asp Val
        35                  40                  45

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

Ala Leu Gly Tyr Val Val Lys Val Pro Val Ser Ser Phe Glu Asn Lys
65                  70                  75                  80

Lys Val Asp Ile Ser Asp Ile Glu Val Ile Thr Asn Gly Asn Leu Asp
                85                  90                  95

Asp Val Pro Tyr Lys Ala Asn Ser Ser Lys Tyr Asn Tyr Pro Asp Ile
            100                 105                 110

Lys Thr Lys Asp Ser Ser Leu Gln Tyr Val Arg Ser Gly Tyr Val Ile
        115                 120                 125

Asp Gly Glu His Ser Gly Ser Asn Glu Lys Gly Tyr Val Tyr Tyr Lys
    130                 135                 140

Gly Asn Ser Pro Ala Lys Glu Leu Pro Val Asn Gln Leu Leu Thr Tyr
145                 150                 155                 160

Thr Gly Ser Trp Asp Phe Thr Ser Asn Ala Asn Leu Asn Asn Glu Glu
                165                 170                 175

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

Lys Arg Val Gly Leu Val Ser Gly Asp Ala Lys Pro Ala Lys His Lys
        195                 200                 205
```

```
Tyr Thr Ser Gln Phe Glu Val Asp Phe Ala Thr Lys Lys Met Thr Gly
    210                 215                 220

Lys Leu Ser Asp Lys Glu Lys Thr Ile Tyr Thr Val Asn Ala Asp Ile
225                 230                 235                 240

Arg Gly Asn Arg Phe Thr Gly Ala Ala Thr Ala Ser Asp Lys Asn Lys
                245                 250                 255

Gly Lys Gly Glu Ser Tyr Asn Phe Phe Ser Ala Asp Ser Gln Ser Leu
            260                 265                 270

Glu Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Met Ala Gly Lys Phe
        275                 280                 285

Val Ala Asn Asp Lys Ser Leu Phe Ala Val Phe Ser Ala Lys His Asn
    290                 295                 300

Gly Ser Asn Val Asn Thr Val Arg Ile Ile Asp Ala Ser Lys Ile Asp
305                 310                 315                 320

Leu Thr Asn Phe Ser Ile Ser Glu Leu Asn Asn Phe Gly Asp Ala Ser
                325                 330                 335

Val Leu Ile Ile Asp Gly Lys Lys Ile Lys Leu Ala Gly Ser Gly Phe
            340                 345                 350

Thr Asn Lys His Thr Ile Glu Ile Asn Gly Lys Thr Met Val Ala Val
        355                 360                 365

Ala Cys Cys Ser Asn Leu Glu Tyr Met Lys Phe Gly Gln Leu Trp Gln
    370                 375                 380

Gln Ala Glu Gly Gly Lys Pro Glu Asn Asn Ser Leu Phe Leu Gln Gly
385                 390                 395                 400

Glu Arg Thr Ala Thr Asp Lys Met Pro Lys Gly Gly Asn Tyr Lys Tyr
                405                 410                 415

Ile Gly Thr Trp Asp Ala Gln Val Ser Lys Glu Asn Asn Trp Val Ala
            420                 425                 430

Thr Ala Asp Asp Asp Arg Lys Ala Gly Tyr Arg Thr Glu Phe Asp Val
        435                 440                 445

Asp Phe Gly Asn Lys Asn Leu Ser Gly Lys Leu Phe Asp Lys Asn Gly
    450                 455                 460

Val Asn Pro Val Phe Thr Val Asp Ala Lys Ile Asp Gly Asn Gly Phe
465                 470                 475                 480

Thr Gly Lys Ala Lys Thr Ser Asp Asp Gly Phe Ala Leu Asp Ser Gly
                485                 490                 495

Ser Ser Arg Tyr Glu Asn Val Lys Phe Asn Asp Val Ala Val Ser Gly
            500                 505                 510
```

```
Gly Phe Tyr Gly Pro Thr Ala Ala Glu Leu Gly Gly Gln Phe His His
        515                 520                 525

Lys Ser Glu Asn Gly Ser Val Gly Ala Val Phe Gly
    530                 535                 540
```

<210> 113

<211> 590

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 113

```
Met His Phe Lys Leu Asn Pro Tyr Ala Leu Ala Phe Thr Ser Leu Phe
1               5                   10                  15

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

Arg Pro Asn Gln Thr Ala Lys Ala Glu Lys Ala Thr Thr Ser Tyr Gln
        35                  40                  45

Asp Glu Glu Thr Lys Lys Lys Thr Lys Glu Glu Leu Asp Lys Leu Met
    50                  55                  60

Glu Pro Ala Leu Gly Tyr Glu Thr Gln Ile Leu Arg Arg Asn Lys Ala
65                  70                  75                  80

Pro Lys Thr Glu Thr Gly Glu Lys Arg Asn Glu Arg Val Val Glu Leu
                85                  90                  95

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

Pro His Leu Asp Glu Leu Asn Gly Lys Thr Thr Ser Asn Asp Val Tyr
        115                 120                 125

His Ser His Asp Ser Lys Arg Leu Asp Lys Asn Arg Asp Leu Lys Tyr
    130                 135                 140

Val Arg Ser Gly Tyr Val Tyr Asp Gly Ser Phe Asn Glu Ile Arg Arg
145                 150                 155                 160

Asn Asp Ser Gly Phe His Val Phe Lys Gln Gly Ile Asp Gly Tyr Val
                165                 170                 175

Tyr Tyr Leu Gly Val Thr Pro Ser Lys Glu Leu Pro Lys Gly Lys Val
            180                 185                 190

Ile Ser Tyr Lys Gly Thr Trp Asp Phe Val Ser Asn Ile Asn Leu Asp
        195                 200                 205

Arg Glu Ile Asp Gly Phe Asp Thr Ser Gly Asp Gly Lys Asn Val Ser
    210                 215                 220

Ala Thr Ser Ile Thr Glu Thr Val Asn Arg Asp His Lys Val Gly Glu
```

```
Ala Thr Ser Ile Thr Glu Thr Val Asn Arg Asp His Lys Val Gly Glu
225                 230                 235                 240

Lys Leu Gly Asp Asn Glu Val Lys Gly Val Ala His Ser Ser Glu Phe
                245                 250                 255

Ala Val Asp Phe Asp Asn Lys Lys Leu Thr Gly Ser Leu Tyr Arg Asn
            260                 265                 270

Gly Tyr Ile Asn Arg Asn Lys Ala Gln Glu Val Thr Lys Arg Tyr Ser
        275                 280                 285

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

Glu Lys Ala Gly Asp Pro Ile Phe Thr Asp Ser Asn Tyr Leu Glu Gly
305                 310                 315                 320

Gly Phe Tyr Gly Pro Lys Ala Glu Glu Met Ala Gly Lys Phe Phe Thr
                325                 330                 335

Asn Asn Lys Ser Leu Phe Ala Val Phe Ala Ala Lys Ser Glu Asn Gly
            340                 345                 350

Glu Thr Thr Thr Glu Arg Ile Ile Asp Ala Thr Lys Ile Asp Leu Thr
        355                 360                 365

Gln Phe Asn Ala Lys Glu Leu Asn Asn Phe Gly Asp Ala Ser Val Leu
    370                 375                 380

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

Ser Lys Thr Val Glu Ile Asn Gly Lys Thr Met Val Ala Val Ala Cys
                405                 410                 415

Cys Ser Asn Leu Glu Tyr Met Lys Phe Gly Gln Leu Trp Gln Lys Glu
            420                 425                 430

Gly Lys Gln Gln Val Lys Asp Asn Ser Leu Phe Leu Gln Gly Glu Arg
        435                 440                 445

Thr Ala Thr Asp Lys Met Pro Ala Gly Gly Asn Tyr Lys Tyr Val Gly
    450                 455                 460

Thr Trp Asp Ala Leu Val Ser Lys Gly Thr Asn Trp Ile Ala Glu Ala
465                 470                 475                 480

Asp Asn Asn Arg Glu Ser Gly Tyr Arg Thr Glu Phe Asp Val Asn Phe
                485                 490                 495

Ser Asp Lys Lys Val Asn Gly Lys Leu Phe Asp Lys Gly Gly Val Asn
            500                 505                 510

Pro Val Phe Thr Val Asp Ala Thr Ile Asn Gly Asn Gly Phe Ile Gly
        515                 520                 525
```

```
Ser Ala Lys Thr Ser Asp Ser Gly Phe Ala Leu Asp Ala Gly Ser Ser
    530                 535                 540

Gln His Gly Asn Ala Val Phe Ser Asp Ile Lys Val Asn Gly Gly Phe
545                 550                 555                 560

Tyr Gly Pro Thr Ala Gly Glu Leu Gly Gly Gln Phe His His Lys Ser
                565                 570                 575

Asp Asn Gly Ser Val Gly Ala Val Phe Gly Ala Lys Arg Gln
            580                 585                 590
```

<210> 114

<211> 540

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 114

```
Met His Phe Lys Leu Asn Pro Tyr Ala Leu Ala Phe Thr Ser Leu Phe
1               5                   10                  15

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

Arg Pro Asn Lys Thr Thr Gly Val Ser Lys Glu Glu Tyr Lys Asp Val
        35                  40                  45

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

Ala Leu Gly Tyr Val Val Lys Val Pro Val Ser Ser Phe Glu Asn Lys
65                  70                  75                  80

Lys Val Asp Ile Ser Asp Ile Glu Val Ile Thr Asn Gly Asn Leu Asp
                85                  90                  95

Asp Val Pro Tyr Lys Ala Asn Ser Ser Lys Tyr Asn Tyr Pro Asp Ile
            100                 105                 110

Lys Thr Lys Asp Ser Ser Leu Gln Tyr Val Arg Ser Gly Tyr Val Ile
        115                 120                 125

Asp Gly Glu His Ser Gly Ser Asn Glu Lys Gly Tyr Val Tyr Tyr Lys
    130                 135                 140

Gly Asn Ser Pro Ala Lys Glu Leu Pro Val Asn Gln Leu Leu Thr Tyr
145                 150                 155                 160

Thr Gly Ser Trp Asp Phe Thr Ser Asn Ala Asn Leu Asn Asn Glu Glu
                165                 170                 175

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

Lys Arg Val Gly Leu Val Ser Gly Asp Ala Lys Pro Ala Lys His Lys
        195                 200                 205
```

```
Tyr Thr Ser Gln Phe Glu Val Asp Phe Ala Thr Lys Lys Met Thr Gly
    210                 215                 220

Lys Leu Ser Asp Lys Glu Lys Thr Ile Tyr Thr Val Asn Ala Asp Ile
225                 230                 235                 240

Arg Gly Asn Arg Phe Thr Gly Ala Ala Thr Ala Ser Asp Lys Asn Lys
                245                 250                 255

Gly Lys Gly Glu Ser Tyr Asn Phe Phe Ser Ala Asp Ser Gln Ser Leu
            260                 265                 270

Glu Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Met Ala Gly Lys Phe

        275                 280                 285

Val Ala Asn Asp Lys Ser Leu Phe Ala Val Phe Ser Ala Lys His Asn
    290                 295                 300

Gly Ser Asn Val Asp Thr Val Arg Ile Ile Asp Ala Ser Lys Ile Asp
305                 310                 315                 320

Leu Thr Asn Phe Ser Ile Ser Glu Leu Asn Asn Phe Gly Asp Ala Ser
                325                 330                 335

Val Leu Ile Ile Asp Gly Lys Lys Ile Lys Leu Ala Gly Ser Gly Phe
            340                 345                 350

Thr Asn Lys His Thr Ile Glu Ile Asn Gly Lys Thr Met Val Ala Val
        355                 360                 365

Ala Cys Cys Ser Asn Leu Glu Tyr Met Lys Phe Gly Gln Leu Trp Gln
    370                 375                 380

Gln Ala Glu Gly Gly Lys Pro Glu Asn Asn Ser Leu Phe Leu Gln Gly
385                 390                 395                 400

Glu Arg Thr Ala Thr Asp Lys Met Pro Lys Gly Gly Asn Tyr Lys Tyr
                405                 410                 415

Ile Gly Thr Trp Asp Ala Gln Val Ser Lys Glu Asn Asn Trp Val Ala
            420                 425                 430

Thr Ala Asp Asp Asp Arg Lys Ala Gly Tyr Arg Thr Glu Phe Asp Val
        435                 440                 445

Asp Phe Gly Asn Lys Asn Leu Ser Gly Lys Leu Phe Asp Lys Asn Gly
    450                 455                 460

Val Asn Pro Val Phe Thr Val Asp Ala Lys Ile Asp Gly Asn Gly Phe
465                 470                 475                 480

Thr Gly Lys Ala Lys Thr Ser Asp Ala Gly Phe Ala Leu Asp Ser Gly
                485                 490                 495
```

```
Ser Ser Arg Tyr Glu Asn Val Lys Phe Asn Asp Val Ala Val Ser Gly
            500                 505                 510

Gly Phe Tyr Gly Pro Thr Ala Ala Glu Leu Gly Gly Gln Phe His His
        515                 520                 525

Lys Ser Glu Asn Gly Ser Val Gly Ala Val Phe Gly
    530                 535                 540
```

<210> 115

<211> 545

<212> PRT

<213> Haemophilus parasuis

<400> 115

```
Met His Phe Lys Leu Asn Pro Tyr Ala Leu Ala Phe Thr Ser Leu Phe
1               5                   10                  15

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

Gln Pro Asn Lys Thr Thr Gly Val Ser Lys Glu Glu Tyr Gln Asp Val
        35                  40                  45

Glu Thr Asp Lys Lys Val Lys Glu Gln Leu Gly Glu Leu Met Glu Pro
    50                  55                  60

Ala Leu Gly Tyr Val Val Lys Val Pro Val Ser Gln Ser Gly Ala Arg
65                  70                  75                  80

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

Lys Ile Pro Asn His Glu Thr Ile Lys Ser Val Ala Glu Gln Asn Tyr
            100                 105                 110

Gly Trp Val Val Asp Lys Thr Ala Asp Lys Thr Met Lys Tyr Val Arg
        115                 120                 125

Ser Gly Tyr Ala Ile Asp Val Asp His Tyr Gly Thr Arg Asp Lys Gly
    130                 135                 140

Tyr Val Phe Tyr Lys Gly Ile Asn Pro Ser Lys Glu Leu Pro Gln Gly
145                 150                 155                 160

Leu Val Leu Thr Tyr Gln Gly Glu Trp Asp Phe Thr Ser Asp Ala Asn
                165                 170                 175

Leu Asp Ala Lys Arg Pro Asn Ser Asn Pro Glu Phe Asn Gly Tyr Gly
            180                 185                 190

Pro Gly Gln Arg Ile Ala Thr Thr Ser Ala Asn Ala Lys Gly Arg Thr
        195                 200                 205

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

```
    210                 215                 220

Lys Leu Asn Ser Lys Thr Ala Asn Thr Glu Ser Leu Glu Arg Tyr Ser
225                 230                 235                 240

Ile Glu Ala Glu Pro Lys Gly Asn Arg Phe Arg Gly Lys Ala Ile Ala
                245                 250                 255

Lys Asp Thr Ser Asp Ala Ile Leu Gly Lys Ser Ser Asp Tyr Leu Glu
            260                 265                 270

Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Ala Gly Lys Phe Ile
        275                 280                 285

Thr Asn Asp Lys Ser Leu Phe Ala Val Phe Ser Ala Lys His Asn Gly
    290                 295                 300

Ser Asn Val Asp Thr Val Arg Ile Ile Asp Ala Ser Lys Ile Asp Leu
305                 310                 315                 320

Thr His Phe Asn Ser Ser Glu Leu Thr Asn Phe Gly Asp Ala Ser Val
                325                 330                 335

Leu Ile Ile Asp Gly Lys Lys Met Asp Leu Ala Gly Thr Asp Phe Lys
            340                 345                 350

Asn Ser Lys Thr Ile Glu Ile Asn Gly Lys Thr Met Val Ala Val Ala
        355                 360                 365

Cys Cys Ser Asn Leu Glu Tyr Met Lys Phe Gly Gln Leu Trp Gln Lys
    370                 375                 380

Glu Gly Glu Thr Ala Lys Asp Asn Ser Leu Phe Leu Gln Gly Glu Arg
385                 390                 395                 400

Thr Thr Thr Asp Lys Met Pro Lys Gly Gly Asn Tyr Lys Tyr Ile Gly
                405                 410                 415

Thr Trp Asp Ala Gln Val Ser Lys Glu Asn Asn Trp Val Ala Thr Ala
            420                 425                 430

Asp Asp Asp Arg Lys Ala Gly Tyr Arg Thr Glu Phe Asp Val Asp Phe
        435                 440                 445

Gly Asn Lys Asn Leu Ser Gly Lys Leu Phe Asp Lys Asn Gly Val Asn
    450                 455                 460

Pro Val Phe Thr Val Asp Ala Lys Ile Asn Gly Asn Gly Phe Thr Gly
465                 470                 475                 480

Lys Ala Lys Thr Ser Asp Ala Gly Phe Ala Leu Asp Ser Asp Ser Ser
                485                 490                 495

Arg Tyr Asp Asn Val Lys Phe Ser Asp Val Ala Val Asn Gly Gly Phe
            500                 505                 510

Tyr Gly Pro Thr Ala Ala Glu Leu Gly Gly Gln Phe Phe His Lys Ser
        515                 520                 525
```

515 520 525

Asp Asn Gly Ser Val Gly Ala Ile Phe Gly Ala Lys Arg Gln Val Lys
530 535 540

Lys
545

<210> 116
<211> 1740
<212> DNA
<213> Neisseria meningitidis

<400> 116

tgtctgggtg gcggcggcag tttcgatttg gacagcgtgg aaaccgtgca agatatgcac 60

tccaaaccta agtatgagga tgaaaaaagc cagcctgaaa gccaacagga tgtatcggaa 120

aacagcggcg cggcttatgg ctttgcagta aaactacctc gccggaatgc acattttaat 180

cctaaatata aggaaaagca caaaccattg ggttcaatgg attggaaaaa actgcaaaga 240

ggagaaccaa atagttttag tgagagggat gaattggaaa aaaaacgggg tagttctgaa 300

cttattgaat caaaatggga agatgggcaa agtcgtgtag ttggttatac aaatttcact 360

tatgtccgtt cgggatatgt ttaccttaat aaaaataata ttgatattaa gaataatata 420

gttctttttg gacctgacgg atatctttac tataaaggga aagaaccttc caaggagctg 480

ccatcggaaa agataactta taaaggtact tgggattatg ttactgatgc tatggaaaaa 540

caaaggtttg aaggattggg tagtgcagca ggaggagata aatcgggggc gttgtctgca 600

ttagaagaag gggtattgcg taatcaggca gaggcatcat ccggtcatac cgattttggt 660

atgactagtg agtttgaggt tgatttttct gataaaacaa taaagggcac actttatcgt 720

aacaaccgta ttactcaaaa taatagtgaa aacaaacaaa taaaaactac gcgttacacc 780

attcaagcaa ctcttcacgg caaccgtttc aaaggtaagg cgttggcggc agataaaggt 840

gcaacaaatg gaagtcatcc ctttatttcc gactccgaca gtttggaagg cggattttac 900

gggccgaaag gcgaggaact tgccggtaaa ttcttgagca acgacaacaa agttgcagcg 960

gtgtttggtg cgaagcagaa agataagaag gatggggaaa acgcggcagg gcctgcaacg 1020

gaaaccgtga tagatgcata ccgtattacc ggcgaggagt ttaagaaaga gcaaatagac 1080

agttttggag atgtgaaaaa gctgctggtt gacggagtgg agctttcact gctgccgtct 1140

gagggcaata aggcggcatt tcagcacgag attgagcaaa acggcgtgaa ggcaacggtg 1200

tgttgttcca acttggatta catgagtttt gggaagctgt caaaagaaaa taaagacgat 1260

atgttcctgc aaggtgtccg cactccagta tccgatgtgg cggcaaggac ggaggcaaac 1320

gccaaatatc gcggtacttg gtacggatat attgccaacg gcacaagctg gagcggcgaa 1380

gcctccaatc aggaaggtgg taatagggca gagtttgacg tggatttttc cactaaaaaa 1440

atcagtggca cactgacggc aaaagaccgt acgtctcctg cgtttactat tactgccatg 1500

attaaggaca acggtttttc aggtgtggcg aaaaccggtg aaaacggctt tgcgctggat 1560

ccgcaaaata ccggaaattc ccactatacg catattgaag ccactgtatc cggcggtttc 1620

tacggcaaaa acgccatcga gatgggcgga tcgttctcat ttccgggaaa tgcaccagag 1680

ggaaaacaag aaaaagcatc ggtggtattc ggtgcgaaac gccaacagct tgtgcaataa 1740

<210> 117

<211> 579

<212> PRT

<213> Neisseria meningitidis

<400> 117

```
Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser Val Glu Thr Val
1               5                   10                  15

Gln Asp Met His Ser Lys Pro Lys Tyr Glu Asp Glu Lys Ser Gln Pro
            20                  25                  30

Glu Ser Gln Gln Asp Val Ser Glu Asn Ser Gly Ala Ala Tyr Gly Phe
        35                  40                  45

Ala Val Lys Leu Pro Arg Arg Asn Ala His Phe Asn Pro Lys Tyr Lys
    50                  55                  60

Glu Lys His Lys Pro Leu Gly Ser Met Asp Trp Lys Lys Leu Gln Arg
65                  70                  75                  80

Gly Glu Pro Asn Ser Phe Ser Glu Arg Asp Glu Leu Glu Lys Lys Arg
                85                  90                  95

Gly Ser Ser Glu Leu Ile Glu Ser Lys Trp Glu Asp Gly Gln Ser Arg
            100                 105                 110

Val Val Gly Tyr Thr Asn Phe Thr Tyr Val Arg Ser Gly Tyr Val Tyr

        115                 120                 125

Leu Asn Lys Asn Asn Ile Asp Ile Lys Asn Asn Ile Val Leu Phe Gly
    130                 135                 140

Pro Asp Gly Tyr Leu Tyr Tyr Lys Gly Lys Glu Pro Ser Lys Glu Leu
145                 150                 155                 160

Pro Ser Glu Lys Ile Thr Tyr Lys Gly Thr Trp Asp Tyr Val Thr Asp
                165                 170                 175

Ala Met Glu Lys Gln Arg Phe Glu Gly Leu Gly Ser Ala Ala Gly Gly
            180                 185                 190

Asp Lys Ser Gly Ala Leu Ser Ala Leu Glu Glu Gly Val Leu Arg Asn
        195                 200                 205

Gln Ala Glu Ala Ser Ser Gly His Thr Asp Phe Gly Met Thr Ser Glu
    210                 215                 220

Phe Glu Val Asp Phe Ser Asp Lys Thr Ile Lys Gly Thr Leu Tyr Arg
225                 230                 235                 240
```

```
Asn Asn Arg Ile Thr Gln Asn Asn Ser Glu Asn Lys Gln Ile Lys Thr
                245                 250                 255

Thr Arg Tyr Thr Ile Gln Ala Thr Leu His Gly Asn Arg Phe Lys Gly
            260                 265                 270

Lys Ala Leu Ala Ala Asp Lys Gly Ala Thr Asn Gly Ser His Pro Phe
        275                 280                 285

Ile Ser Asp Ser Asp Ser Leu Glu Gly Gly Phe Tyr Gly Pro Lys Gly
    290                 295                 300

Glu Glu Leu Ala Gly Lys Phe Leu Ser Asn Asp Asn Lys Val Ala Ala
305                 310                 315                 320

Val Phe Gly Ala Lys Gln Lys Asp Lys Lys Asp Gly Glu Asn Ala Ala
                325                 330                 335

Gly Pro Ala Thr Glu Thr Val Ile Asp Ala Tyr Arg Ile Thr Gly Glu
            340                 345                 350

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

Leu Val Asp Gly Val Glu Leu Ser Leu Leu Pro Ser Glu Gly Asn Lys
    370                 375                 380

Ala Ala Phe Gln His Glu Ile Glu Gln Asn Gly Val Lys Ala Thr Val
385                 390                 395                 400

Cys Cys Ser Asn Leu Asp Tyr Met Ser Phe Gly Lys Leu Ser Lys Glu
                405                 410                 415

Asn Lys Asp Asp Met Phe Leu Gln Gly Val Arg Thr Pro Val Ser Asp
            420                 425                 430

Val Ala Ala Arg Thr Glu Ala Asn Ala Lys Tyr Arg Gly Thr Trp Tyr
        435                 440                 445

Gly Tyr Ile Ala Asn Gly Thr Ser Trp Ser Gly Glu Ala Ser Asn Gln
    450                 455                 460

Glu Gly Gly Asn Arg Ala Glu Phe Asp Val Asp Phe Ser Thr Lys Lys
465                 470                 475                 480

Ile Ser Gly Thr Leu Thr Ala Lys Asp Arg Thr Ser Pro Ala Phe Thr
                485                 490                 495

Ile Thr Ala Met Ile Lys Asp Asn Gly Phe Ser Gly Val Ala Lys Thr
            500                 505                 510

Gly Glu Asn Gly Phe Ala Leu Asp Pro Gln Asn Thr Gly Asn Ser His
        515                 520                 525

Tyr Thr His Ile Glu Ala Thr Val Ser Gly Gly Phe Tyr Gly Lys Asn
```

```
    530                 535                 540

Ala Ile Glu Met Gly Gly Ser Phe Ser Phe Pro Gly Asn Ala Pro Glu
545                 550                 555                 560

Gly Lys Gln Glu Lys Ala Ser Val Val Phe Gly Ala Lys Arg Gln Gln
                565                 570                 575

Leu Val Gln
```

<210> 118

<211> 762

<212> DNA

<213> Neisseria meningitidis

<400> 118

```
cagaaagata agaaggatgg ggaaaacgcg gcagggcctg caacggaaac cgtgatagat       60

gcataccgta ttaccggcga ggagtttaag aaagagcaaa tagacagttt tggagatgtg      120

aaaaagctgc tggttgacgg agtggagctt tcactgctgc cgtctgaggg caataaggcg      180

gcatttcagc acgagattga gcaaaacggc gtgaaggcaa cggtgtgttg ttccaacttg      240

gattacatga gttttgggaa gctgtcaaaa gaaaataaag acgatatgtt cctgcaaggt      300

gtccgcactc cagtatccga tgtggcggca aggacggagg caaacgccaa atatcgcggt      360

acttggtacg gatatattgc caacggcaca agctggagcg gcgaagcctc caatcaggaa      420

ggtggtaata gggcagagtt tgacgtggat ttttccacta aaaaaatcag tggcacactg      480

acggcaaaag accgtacgtc tcctgcgttt actattactg ccatgattaa ggacaacggt      540

ttttcaggtg tggcgaaaac cggtgaaaac ggctttgcgc tggatccgca aaataccgga      600

aattcccact atacgcatat tgaagccact gtatccggcg gtttctacgg caaaaacgcc      660

atcgagatgg gcggatcgtt ctcatttccg ggaaatgcac cagagggaaa acaagaaaaa      720

gcatcggtgg tattcggtgc gaaacgccaa cagcttgtgc aa                         762
```

<210> 119

<211> 254

<212> PRT

<213> Neisseria meningitidis

<400> 119

```
Gln Lys Asp Lys Lys Asp Gly Glu Asn Ala Ala Gly Pro Ala Thr Glu
1               5                   10                  15

Thr Val Ile Asp Ala Tyr Arg Ile Thr Gly Glu Glu Phe Lys Lys Glu
            20                  25                  30

Gln Ile Asp Ser Phe Gly Asp Val Lys Lys Leu Leu Val Asp Gly Val
        35                  40                  45

Glu Leu Ser Leu Leu Pro Ser Glu Gly Asn Lys Ala Ala Phe Gln His
    50                  55                  60
```

```
Glu Ile Glu Gln Asn Gly Val Lys Ala Thr Val Cys Cys Ser Asn Leu
65                  70                  75                  80

Asp Tyr Met Ser Phe Gly Lys Leu Ser Lys Glu Asn Lys Asp Asp Met
                85                  90                  95

Phe Leu Gln Gly Val Arg Thr Pro Val Ser Asp Val Ala Ala Arg Thr
            100                 105                 110

Glu Ala Asn Ala Lys Tyr Arg Gly Thr Trp Tyr Gly Tyr Ile Ala Asn
        115                 120                 125

Gly Thr Ser Trp Ser Gly Glu Ala Ser Asn Gln Glu Gly Gly Asn Arg
    130                 135                 140

Ala Glu Phe Asp Val Asp Phe Ser Thr Lys Lys Ile Ser Gly Thr Leu
145                 150                 155                 160

Thr Ala Lys Asp Arg Thr Ser Pro Ala Phe Thr Ile Thr Ala Met Ile
                165                 170                 175

Lys Asp Asn Gly Phe Ser Gly Val Ala Lys Thr Gly Glu Asn Gly Phe
            180                 185                 190

Ala Leu Asp Pro Gln Asn Thr Gly Asn Ser His Tyr Thr His Ile Glu
        195                 200                 205

Ala Thr Val Ser Gly Gly Phe Tyr Gly Lys Asn Ala Ile Glu Met Gly
    210                 215                 220

Gly Ser Phe Ser Phe Pro Gly Asn Ala Pro Glu Gly Lys Gln Glu Lys
225                 230                 235                 240

Ala Ser Val Val Phe Gly Ala Lys Arg Gln Gln Leu Val Gln
                245                 250
```

<210> 120

<211> 970

<212> DNA

<213> Neisseria meningitidis

<400> 120

```
tgtctgggtg gcggcggcag tttcgatttg gacagcgtgg aaaccgtgca agatatgcac       60

tccaaaccta agtatgagga tgaaaaaagc cagcctgaaa gccaacagga tgtatcggaa      120

aacagcggcg cggcttatgg ctttgcagta aaactacctc gccggaatgc acattttaat      180

cctaaatata aggaaaagca caaaccattg ggttcaatgg attggaaaaa actgcaaaga      240

ggagaaccaa atagttttag tgagagggat gaattggaaa aaaaacgggg tagttctgaa      300

cttattgaat caaaatggga agatgggcaa agtcgtgtag ttggttatac aaatttcact      360

tatgtccgtt cgggatatgt ttaccttaat aaaaataata ttgatattaa gaataatata      420

gttctttttg gacctgacgg atatctttac tataaaggga aagaaccttc caaggagctg      480

ggatgggaaa agataaactta taaaggtact tgggattatg ttactgatgc tatggaaaaa      540
```

caaaggtttg aaggattggg tagtgcagca ggaggagata aatcgggggc gttgtctgca 600

ttagaagaag gggtattgcg taatcaggca gaggcatcat ccggtcatac cgattttggt 660

atgactagtg agtttgaggt tgatttttct gataaaacaa taaagggcac actttatcgt 720

aacaaccgta ttactcaaaa taatagtgaa aacaaacaaa taaaaactac gcgttacacc 780

attcaagcaa ctcttcacgg caaccgtttc aaaggtaagg cgttggcggc agataaaggt 840

gcaacaaatg gaagtcatcc ctttatttcc gactccgaca gtttggaagg cggattttac 900

gggccgaaag gcgaggaact tgccggtaaa ttcttgagca acgacaacaa agttgcagcg 960

gtgtttggtg 970

<210> 121

<211> 320

<212> PRT

<213> Neisseria meningitidis

<400> 121

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

Gln Asp Met His Ser Lys Pro Lys Tyr Glu Asp Glu Lys Ser Gln Pro
20 25 30

Glu Ser Gln Gln Asp Val Ser Glu Asn Ser Gly Ala Ala Tyr Gly Phe
35 40 45

Ala Val Lys Leu Pro Arg Arg Asn Ala His Phe Asn Pro Lys Tyr Lys
50 55 60

Glu Lys His Lys Pro Leu Gly Ser Met Asp Trp Lys Lys Leu Gln Arg
65 70 75 80

Gly Glu Pro Asn Ser Phe Ser Glu Arg Asp Glu Leu Glu Lys Lys Arg
85 90 95

Gly Ser Ser Glu Leu Ile Glu Ser Lys Trp Glu Asp Gly Gln Ser Arg
100 105 110

Val Val Gly Tyr Thr Asn Phe Thr Tyr Val Arg Ser Gly Tyr Val Tyr
115 120 125

Leu Asn Lys Asn Asn Ile Asp Ile Lys Asn Asn Ile Val Leu Phe Gly
130 135 140

Pro Asp Gly Tyr Leu Tyr Tyr Lys Gly Lys Glu Pro Ser Lys Glu Leu
145 150 155 160

Pro Ser Glu Lys Ile Thr Tyr Lys Gly Thr Trp Asp Tyr Val Thr Asp
165 170 175

Ala Met Glu Lys Gln Arg Phe Glu Gly Leu Gly Ser Ala Ala Gly Gly
180 185 190

```
Asp Lys Ser Gly Ala Leu Ser Ala Leu Glu Glu Gly Val Leu Arg Asn
        195                 200                 205

Gln Ala Glu Ala Ser Ser Gly His Thr Asp Phe Gly Met Thr Ser Glu
    210                 215                 220

Phe Glu Val Asp Phe Ser Asp Lys Thr Ile Lys Gly Thr Leu Tyr Arg
225                 230                 235                 240

Asn Asn Arg Ile Thr Gln Asn Asn Ser Glu Asn Lys Gln Ile Lys Thr
                245                 250                 255

Thr Arg Tyr Thr Ile Gln Ala Thr Leu His Gly Asn Arg Phe Lys Gly
            260                 265                 270

Lys Ala Leu Ala Ala Asp Lys Gly Ala Thr Asn Gly Ser His Pro Phe
        275                 280                 285

Ile Ser Asp Ser Asp Ser Leu Glu Gly Gly Phe Tyr Gly Pro Lys Gly
    290                 295                 300

Glu Glu Leu Ala Gly Lys Phe Leu Ser Asn Asp Asn Lys Val Ala Ala
305                 310                 315                 320
```

<210> 122

<211> 2060

<212> DNA

<213> Neisseria meningitidis

<400> 122

```
tgtctgggcg gcggcggcag tttcgatctt gattctgtcg ataccgaagc cccgcgtccc       60

gcgccaaagt atcaagatgt ttcttccgaa aaaccgcaag cccaaaaaga ccaaggcgga      120

tacggttttg cgatgaggtt gaaacggagg aattggtatc cgggggcaga agaaagcgag      180

gttaaactga acgagagtga ttgggaggcg acgggattgc cgacaaaacc caaggaactt      240

cctaaacggc aaaaatcggt tattgaaaaa gtagaaacag acggcgacag cgatatttat      300

tcttcccccc atctcacacc atcaaaccat caaaacggca gcgctggcaa cggtgtaaat      360

caacctaaaa atcaggcaac aggtcacgaa aatttccaat atgtttattc cggttggttt      420

tataaacatg cagcgagtga aaaagatttc agtaacaaaa aaattaagtc aggcgacgat      480

ggttatatct tctatcacgg tgaaaaacct tcccgacaac ttcctgcttc tggaaaagtt      540

atctacaaag gtgtgtggca ttttgtaacc gatacaaaaa agggtcaaga ttttcgtgaa      600

attatccagc cttcaaaaaa acaaggcgac aggtatagcg gattttctgg tgatggcagc      660

gaagaatatt ccaacaaaaa cgaatccacg ctgaaagatg atcacgaggg ttatggtttt      720

acctcgaatt tagaagtgga tttcggcaat aagaaattga cgggtaaatt aatacgcaat      780

aatgcgagcc taaataataa tactaataat gacaaacata ccacccaata ctacagcctt      840

gatgcacaaa taacaggcaa ccgcttcaac ggcacggcaa cggcaactga caaaaaggag      900

aatgaaacca aactacatcc ctttgtttcc gactcgtctt ctttgaggcg cggcttttcc      960
```

ggcccgcagg gtgaggaatt gggtttccgc tttttgagcg acgatcaaaa agttgccgtt 1020

gtcggcagcg cgaaaaccaa agacaaactg gaaaatggcg cggcggcttc aggcagcaca 1080

ggtgcggcag catcgggcgg tgcggcaggc acgtcgtctg aaaacagtaa gctgaccacg 1140

gttttggatg cggttgaatt gacactaaac gacaagaaaa tcaaaaatct cgacaacttc 1200

agcaatgccg cccaactggt tgtcgacggc attatgattc cgctcctgcc caaggattcc 1260

gaaagcggga acactcaggc agataaaggt aaaaacggcg gaacagaatt tacccgcaaa 1320

tttgaacaca cgccggaaag tgataaaaaa gacgcccaag caggtacgca gacgaatggg 1380

gcgcaaaccg cttcaaatac ggcaggtgat accaatggca aaacaaaaac ctatgaagtc 1440

gaagtctgct gttccaacct caattatctg aaatacggaa tgttgacgcg caaaaacagc 1500

aagtccgcga tgcaggcagg aggaaacagt agtcaagctg atgctaaaac ggaacaagtt 1560

gaacaaagta tgttcctcca aggcgagcgt accgatgaaa aagagattcc aaccgaccaa 1620

aacgtcgttt atcgggggtc ttggtacggg catattgcca acggcacaag ctggagcggc 1680

aatgcttctg ataaagaggg cggcaacagg gcggaattta ctgtgaattt tgccgataaa 1740

aaaattaccg gcaagttaac cgctgaaaac aggcaggcgc aaacctttac cattgaggga 1800

atgattcagg gcaacggctt tgaaggtacg gcgaaaactg ctgagtcagg ttttgatctc 1860

gatcaaaaaa ataccacccg cacgcctaag gcatatatca cagatgccaa ggtaaagggc 1920

ggtttttacg ggcctaaagc cgaagagttg ggcggatggt ttgcctatcc gggcgataaa 1980

caaacggaaa aggcaacagc tacatccagc gatggaaatt cagcaagcag cgcgaccgtg 2040

gtattcggtg cgaaacgcca 2060

<210> 123

<211> 680

<212> PRT

<213> Neisseria meningitidis

<400> 123

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

Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser Ser Glu Lys Pro
20 25 30

Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Leu Lys
35 40 45

Arg Arg Asn Trp Tyr Pro Gly Ala Glu Glu Ser Glu Val Lys Leu Asn
50 55 60

Glu Ser Asp Trp Glu Ala Thr Gly Leu Pro Thr Lys Pro Lys Glu Leu
65 70 75 80

Pro Lys Arg Gln Lys Ser Val Ile Glu Lys Val Glu Thr Asp Gly Asp
85 90 95

Ser Asp Ile Tyr Ser Ser Pro Tyr Leu Thr Pro Ser Asn His Gln Asn
100 105 110

```
            100                 105                 110

Gly Ser Ala Gly Asn Gly Val Asn Gln Pro Lys Asn Gln Ala Thr Gly
        115                 120                 125

His Glu Asn Phe Gln Tyr Val Tyr Ser Gly Trp Phe Tyr Lys His Ala
    130                 135                 140

Ala Ser Glu Lys Asp Phe Ser Asn Lys Lys Ile Lys Ser Gly Asp Asp
145                 150                 155                 160

Gly Tyr Ile Phe Tyr His Gly Glu Lys Pro Ser Arg Gln Leu Pro Ala
                165                 170                 175

Ser Gly Lys Val Ile Tyr Lys Gly Val Trp His Phe Val Thr Asp Thr
            180                 185                 190

Lys Lys Gly Gln Asp Phe Arg Glu Ile Ile Gln Pro Ser Lys Lys Gln
        195                 200                 205

Gly Asp Arg Tyr Ser Gly Phe Ser Gly Asp Gly Ser Glu Glu Tyr Ser
    210                 215                 220

Asn Lys Asn Glu Ser Thr Leu Lys Asp Asp His Glu Gly Tyr Gly Phe
225                 230                 235                 240

Thr Ser Asn Leu Glu Val Asp Phe Gly Asn Lys Lys Leu Thr Gly Lys
                245                 250                 255

Leu Ile Arg Asn Asn Ala Ser Leu Asn Asn Asn Thr Asn Asn Asp Lys
            260                 265                 270

His Thr Thr Gln Tyr Tyr Ser Leu Asp Ala Gln Ile Thr Gly Asn Arg

        275                 280                 285

Phe Asn Gly Thr Ala Thr Ala Thr Asp Lys Lys Glu Asn Glu Thr Lys
    290                 295                 300

Leu His Pro Phe Val Ser Asp Ser Ser Ser Leu Ser Gly Gly Phe Phe
305                 310                 315                 320

Gly Pro Gln Gly Glu Glu Leu Gly Phe Arg Phe Leu Ser Asp Asp Gln
                325                 330                 335

Lys Val Ala Val Val Gly Ser Ala Lys Thr Lys Asp Lys Leu Glu Asn
            340                 345                 350

Gly Ala Ala Ala Ser Gly Ser Thr Gly Ala Ala Ala Ser Gly Gly Ala
        355                 360                 365

Ala Gly Thr Ser Ser Glu Asn Ser Lys Leu Thr Thr Val Leu Asp Ala
    370                 375                 380

Val Glu Leu Thr Leu Asn Asp Lys Lys Ile Lys Asn Leu Asp Asn Phe
385                 390                 395                 400
```

```
Ser Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met Ile Pro Leu Leu
                405                 410                 415

Pro Lys Asp Ser Glu Ser Gly Asn Thr Gln Ala Asp Lys Gly Lys Asn
            420                 425                 430

Gly Gly Thr Glu Phe Thr Arg Lys Phe Glu His Thr Pro Glu Ser Asp
        435                 440                 445

Lys Lys Asp Ala Gln Ala Gly Thr Gln Thr Asn Gly Ala Gln Thr Ala
    450                 455                 460

Ser Asn Thr Ala Gly Asp Thr Asn Gly Lys Thr Lys Thr Tyr Glu Val
465                 470                 475                 480

Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr Gly Met Leu Thr
                485                 490                 495

Arg Lys Asn Ser Lys Ser Ala Met Gln Ala Gly Gly Asn Ser Ser Gln
            500                 505                 510

Ala Asp Ala Lys Thr Glu Gln Val Glu Gln Ser Met Phe Leu Gln Gly
        515                 520                 525

Glu Arg Thr Asp Glu Lys Glu Ile Pro Thr Asp Gln Asn Val Val Tyr
    530                 535                 540

Arg Gly Ser Trp Tyr Gly His Ile Ala Asn Gly Thr Ser Trp Ser Gly
545                 550                 555                 560

Asn Ala Ser Asp Lys Glu Gly Gly Asn Arg Ala Glu Phe Thr Val Asn
                565                 570                 575

Phe Ala Asp Lys Lys Ile Thr Gly Lys Leu Thr Ala Glu Asn Arg Gln
            580                 585                 590

Ala Gln Thr Phe Thr Ile Glu Gly Met Ile Gln Gly Asn Gly Phe Glu
        595                 600                 605

Gly Thr Ala Lys Thr Ala Glu Ser Gly Phe Asp Leu Asp Gln Lys Asn
    610                 615                 620

Thr Thr Arg Thr Pro Lys Ala Tyr Ile Thr Asp Ala Lys Val Lys Gly
625                 630                 635                 640

Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr
                645                 650                 655

Pro Gly Asp Lys Gln Thr Glu Lys Ala Thr Ala Thr Ser Ser Asp Gly
            660                 665                 670

Asn Ser Ala Ser Ser Ala Thr Val
        675                 680
```

<210> 124

<211> 1030
<212> DNA
<213> Neisseria meningitidis

<400> 124

```
accaaagaca aactggaaaa tggcgcggcg gcttcaggca gcacaggtgc ggcagcatcg       60

ggcggtgcgg caggcacgtc gtctgaaaac agtaagctga ccacggtttt ggatgcggtt      120

gaattgacac taaacgacaa gaaaatcaaa aatctcgaca acttcagcaa tgccgcccaa      180

ctggttgtcg acggcattat gattccgctc ctgcccaagg attccgaaag cgggaacact      240

caggcagata aaggtaaaaa cggcggaaca gaatttaccc gcaaatttga acacacgccg      300

gaaagtgata aaaaagacgc ccaagcaggt acgcagacga atggggcgca aaccgcttca      360

aatacggcag gtgataccaa tggcaaaaca aaaacctatg aagtcgaagt ctgctgttcc      420

aacctcaatt atctgaaata cggaatgttg acgcgcaaaa acagcaagtc cgcgatgcag      480

gcaggaggaa acagtagtca agctgatgct aaaacggaac aagttgaaca aagtatgttc      540

ctccaaggcg agcgtaccga tgaaaaagag attccaaccg accaaaacgt cgtttatcgg      600

gggtcttggt acgggcatat tgccaacggc acaagctgga gcggcaatgc ttctgataaa      660

gagggcggca acagggcgga atttactgtg aattttgccg ataaaaaaat taccggcaag      720

ttaaccgctg aaaacaggca ggcgcaaacc tttaccattg agggaatgat tcagggcaac      780

ggctttgaag gtacggcgaa aactgctgag tcaggttttg atctcgatca aaaaaatacc      840

acccgcacgc ctaaggcata tatcacagat gccaaggtaa agggcggttt ttacgggcct      900

aaagccgaag agttgggcgg atggtttgcc tatccgggcg ataaacaaac ggaaaaggca      960

acagctacat ccagcgatgg aaattcagca agcagcgcga ccgtggtatt cggtgcgaaa     1020

cgccaacagc                                                            1030
```

<210> 125
<211> 343
<212> PRT
<213> Neisseria meningitidis

<400> 125

```
Thr Lys Asp Lys Leu Glu Asn Gly Ala Ala Ala Ser Gly Ser Thr Gly
1               5                  10                  15

Ala Ala Ala Ser Gly Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys
            20                  25                  30

Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys
        35                  40                  45

Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
    50                  55                  60

Gly Ile Met Ile Pro Leu Leu Pro Lys Asp Ser Glu Ser Gly Asn Thr
65                  70                  75                  80
```

```
Gln Ala Asp Lys Gly Lys Asn Gly Gly Thr Glu Phe Thr Arg Lys Phe
                85                  90                  95

Glu His Thr Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln
            100                 105                 110

Thr Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly
        115                 120                 125

Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
    130                 135                 140

Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln
145                 150                 155                 160

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

Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro
            180                 185                 190

Thr Asp Gln Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala
        195                 200                 205

Asn Gly Thr Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly Asn
    210                 215                 220

Arg Ala Glu Phe Thr Val Asn Phe Ala Asp Lys Lys Ile Thr Gly Lys
225                 230                 235                 240

Leu Thr Ala Glu Asn Arg Gln Ala Gln Thr Phe Thr Ile Glu Gly Met
                245                 250                 255

Ile Gln Gly Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala Glu Ser Gly
            260                 265                 270

Phe Asp Leu Asp Gln Lys Asn Thr Thr Arg Thr Pro Lys Ala Tyr Ile
        275                 280                 285

Thr Asp Ala Lys Val Lys Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu
    290                 295                 300

Leu Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Glu Lys Ala
305                 310                 315                 320

Thr Ala Thr Ser Ser Asp Gly Asn Ser Ala Ser Ser Ala Thr Val Val
                325                 330                 335

Phe Gly Ala Lys Arg Gln Gln
            340
```

<210> 126

<211> 1030

<212> DNA

<213> Neisseria meningitidis

<400> 126

```
tgtctgggcg gcggcggcag tttcgatctt gattctgtcg ataccgaagc cccgcgtccc       60

gcgccaaagt atcaagatgt ttcttccgaa aaaccgcaag cccaaaaaga ccaaggcgga      120

tacggttttg cgatgaggtt gaaacggagg aattggtatc cgggggcaga agaaagcgag      180

gttaaactga acgagagtga ttgggaggcg acgggattgc cgacaaaacc caaggaactt      240

cctaaacggc aaaaatcggt tattgaaaaa gtagaaacag acggcgacag cgatatttat      300

tcttcccccc atctcacacc atcaaaccat caaaacggca gcgctggcaa cggtgtaaat      360

caacctaaaa atcaggcaac aggtcacgaa aatttccaat atgtttattc cggttggttt      420

tataaacatg cagcgagtga aaaagatttc agtaacaaaa aaattaagtc aggcgacgat      480

ggttatatct tctatcacgg tgaaaaacct tcccgacaac ttcctgcttc tggaaaagtt      540

atctacaaag gtgtgtggca ttttgtaacc gatacaaaaa agggtcaaga ttttcgtgaa      600

attatccagc cttcaaaaaa acaaggcgac aggtatagcg gattttctgg tgatggcagc      660

gaagaatatt ccaacaaaaa cgaatccacg ctgaaagatg atcacgaggg ttatggtttt      720

acctcgaatt tagaagtgga tttcggcaat aagaaattga cgggtaaatt aatacgcaat      780

aatgcgagcc taaataataa tactaataat gacaaacata ccacccaata ctacagcctt      840

gatgcacaaa taacaggcaa ccgcttcaac ggcacggcaa cggcaactga caaaaaggag      900

aatgaaacca aactacatcc ctttgtttcc gactcgtctt ctttgagcgg cggctttttc      960

ggcccgcagg gtgaggaatt gggtttccgc tttttgagcg acgatcaaaa agttgccgtt     1020

gtcggcagcg                                                            1030
```

<210> 127

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 127

```
Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser Val Asp Thr Glu
1               5                  10                  15

Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser Ser Glu Lys Pro
            20                  25                  30

Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Leu Lys
        35                  40                  45

Arg Arg Asn Trp Tyr Pro Gly Ala Glu Glu Ser Glu Val Lys Leu Asn
    50                  55                  60

Glu Ser Asp Trp Glu Ala Thr Gly Leu Pro Thr Lys Pro Lys Glu Leu
65                  70                  75                  80

Pro Lys Arg Gln Lys Ser Val Ile Glu Lys Val Glu Thr Asp Gly Asp
                85                  90                  95

Ser Asp Ile Tyr Ser Ser Pro Tyr Leu Thr Pro Ser Asn His Gln Asn
```

```
            100                 105                 110

Gly Ser Ala Gly Asn Gly Val Asn Gln Pro Lys Asn Gln Ala Thr Gly
        115                 120                 125

His Glu Asn Phe Gln Tyr Val Tyr Ser Gly Trp Phe Tyr Lys His Ala
    130                 135                 140

Ala Ser Glu Lys Asp Phe Ser Asn Lys Lys Ile Lys Ser Gly Asp Asp
145                 150                 155                 160

Gly Tyr Ile Phe Tyr His Gly Glu Lys Pro Ser Arg Gln Leu Pro Ala
                165                 170                 175

Ser Gly Lys Val Ile Tyr Lys Gly Val Trp His Phe Val Thr Asp Thr
            180                 185                 190

Lys Lys Gly Gln Asp Phe Arg Glu Ile Ile Gln Pro Ser Lys Lys Gln
        195                 200                 205

Gly Asp Arg Tyr Ser Gly Phe Ser Gly Asp Gly Ser Glu Glu Tyr Ser
    210                 215                 220

Asn Lys Asn Glu Ser Thr Leu Lys Asp Asp His Glu Gly Tyr Gly Phe
225                 230                 235                 240

Thr Ser Asn Leu Glu Val Asp Phe Gly Asn Lys Lys Leu Thr Gly Lys
                245                 250                 255

Leu Ile Arg Asn Asn Ala Ser Leu Asn Asn Asn Thr Asn Asn Asp Lys
            260                 265                 270

His Thr Thr Gln Tyr Tyr Ser Leu Asp Ala Gln Ile Thr Gly Asn Arg
        275                 280                 285

Phe Asn Gly Thr Ala Thr Ala Thr Asp Lys Lys Glu Asn Glu Thr Lys
    290                 295                 300

Leu His Pro Phe Val Ser Asp Ser Ser Ser Leu Ser Gly Gly Phe Phe
305                 310                 315                 320

Gly Pro Gln Gly Glu Glu Leu Gly Phe Arg Phe Leu Ser Asp Asp Gln
                325                 330                 335

Lys Val Ala Val
            340
```

<210> 128

<211> 735

<212> DNA

<213> Neisseria meningitidis

<400> 128

```
ggatcctcgt ctgaaaacag taagctgacc acggttttgg atgcggttga attgacacta       60

aacgacaaga aaatcaaaaa tctcgacaac ttcagcaatg ccgcccaact ggttgtcgac      120
```

```
ggcattatga ttgatctggc cggaacagaa tttacccgca aatttgaaca cacgattaac      180

ggcaaaacct atgaagtcga agtctgctgt tccaacctca attatctgaa atacggaatg      240

ttgacgcgca aaggcaaaca ggttgaacaa agtatgttcc tccaaggcga gcgtaccgat      300

gaaaaagaga ttccaaccga ccaaaacgtc gtttatcggg ggtcttggta cgggcatatt      360

gccaacggca caagctggag cggcaatgct tctgataaag agggcggcaa cagggcggaa      420

tttactgtga attttgccga taaaaaaatt accggcaagt taaccgctga aaacaggcag      480

gcgcaaacct ttaccattga gggaatgatt cagggcaacg gctttgaagg tacggcgaaa      540

actgctgagt caggttttga tctcgatcaa aaaaatacca cccgcacgcc taaggcatat      600

atcacagatg ccaaggtaaa gggcggtttt tacgggccta aagccgaaga gttgggcgga      660

tggtttgcct atcataaaag cgataacggc agcgcgaccg tggtattcgg tgcgaaacgc      720

caacagcctg tgcaa                                                       735
```

<210> 129

<211> 245

<212> PRT

<213> Neisseria meningitidis

<400> 129

```
Gly Ser Ser Ser Glu Asn Ser Lys Leu Thr Thr Val Leu Asp Ala Val
1               5                   10                  15

Glu Leu Thr Leu Asn Asp Lys Lys Ile Lys Asn Leu Asp Asn Phe Ser
            20                  25                  30

Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met Ile Asp Leu Ala Gly
        35                  40                  45

Thr Glu Phe Thr Arg Lys Phe Glu His Thr Ile Asn Gly Lys Thr Tyr
    50                  55                  60

Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr Gly Met
65                  70                  75                  80

Leu Thr Arg Lys Gly Lys Gln Val Glu Gln Ser Met Phe Leu Gln Gly
                85                  90                  95

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

Arg Gly Ser Trp Tyr Gly His Ile Ala Asn Gly Thr Ser Trp Ser Gly
        115                 120                 125

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

Phe Ala Asp Lys Lys Ile Thr Gly Lys Leu Thr Ala Glu Asn Arg Gln
145                 150                 155                 160

Ala Gln Thr Phe Thr Ile Glu Gly Met Ile Gln Gly Asn Gly Phe Glu
                165                 170                 175
```

```
Gly Thr Ala Lys Thr Ala Glu Ser Gly Phe Asp Leu Asp Gln Lys Asn
            180                 185                 190

Thr Thr Arg Thr Pro Lys Ala Tyr Ile Thr Asp Ala Lys Val Lys Gly
        195                 200                 205

Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr
    210                 215                 220

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

Gln Gln Pro Val Gln
                245
```

<210> 130

<211> 945

<212> DNA

<213> Neisseria meningitidis

<400> 130

```
ggatcctcgt ctgaaaacag taagctgacc acggttttgg atgcggttga attgacacta       60

aacgacaaga aaatcaaaaa tctcgacaac ttcagcaatg ccgcccaact ggttgtcgac      120

ggcattatga ttccactcct cccagccaca aaagccgtct ttgatgagaa ccgcaaatac      180

ggcccggaat ttacccgcaa atttgaacac acggccaagg aaatcacaga gttgttgggc      240

agccgggctt tgctcaacgg caacagccgc aatacaaaag ccaccgcgcg ccgtacccgc      300

acctatgaag tcgaagtctg ctgttccaac ctcaattatc tgaaatacgg aatgttgacg      360

cgcaaagtta cttgggaaaa tgtgcggcaa actgccggcg gcgcagtcaa ccaacacaaa      420

aatgtcggcg tttacaaccg atatgccgtt gaacaaagta tgttcctcca aggcgagcgt      480

accgatgaaa aagagattcc aaccgaccaa aacgtcgttt atcgggggtc ttggtacggg      540

catattgcca acggcacaag ctggagcggc aatgcttctg ataaagaggg cggcaacagg      600

gcggaattta ctgtgaattt tgccgataaa aaaattaccg gcaagttaac cgctgaaaac      660

aggcaggcgc aaacctttac cattgaggga atgattcagg gcaacggctt tgaaggtacg      720

gcgaaaactg ctgagtcagg ttttgatctc gatcaaaaaa ataccacccg cacgcctaag      780

gcatatatca cagatgccaa ggtaaagggc ggtttttacg ggcctaaagc cgaagagttg      840

ggcggatggt ttgcctatac cgcgcaggcg gcattgggcg ggacgaggac ggcgggcagc      900

agcgcgaccg tggtattcgg tgcgaaacgc caacagcctg tgcaa                      945
```

<210> 131

<211> 315

<212> PRT

<213> Neisseria meningitidis

<400> 131

```
Gly Ser Ser Ser Glu Asn Ser Lys Leu Thr Thr Val Leu Asp Ala Val
```

```
1               5                   10                  15

Glu Leu Thr Leu Asn Asp Lys Lys Ile Lys Asn Leu Asp Asn Phe Ser
            20                  25                  30

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

Ala Thr Lys Ala Val Phe Asp Glu Asn Arg Lys Tyr Gly Pro Glu Phe
    50                  55                  60

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

Ser Arg Ala Leu Leu Asn Gly Asn Ser Arg Asn Thr Lys Ala Thr Ala
                85                  90                  95

Arg Arg Thr Arg Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn
            100                 105                 110

Tyr Leu Lys Tyr Gly Met Leu Thr Arg Lys Val Thr Trp Glu Asn Val
        115                 120                 125

Arg Gln Thr Ala Gly Gly Ala Val Asn Gln His Lys Asn Val Gly Val
    130                 135                 140

Tyr Asn Arg Tyr Ala Val Glu Gln Ser Met Phe Leu Gln Gly Glu Arg
145                 150                 155                 160

Thr Asp Glu Lys Glu Ile Pro Thr Asp Gln Asn Val Val Tyr Arg Gly
                165                 170                 175

Ser Trp Tyr Gly His Ile Ala Asn Gly Thr Ser Trp Ser Gly Asn Ala
            180                 185                 190

Ser Asp Lys Glu Gly Gly Asn Arg Ala Glu Phe Thr Val Asn Phe Ala
        195                 200                 205

Asp Lys Lys Ile Thr Gly Lys Leu Thr Ala Glu Asn Arg Gln Ala Gln
    210                 215                 220

Thr Phe Thr Ile Glu Gly Met Ile Gln Gly Asn Gly Phe Glu Gly Thr
225                 230                 235                 240

Ala Lys Thr Ala Glu Ser Gly Phe Asp Leu Asp Gln Lys Asn Thr Thr
                245                 250                 255

Arg Thr Pro Lys Ala Tyr Ile Thr Asp Ala Lys Val Lys Gly Gly Phe
            260                 265                 270

Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Thr Ala
        275                 280                 285

Gln Ala Ala Leu Gly Gly Thr Arg Thr Ala Gly Ser Ser Ala Thr Val
    290                 295                 300
```

```
Val Phe Gly Ala Lys Arg Gln Gln Pro Val Gln
305                 310                 315
```

<210> 132

<211> 670

<212> PRT

<213> Neisseria meningitidis

<400> 132

```
Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser Val Asp Thr Glu
1               5                   10                  15

Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser Ser Glu Lys Pro
            20                  25                  30

Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Phe Lys
        35                  40                  45

Arg Arg Asn Trp His Pro Arg Val Asn Pro Lys Glu Asp Lys Ile Glu
    50                  55                  60

Leu Ser Glu Asn Asp Trp Glu Gln Thr Asp Asn Gly Asn Ile Lys Thr
65                  70                  75                  80

Pro Ser Lys Gln Lys Asn Ile Ile Asn Ala Leu Leu Gly Ser Glu Gly
                85                  90                  95

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

Thr Asp His His Asn Phe Gln Tyr Val Trp Ser Gly Phe Phe Tyr Lys
        115                 120                 125

His Ile Gln Thr Lys Phe Glu Thr Thr Gly Gly Lys Met Thr Ala Arg
    130                 135                 140

Ser Gly Pro Asp Gly Tyr Ile Phe Tyr Lys Gly Lys Asp Pro Ser Arg
145                 150                 155                 160

Lys Leu Pro Val Ser Gly Glu Val Met Tyr Lys Gly Thr Trp Asp Phe
                165                 170                 175

Leu Thr Asp Val Lys Ala Asn Gln Lys Phe Thr Asp Leu Gly Asn Ala
            180                 185                 190

Ser Thr Lys Pro Gly Asp Arg Tyr Ser Ala Phe Ser Gly Glu Leu Asp
        195                 200                 205

Tyr Ile Val Lys Gln Glu Asn Asp Lys Lys Asp Gly His Val Gly Leu
    210                 215                 220

Gly Leu Thr Thr Glu Ile Thr Val Asp Phe Glu Lys Lys Thr Leu Ser
225                 230                 235                 240

Gly Lys Leu Ile Lys Asn Asn Ser Val Ile Thr Thr Asn Asn Asp Lys
                245                 250                 255
```

```
His Thr Thr Gln Tyr Tyr Ser Leu Glu Ala Thr Leu Lys Gly Asn Arg
            260                 265                 270

Phe Asn Gly Lys Ala Thr Ala Thr Asp Lys Pro Lys Glu Asn Glu Ile
        275                 280                 285

Lys Gln His Pro Phe Val Ser Asp Ser Ser Ser Leu Ser Gly Gly Phe
    290                 295                 300

Phe Gly Pro Gln Gly Glu Glu Leu Gly Phe Arg Phe Leu Ser Asp Asp

305                 310                 315                 320

Lys Lys Val Ala Val Val Gly Ser Ala Lys Thr Lys Asp Lys Ala Glu
                325                 330                 335

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

Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys Leu Thr
        355                 360                 365

Thr Val Leu Asp Ala Val Glu Leu Lys Ser Gly Asp Lys Glu Val Lys
    370                 375                 380

Lys Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp Gly Ile
385                 390                 395                 400

Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly Ser Asn Gln Ala
                405                 410                 415

Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe Asn His
            420                 425                 430

Thr Pro Lys Ser Asp Glu Lys Asp Thr Gln Ala Gly Thr Ala Glu Asn
        435                 440                 445

Gly Asn Pro Ala Ala Ser Asn Thr Ala Gly Asp Ala Asn Gly Lys Thr
    450                 455                 460

Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys
465                 470                 475                 480

Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln Ala Gly
                485                 490                 495

Glu Ser Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu Gln Ser
            500                 505                 510

Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Asn Asp
        515                 520                 525

Gln Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Asn Gly
    530                 535                 540
```

```
Thr Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly Asn Arg Ala
545                 550                 555                 560

Asp Phe Thr Val Asn Phe Gly Thr Lys Lys Ile Asn Gly Thr Leu Thr
                565                 570                 575

Ala Asp Asn Arg Gln Ala Ala Thr Phe Thr Ile Val Gly Asp Ile Glu
            580                 585                 590

Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala Asp Ser Gly Phe Asp
        595                 600                 605

Leu Asp Gln Ser Asn Asn Thr Arg Thr Pro Lys Ala Tyr Ile Thr Asn
    610                 615                 620

Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly
625                 630                 635                 640

Gly Trp Phe Ala Tyr Ser Asp Asp Lys Gln Thr Lys Asn Ala Thr Asp
                645                 650                 655

Ala Ser Gly Asn Gly Asn Ser Ala Ser Ser Ala Thr Val Val
            660                 665                 670
```

<210> 133

<211> 660

<212> PRT

<213> Neisseria meningitidis

<400> 133

```
Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser Val Asp Thr Glu
1               5                   10                  15

Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser Ser Glu Lys Pro
            20                  25                  30

Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Phe Lys
        35                  40                  45

Arg Arg Asn Trp Tyr Gln Arg Ala Asn Pro Lys Glu Asp Glu Ile Lys
    50                  55                  60

Leu Ser Glu Asp Asp Trp Glu Gln Thr Asp Asp Gly Asp Ile Lys Asn
65                  70                  75                  80

Pro Ser Lys Gln Lys Asn Ile Ile Asn Ala Leu Pro Gly Asn Asn Glu
                85                  90                  95

Gly Ala Leu Leu Gln Asp Ser Ser Gln Glu Asn Gln Gly Ile Ser Lys
            100                 105                 110

Val Lys Asp Tyr His Asn Phe Gln Tyr Val Trp Ser Gly Phe Phe Tyr
        115                 120                 125

Lys Gln Ile Lys Asn Thr Ile Glu Lys Asn Gly Ser Ser Ile Thr Ala
```

```
    130                 135                 140

Ala Arg Asn Gly Pro Asp Gly Tyr Ile Phe Tyr Lys Gly Lys Asp Pro
145                 150                 155                 160

Ser Arg Lys Leu Pro Val Ser Gly Glu Val Met Tyr Lys Gly Thr Trp
                165                 170                 175

Asp Phe Leu Thr Asp Val Lys Ala Asn Gln Lys Phe Thr Asp Leu Gly
            180                 185                 190

Asn Ala Ser Thr Lys Pro Gly Asp Arg Tyr Ser Ala Phe Ser Gly Glu
        195                 200                 205

Leu Asp Tyr Ile Val Lys Gln Glu Asn Asp Lys Lys Asp Gly His Val
    210                 215                 220

Gly Leu Gly Leu Thr Thr Glu Ile Thr Val Asp Phe Glu Lys Lys Thr
225                 230                 235                 240

Leu Ser Gly Lys Leu Ile Lys Asn Asn Ser Val Ile Thr Thr Asn Asn
                245                 250                 255

Asp Lys His Thr Thr Gln Tyr Tyr Ser Leu Glu Ala Thr Leu Lys Gly
            260                 265                 270

Asn Arg Phe Asn Gly Lys Ala Thr Ala Thr Asp Lys Pro Lys Glu Asn
        275                 280                 285

Glu Thr Lys Gln His Pro Phe Val Ser Asp Ser Ser Ser Leu Ser Gly
    290                 295                 300

Gly Phe Phe Gly Pro Gln Gly Glu Glu Leu Gly Phe Arg Phe Leu Ser
305                 310                 315                 320

Asp Asp Lys Lys Val Ala Val Val Gly Ser Ala Lys Thr Lys Asp Lys
                325                 330                 335

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

Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys Leu Thr Thr Val
        355                 360                 365

Leu Asp Ala Val Glu Leu Lys Ser Gly Gly Lys Glu Val Lys Asn Leu
    370                 375                 380

Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met Ile
385                 390                 395                 400

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

Gly Lys Asn Gly Gly Thr Glu Phe Thr Arg Lys Phe Glu His Thr Pro
            420                 425                 430

Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Ala Glu Asn Gly Asn
        435                 440                 445
```

```
        435                 440                 445

Pro Ala Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly Lys Thr Lys Thr
    450                 455                 460

Tyr Ala Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr Gly
465                 470                 475                 480

Leu Leu Thr Arg Lys Thr Ala Gly Asn Thr Gly Glu Gly Gly Asn Gly
                485                 490                 495

Ala Ala Gln Thr Asp Ala Gln Ser Met Phe Leu Gln Gly Glu Arg Thr
            500                 505                 510

Asp Glu Lys Glu Ile Pro Asn Asp Gln Asn Ile Val Tyr Arg Gly Ser
        515                 520                 525

Trp Tyr Gly His Ile Ala Asn Gly Thr Ser Trp Ser Gly Asn Ala Ser
    530                 535                 540

Asp Lys Glu Gly Gly Asn Arg Ala Glu Phe Thr Val Asn Phe Ala Asp
545                 550                 555                 560

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

Phe Thr Ile Thr Ala Thr Ile Gln Gly Asn Gly Phe Glu Gly Thr Ala
            580                 585                 590

Lys Thr Gly Asp Asp Gly Phe Ala Leu Asp Thr Lys Asn Thr Val Asp
        595                 600                 605

Thr His Lys Ala His Ile Thr Asp Ala Asn Val Gln Gly Gly Phe Tyr
    610                 615                 620

Gly Pro Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly Asp
625                 630                 635                 640

Arg Gln Ala Gln Pro Ser Ala Ser Gly Ser Gly Thr Ser Ala Ala Asn
                645                 650                 655

Ser Ala Thr Val
            660
```

<210> 134

<211> 640

<212> PRT

<213> Neisseria meningitidis

<400> 134

```
Pro Ala Pro Lys Tyr Gln Asp Val Ser Ser Glu Lys Pro Gln Ala Gln
1               5                   10                  15

Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Leu Lys Arg Arg Asn
            20                  25                  30

Trp His Thr Gln Ala Asn Pro Lys Glu Asp Glu Ile Lys Leu Ser Glu
```

```
Trp His Thr Gln Ala Asn Pro Lys Glu Asp Glu Ile Lys Leu Ser Glu
        35                  40                  45

Asn Asp Trp Glu Ala Thr Gly Leu Pro Gly Asn Pro Lys Asn Leu Pro
    50                  55                  60

Glu Arg Gln Lys Ser Val Ile Glu Lys Val Glu Thr Asp Asp Gly Ser
65                  70                  75                  80

Asn Ile Tyr Ser Ser Pro Tyr Leu Thr Gln Ser Asn His Pro Asn Gly
                85                  90                  95

Asn Thr Gly Asn Gly Thr Asn Leu Pro Lys Asn Glu Val Thr Asp Tyr
            100                 105                 110

Lys Asp Phe Lys Tyr Val Tyr Ser Gly Trp Phe Tyr Lys His Ala Lys
        115                 120                 125

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

Tyr Ile Phe Tyr His Gly Lys Glu Pro Ser Arg Gln Leu Pro Val Ser
145                 150                 155                 160

Glu Lys Ile Thr Tyr Lys Gly Val Trp His Phe Val Thr Asp Thr Lys
                165                 170                 175

Asn Gly Gln Lys Phe Tyr Asp Ile Ile Gln Pro Ser Lys Lys Gln Gly
            180                 185                 190

Asp Arg Tyr Ser Gly Phe Ser Gly Asp Asp Asp Glu Gln Tyr Ser Asn
        195                 200                 205

Lys Asn Asp Met Leu Lys Gly Asp His Glu Gly Tyr Gly Phe Thr Ser
    210                 215                 220

Asn Leu Glu Val Asp Phe Asp Asp Lys Lys Leu Thr Gly Lys Leu Ile
225                 230                 235                 240

Arg Asn Asp Lys Val Thr Asn Ala Thr Thr Gly Asn Lys His Thr Thr
                245                 250                 255

Gln Tyr Tyr Ser Leu Glu Ala Gln Val Thr Gly Asn Arg Phe Asn Gly
            260                 265                 270

Lys Ala Ile Ala Thr Asp Lys Pro Gln Glu Asn Gly Thr Lys Gln His
        275                 280                 285

Pro Phe Val Ser Asp Ser Ser Ser Leu Ser Gly Gly Phe Phe Gly Pro
    290                 295                 300

Gln Gly Glu Glu Leu Gly Phe Arg Phe Leu Ser Asp Asp Gln Lys Val
305                 310                 315                 320

Ala Val Val Gly Ser Ala Lys Thr Lys Asp Lys Pro Ala Asn Gly Asn
                325                 330                 335
```

```
Thr Ala Ala Ala Ser Gly Gly Thr Asp Ala Ala Ala Ser Gly Gly Thr
            340                 345                 350

Ala Gly Thr Pro Ser Glu Ser Thr Lys Leu Thr Thr Val Leu Asp Ala
        355                 360                 365

Val Glu Leu Lys Ser Gly Asp Lys Glu Val Lys Lys Leu Asp Asn Phe
    370                 375                 380

Ser Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met Ile Pro Leu Leu
385                 390                 395                 400

Pro Glu Ala Ser Glu Ser Gly Asn Asn Gln Ala Asn Gln Gly Thr Asn
                405                 410                 415

Gly Gly Thr Ala Phe Thr Arg Lys Phe Asn His Thr Pro Lys Ser Asp

            420                 425                 430

Glu Lys Asp Thr Gln Ala Gly Thr Ala Glu Asn Gly Asn Pro Ala Ala
        435                 440                 445

Ser Asn Thr Ala Gly Asp Ala Asn Gly Lys Thr Lys Thr Tyr Glu Val
    450                 455                 460

Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr Gly Leu Leu Thr
465                 470                 475                 480

Arg Lys Thr Ala Gly Asn Thr Gly Glu Gly Gly Asn Gly Ser Pro Thr
                485                 490                 495

Ala Ala Gln Thr Asp Ala Gln Ser Met Phe Leu Gln Gly Glu Arg Thr
            500                 505                 510

Asp Glu Lys Glu Ile Pro Lys Glu Gln Gln Asp Ile Val Tyr Arg Gly
        515                 520                 525

Ser Trp Tyr Gly His Ile Ala Asn Gly Thr Ser Trp Ser Gly Asn Ala
    530                 535                 540

Ser Asp Lys Glu Gly Gly Asn Arg Ala Glu Phe Thr Val Asn Phe Gly
545                 550                 555                 560

Asp Lys Lys Ile Thr Gly Thr Leu Thr Ala Asp Asn Arg Gln Ala Ala
                565                 570                 575

Thr Phe Thr Ile Glu Gly Asp Ile Glu Gly Asn Gly Phe Ser Gly Thr
            580                 585                 590

Ala Lys Thr Asp Asn Leu Gly Phe Asp Leu Asp Gln Ser Asp Asn Thr
        595                 600                 605

Arg Thr Pro Lys Ala Tyr Ile Thr Asp Ala Lys Val Gln Gly Gly Phe
    610                 615                 620
```

```
Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly
625                 630                 635                 640
```

<210> 135

<211> 700

<212> PRT

<213> Neisseria meningitidis

<400> 135

```
Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser Val Asp Thr Glu

1               5                   10                  15

Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser Ser Glu Lys Pro
            20                  25                  30

Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Leu Lys
        35                  40                  45

Arg Arg Asn Trp His Pro Gln Ala Asn Pro Lys Glu Asp Glu Ile Lys
    50                  55                  60

Leu Ser Glu Asn Asp Trp Glu Ala Thr Gly Leu Pro Gly Asn Pro Lys
65                  70                  75                  80

Asn Leu Pro Glu Arg Gln Lys Ser Val Ile Glu Lys Val Lys Thr Gly
                85                  90                  95

Ser Asp Ser Asn Ile Tyr Ser Ser Pro Tyr Leu Thr Gln Ser Asn His
            100                 105                 110

Gln Asn Gly Ser Ala Asn Gln Pro Lys Asn Glu Val Lys Asp Tyr Lys
        115                 120                 125

Glu Phe Lys Tyr Val Tyr Ser Gly Trp Phe Tyr Lys His Ala Lys Leu
    130                 135                 140

Glu Ile Ile Lys Glu Asn Asn Leu Ile Lys Gly Ala Lys Ser Gly Asp
145                 150                 155                 160

Asp Gly Tyr Ile Phe Tyr His Gly Glu Lys Pro Ser Arg Gln Leu Pro
                165                 170                 175

Val Ser Gly Glu Val Thr Tyr Lys Gly Val Trp His Phe Val Thr Asp
            180                 185                 190

Thr Lys Gln Gly Gln Lys Phe Asn Asp Ile Leu Gly Thr Ser Lys Lys
        195                 200                 205

Gln Gly Asp Arg Tyr Ser Gly Phe Pro Gly Asp Asp Gly Glu Glu Tyr
    210                 215                 220

Ser Asn Lys Asn Glu Ala Thr Leu Gln Gly Ser Gln Glu Gly Tyr Gly
225                 230                 235                 240
```

```
Phe Thr Ser Asn Leu Lys Val Asp Phe Asn Lys Lys Lys Leu Thr Gly
                245                 250                 255

Glu Leu Ile Arg Asn Asn Arg Val Thr Asn Ala Thr Ala Asn Asp Lys
            260                 265                 270

Tyr Thr Thr Gln Tyr Tyr Ser Leu Glu Ala Gln Val Thr Gly Asn Arg
        275                 280                 285

Phe Asn Gly Lys Ala Thr Ala Thr Asp Lys Pro Gly Thr Gly Glu Thr
    290                 295                 300

Lys Gln His Pro Phe Val Ser Asp Ser Ser Ser Leu Ser Gly Gly Phe
305                 310                 315                 320

Phe Gly Pro Lys Gly Glu Glu Leu Gly Phe Arg Phe Leu Ser Asn Asp
                325                 330                 335

Gln Lys Val Ala Val Val Gly Ser Ala Lys Thr Gln Asp Lys Ala Ala
            340                 345                 350

Asn Gly Asn Thr Ala Ala Ala Ser Gly Gly Thr Asp Ala Ala Ala Ser
        355                 360                 365

Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys Leu Thr Thr Val
    370                 375                 380

Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys Ile Lys Asn Leu
385                 390                 395                 400

Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met Ile
                405                 410                 415

Pro Leu Leu Pro Glu Thr Ser Glu Ser Gly Ser Asn Gln Ala Asp Lys
            420                 425                 430

Gly Lys Lys Gly Lys Asn Gly Lys Asn Gly Gly Thr Asp Phe Thr Tyr
        435                 440                 445

Lys Thr Thr Tyr Thr Pro Lys Asn Asp Asp Lys Asp Thr Lys Ala Gln
    450                 455                 460

Thr Gly Ala Ala Gly Ser Ser Gly Ala Gln Thr Asp Leu Gly Lys Ala
465                 470                 475                 480

Asp Val Asn Gly Gly Lys Ala Glu Thr Lys Thr Tyr Glu Val Glu Val
                485                 490                 495

Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr Gly Met Leu Thr Arg Lys
            500                 505                 510

Asn Ser Lys Ser Ala Met Gln Ala Gly Gly Asn Ser Ser Gln Ala Asp
        515                 520                 525

Ala Lys Thr Glu Gln Val Glu Gln Ser Met Phe Leu Gln Gly Glu Arg
    530                 535                 540
```

```
Thr Asp Glu Lys Glu Ile Pro Asn Asp Gln Asn Val Val Tyr Arg Gly
545                 550                 555                 560

Ser Trp Tyr Gly His Ile Ala Ser Ser Thr Ser Trp Ser Gly Asn Ala
                565                 570                 575

Ser Asn Ala Thr Ser Gly Asn Arg Ala Glu Phe Thr Val Asn Phe Asp
            580                 585                 590

Thr Lys Lys Ile Asn Gly Thr Leu Thr Ala Glu Asn Arg Gln Glu Ala
        595                 600                 605

Thr Phe Thr Ile Asp Gly Lys Ile Glu Gly Asn Gly Phe Ser Gly Thr
    610                 615                 620

Ala Lys Thr Ala Asp Leu Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr
625                 630                 635                 640

Gly Thr Pro Lys Ala Tyr Ile Thr Asp Ala Lys Val Gln Gly Gly Phe
                645                 650                 655

Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly
            660                 665                 670

Asp Lys Gln Thr Glu Lys Ala Thr Val Ala Ser Gly Asp Gly Asn Ser
        675                 680                 685

Ala Ser Ser Ala Thr Val Val Phe Gly Ala Lys Arg
    690                 695                 700
```

<210> 136

<211> 680

<212> PRT

<213> Neisseria meningitidis

<400> 136

```
Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser Val Asp Thr Glu
1               5                   10                  15

Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Phe Ser Glu Lys Pro
            20                  25                  30

Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Leu Lys
        35                  40                  45

Arg Arg Asn Trp Tyr Pro Gln Ala Lys Glu Asp Glu Val Lys Leu Asp
    50                  55                  60

Glu Ser Asp Trp Glu Ala Thr Gly Leu Pro Asp Glu Pro Lys Glu Leu
65                  70                  75                  80

Pro Lys Arg Gln Lys Ser Val Ile Glu Lys Val Glu Thr Asp Ser Asp
                85                  90                  95

Asn Asn Ile Tyr Ser Ser Pro Tyr Leu Lys Pro Ser Asn His Gln Asn
            100                 105                 110
```

```
Gly Asn Thr Gly Asn Gly Ile Asn Gln Pro Lys Asn Gln Ala Lys Asp
        115                 120                 125

Tyr Glu Asn Phe Lys Tyr Val Tyr Ser Gly Trp Phe Tyr Lys His Ala
    130                 135                 140

Lys Arg Glu Phe Asn Leu Lys Val Glu Pro Lys Ser Ala Lys Asn Gly
145                 150                 155                 160

Asp Asp Gly Tyr Ile Phe Tyr His Gly Lys Glu Pro Ser Arg Gln Leu
                165                 170                 175

Pro Ala Ser Gly Lys Ile Thr Tyr Lys Gly Val Trp His Phe Ala Thr
            180                 185                 190

Asp Thr Lys Lys Gly Gln Lys Phe Arg Glu Ile Ile Gln Pro Ser Lys
        195                 200                 205

Ser Gln Gly Asp Arg Tyr Ser Gly Phe Ser Gly Asp Asp Gly Glu Glu
    210                 215                 220

Tyr Ser Asn Lys Asn Lys Ser Thr Leu Thr Asp Gly Gln Glu Gly Tyr
225                 230                 235                 240

Gly Phe Thr Ser Asn Leu Glu Val Asp Phe His Asn Lys Lys Leu Thr
                245                 250                 255

Gly Lys Leu Ile Arg Asn Asn Ala Asn Thr Asp Asn Asn Gln Ala Thr
            260                 265                 270

Thr Thr Gln Tyr Tyr Ser Leu Glu Ala Gln Val Thr Gly Asn Arg Phe
        275                 280                 285

Asn Gly Lys Ala Thr Ala Thr Asp Lys Pro Gln Gln Asn Ser Glu Thr
    290                 295                 300

Lys Glu His Pro Phe Val Ser Asp Ser Ser Ser Leu Ser Gly Gly Phe
305                 310                 315                 320

Phe Gly Pro Gln Gly Glu Glu Leu Gly Phe Arg Phe Leu Ser Asp Asp
                325                 330                 335

Gln Lys Val Ala Val Val Gly Ser Ala Lys Thr Lys Asp Lys Pro Ala
            340                 345                 350

Asn Gly Asn Thr Ala Ala Ala Ser Gly Gly Thr Asp Ala Ala Ala Ser
        355                 360                 365

Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Gly Lys Leu Thr Thr Val
    370                 375                 380

Leu Asp Ala Val Glu Leu Lys Leu Gly Asp Lys Glu Val Gln Lys Leu
385                 390                 395                 400

Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met Ile
                405                 410                 415
```

```
Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly Asn Asn Gln Ala Asn Gln
            420                 425                 430

Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe Asp His Thr Pro
        435                 440                 445

Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln Thr Asn Gly Ala
    450                 455                 460

Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly Lys Thr Lys Thr
465                 470                 475                 480

Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr Gly
                485                 490                 495

Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln Ala Gly Glu Ser
            500                 505                 510

Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu Gln Ser Met Phe
        515                 520                 525

Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Ser Glu Gln Asn

    530                 535                 540

Ile Val Tyr Arg Gly Ser Trp Tyr Gly Tyr Ile Ala Asn Asp Lys Ser
545                 550                 555                 560

Thr Ser Trp Ser Gly Asn Ala Ser Asn Ala Thr Ser Gly Asn Arg Ala
                565                 570                 575

Glu Phe Thr Val Asn Phe Ala Asp Lys Lys Ile Thr Gly Thr Leu Thr
            580                 585                 590

Ala Asp Asn Arg Gln Glu Ala Thr Phe Thr Ile Asp Gly Asn Ile Lys
        595                 600                 605

Asp Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala Glu Ser Gly Phe Asp
    610                 615                 620

Leu Asp Gln Ser Asn Thr Thr Arg Thr Pro Lys Ala Tyr Ile Thr Asp
625                 630                 635                 640

Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly
                645                 650                 655

Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Lys Asn Ala Thr Asn
            660                 665                 670

Ala Ser Gly Asn Ser Ser Ala Thr
        675                 680
```

<210> 137

<211> 680

<212> PRT

<213> Neisseria meningitidis

<400> 137

```
Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser Val Asp Thr Glu
1               5                  10                  15

Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser Ser Glu Lys Pro
            20                  25                  30

Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Leu Lys
        35                  40                  45

Arg Arg Asn Trp Tyr Pro Gln Ala Lys Glu Asp Glu Val Lys Leu Asp
    50                  55                  60

Glu Ser Asp Trp Glu Ala Thr Gly Leu Pro Asp Glu Pro Lys Glu Leu

65                  70                  75                  80

Pro Lys Arg Gln Lys Ser Val Ile Glu Lys Val Glu Thr Asp Ser Asp
                85                  90                  95

Asn Asn Ile Tyr Ser Ser Pro Tyr Leu Lys Pro Ser Asn His Gln Asn
            100                 105                 110

Gly Asn Thr Gly Asn Gly Ile Asn Gln Pro Lys Asn Gln Ala Lys Asp
        115                 120                 125

Tyr Glu Asn Phe Lys Tyr Val Tyr Ser Gly Trp Phe Tyr Lys His Ala
    130                 135                 140

Lys Arg Glu Phe Asn Leu Lys Val Glu Pro Lys Ser Ala Lys Asn Gly
145                 150                 155                 160

Asp Asp Gly Tyr Ile Phe Tyr His Gly Lys Glu Pro Ser Arg Gln Leu
                165                 170                 175

Pro Ala Ser Gly Lys Ile Thr Tyr Lys Gly Val Trp His Phe Ala Thr
            180                 185                 190

Asp Thr Lys Lys Gly Gln Lys Phe Arg Glu Ile Ile Gln Pro Ser Lys
        195                 200                 205

Ser Gln Gly Asp Arg Tyr Ser Gly Phe Ser Gly Asp Asp Gly Glu Glu
    210                 215                 220

Tyr Ser Asn Lys Asn Lys Ser Thr Leu Thr Asp Gly Gln Glu Gly Tyr
225                 230                 235                 240

Gly Phe Thr Ser Asn Leu Glu Val Asp Phe His Asn Lys Lys Leu Thr
                245                 250                 255

Gly Lys Leu Ile Arg Asn Asn Ala Asn Thr Asp Asn Asn Gln Ala Thr
            260                 265                 270
```

```
Thr Thr Gln Tyr Tyr Ser Leu Glu Ala Gln Val Thr Gly Asn Arg Phe
        275                 280                 285

Asn Gly Lys Ala Thr Ala Thr Asp Lys Pro Gln Asn Ser Glu Thr Lys
    290                 295                 300

Glu His Pro Phe Val Ser Asp Ser Ser Ser Leu Ser Gly Gly Phe Phe
305                 310                 315                 320

Gly Pro Gln Gly Glu Glu Leu Gly Phe Arg Phe Leu Ser Asp Asp Gln
                325                 330                 335

Lys Val Ala Val Val Gly Ser Ala Lys Thr Lys Asp Lys Pro Ala Asn
            340                 345                 350

Gly Asn Thr Ala Ala Ala Ser Gly Gly Thr Asp Ala Ala Ala Ser Asn
        355                 360                 365

Gly Ala Ala Gly Thr Ser Ser Glu Asn Gly Lys Leu Thr Thr Val Leu
    370                 375                 380

Asp Ala Val Glu Leu Lys Leu Gly Asp Lys Glu Val Gln Lys Leu Asp
385                 390                 395                 400

Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met Ile Pro
                405                 410                 415

Leu Leu Pro Glu Ala Ser Glu Ser Gly Asn Asn Gln Ala Asn Gln Gly
            420                 425                 430

Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe Asp His Thr Pro Glu
        435                 440                 445

Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln Thr Asn Gly Ala Gln
    450                 455                 460

Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly Lys Thr Lys Thr Tyr
465                 470                 475                 480

Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr Gly Met
                485                 490                 495

Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln Ala Gly Glu Ser Ser
            500                 505                 510

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

Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Ser Glu Gln Asn Val
    530                 535                 540

Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Asn Gly Thr Ser Trp
545                 550                 555                 560

Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly Asn Arg Ala Glu Phe Thr
                565                 570                 575
```

```
Val Asp Phe Gly Ala Lys Lys Ile Asn Gly Lys Leu Thr Ala Glu Asn
            580                 585                 590

Arg Gln Ala Ala Thr Phe Thr Ile Glu Gly Asp Ile Glu Gly Asn Gly
        595                 600                 605

Phe Ser Gly Thr Ala Lys Thr Ala Glu Ser Gly Phe Asp Leu Asp Gln
    610                 615                 620

Ser Asn Thr Thr Arg Thr Pro Lys Ala Tyr Ile Thr Asp Ala Lys Val
625                 630                 635                 640

Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly Trp Phe
                645                 650                 655

Ala Tyr Pro Gly Asp Lys Gln Thr Lys Asn Ala Thr Asn Ala Ser Gly
            660                 665                 670

Asn Ser Ser Ala Thr Val Val Phe
        675                 680
```

<210> 138

<211> 690

<212> PRT

<213> Neisseria meningitidis

<400> 138

```
Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser Val Asp Thr Glu
1               5                   10                  15

Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser Ser Glu Thr Pro
            20                  25                  30

Lys Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Phe Lys
        35                  40                  45

Arg Leu Asn Arg His Pro Lys Ala Met Pro Gln Glu Asn Glu Val Lys
    50                  55                  60

Leu Lys Asn Asp Asp Trp Glu Val Thr Gly Leu Pro Thr Glu Pro Lys
65                  70                  75                  80

Lys Leu Pro Leu Lys Gln Glu Ser Val Ile Leu Gln Val Gln Ala Ser
                85                  90                  95

Asn Gly Asp Asn Asn Ile Tyr Thr Ser Pro Tyr Leu Thr Gln Ser Ser
            100                 105                 110

His Asn Ser His Asn Gly Ser Val Asn Gly Gly Ala Asn Gln Pro Lys
        115                 120                 125

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

Phe Tyr Lys His Ala Ala Asn Glu Thr Asp Phe Ser Lys Asn Lys Phe
```

```
145                 150                 155                 160

Lys Ser Gly Asp Asp Gly Tyr Ile Phe Tyr His Gly Lys Lys Pro Ser
                165                 170                 175

Arg Gln Leu Pro Ala Ser Gly Lys Val Thr Tyr Lys Gly Val Trp His
            180                 185                 190

Phe Val Thr Asp Thr Lys Lys Gly Gln Lys Phe His Asp Ile Leu Glu
        195                 200                 205

Ala Ser Lys Gly Gln Gly Asp Arg Tyr Ser Gly Phe Ser Gly Asp Glu
    210                 215                 220

Gly Glu Thr Ile Ser Asn Arg Thr Asp Ser Glu Leu Lys Thr Asp Gln
225                 230                 235                 240

Glu Gly Tyr Gly Phe Thr Ser Asn Leu Glu Val Asp Phe Asp Asn Lys
                245                 250                 255

Lys Leu Thr Gly Lys Leu Ile Arg Asn Asp Lys Val Thr Asn Ala Thr
            260                 265                 270

Thr Gly Asp Lys His Thr Thr Gln Tyr Tyr Ser Leu Glu Ala Gln Val
        275                 280                 285

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

Gln Asp Gly Thr Lys Gln His Pro Phe Val Ser Asp Ser Ser Ser Leu
305                 310                 315                 320

Ser Gly Gly Phe Phe Gly Pro Gln Gly Glu Glu Leu Gly Phe Arg Phe
                325                 330                 335

Leu Ser Asn Asp Gln Lys Val Ala Val Val Gly Ser Ala Lys Thr Lys
            340                 345                 350

Asp Lys Ala Glu Ser Gly Lys Thr Val Ala Ala Ser Gly Gly Thr Gly
        355                 360                 365

Ala Ala Ala Ser Gly Gly Ala Ala Asp Met Pro Ser Glu Asn Gly Lys
    370                 375                 380

Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys
385                 390                 395                 400

Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
                405                 410                 415

Gly Ile Met Ile Pro Leu Leu Pro Lys Asp Ser Glu Ser Gly Asn Asn
            420                 425                 430

Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Tyr Lys Thr
        435                 440                 445

Thr Tyr Thr Pro Lys Ser Asp Glu Lys Asp Thr Gln Ala Gly Thr Ala
    450                 455                 460
```

```
    450                 455                 460

Ala Asn Gly Asn Gln Ala Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly
465                 470                 475                 480

Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
                485                 490                 495

Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln
            500                 505                 510

Ala Gly Glu Asn Gly Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu
        515                 520                 525

Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro
    530                 535                 540

Lys Glu Gln Gln Asp Ile Val Tyr Arg Gly Ser Trp Tyr Gly His Ile
545                 550                 555                 560

Ala Gly Ser Thr Ser Trp Ser Gly Asn Ala Ser Asn Ala Thr Ser Gly
                565                 570                 575

Asn Arg Ala Glu Phe Thr Val Asn Phe Asp Thr Lys Lys Ile Asn Gly
            580                 585                 590

Lys Leu Thr Ala Glu Asn Arg Gln Ala Ala Thr Phe Thr Ile Val Gly
        595                 600                 605

Asp Ile Lys Asp Asn Gly Phe Glu Gly Thr Ala Lys Thr Asp Asn Leu

    610                 615                 620

Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr Gly Thr Pro Lys Ala Tyr
625                 630                 635                 640

Ile Thr Asn Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu
                645                 650                 655

Glu Leu Gly Gly Trp Phe Ala Tyr Ser Asp Asp Lys Gln Thr Lys Asn
            660                 665                 670

Ala Thr Asp Ala Ser Gly Asn Gly Asn Ser Ala Ser Ser Ala Thr Val
        675                 680                 685

Val Phe
    690
```

<210> 139

<211> 680

<212> PRT

<213> Neisseria meningitidis

<400> 139

```
Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser Val Asp Thr Glu
1               5                   10                  15
```

```
Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser Ser Glu Lys Pro
            20                  25                  30

Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Leu Lys
        35                  40                  45

Arg Arg Asn Arg His Pro Gln Ala Lys Glu Asp Lys Val Glu Leu Asn
    50                  55                  60

Pro Asn Asp Trp Glu Glu Thr Gly Leu Pro Ser Lys Pro Gln Asn Leu
65                  70                  75                  80

Pro Glu Arg Gln Gln Ser Val Ile Asp Lys Val Lys Thr Asp Asp Gly
                85                  90                  95

Ser Asn Ile Tyr Thr Ser Pro Tyr Leu Thr Gln Ser Asn His Gln Asn
            100                 105                 110

Gly Ser Thr Asn Ser Gly Ala Asn Gln Pro Lys Asn Glu Val Lys Asp
        115                 120                 125

Tyr Lys Asn Phe Lys Tyr Val Tyr Ser Gly Trp Phe Tyr Lys His Ala

    130                 135                 140

Glu Ser Glu Arg Glu Phe Ser Lys Ile Lys Phe Lys Ser Gly Asp Asp
145                 150                 155                 160

Gly Tyr Ile Phe Tyr His Gly Lys Asp Pro Ser Arg Gln Leu Pro Thr
                165                 170                 175

Ser Glu Lys Val Ile Tyr Lys Gly Val Trp His Phe Val Thr Asp Thr
            180                 185                 190

Glu Lys Gly Gln Lys Phe Asn Asp Ile Leu Glu Thr Ser Lys Gly Gln
        195                 200                 205

Gly Asp Arg Tyr Ser Gly Phe Ser Gly Asp Asp Gly Glu Thr Thr Ser
    210                 215                 220

Asn Arg Thr Asp Ser Asn Leu Asn Asp Lys His Glu Gly Tyr Gly Phe
225                 230                 235                 240

Thr Ser Asn Leu Glu Val Asp Phe Gly Ser Lys Lys Leu Thr Gly Lys
                245                 250                 255

Leu Ile Arg Asn Asn Arg Val Thr Asn Ala Thr Thr Asn Asp Lys Tyr
            260                 265                 270

Thr Thr Gln Tyr Tyr Ser Leu Asp Ala Gln Ile Thr Gly Asn Arg Phe
        275                 280                 285

Asn Gly Lys Ala Ile Ala Thr Asp Lys Pro Asp Thr Gly Gly Thr Lys
    290                 295                 300
```

```
Leu His Pro Phe Val Ser Asp Ser Ser Ser Leu Ser Gly Ser Phe Phe
305                 310                 315                 320

Gly Pro Lys Gly Glu Glu Leu Gly Phe Arg Phe Leu Ser Asp Asp Lys
                325                 330                 335

Lys Val Ala Val Val Gly Ser Ala Lys Thr Lys Asp Lys Asn Ala Asn
            340                 345                 350

Gly Asn Thr Pro Ala Ala Ser Ser Gly Ala Gly Ala Ala Thr Met Pro
        355                 360                 365

Ser Glu Thr Arg Leu Thr Thr Val Leu Asp Ala Val Glu Leu Lys Ser
    370                 375                 380

Gly Gly Lys Glu Val Gln Lys Leu Asp Asn Phe Ser Asn Ala Ala Gln
385                 390                 395                 400

Leu Val Val Asp Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu
                405                 410                 415

Ser Gly Lys Asn Gln Ala Asp Lys Gly Lys Asn Gly Gly Thr Ala Phe
            420                 425                 430

Thr Tyr Thr Ile Thr Tyr Thr Pro Glu Ser Asp Lys Lys Asp Thr Gln
        435                 440                 445

Ala Gly Thr Pro Thr Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly
    450                 455                 460

Asp Thr Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser
465                 470                 475                 480

Asn Leu Asn Tyr Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys
                485                 490                 495

Ser Ala Met Gln Ala Gly Glu Ser Ser Ser Gln Ala Asp Ala Lys Thr
            500                 505                 510

Glu Gln Val Glu Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu
        515                 520                 525

Lys Glu Ile Pro Ser Glu Gln Asn Ile Val Tyr Arg Gly Ser Trp Tyr
    530                 535                 540

Gly Tyr Ile Ala Asn Asp Lys Ser Thr Ser Trp Ser Gly Asn Ala Ser
545                 550                 555                 560

Asn Ala Thr Ser Gly Asn Arg Ala Glu Phe Thr Val Asn Phe Ala Asp
                565                 570                 575

Lys Lys Ile Thr Gly Thr Leu Thr Ala Asp Asn Arg Gln Glu Ala Thr
            580                 585                 590

Phe Thr Ile Asp Gly Asn Ile Lys Asp Asn Gly Phe Glu Gly Thr Ala
        595                 600                 605
```

```
Lys Thr Ala Glu Ser Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr Arg
    610                 615                 620

Thr Pro Lys Ala Tyr Ile Thr Asp Ala Lys Val Gln Gly Gly Phe Tyr
625                 630                 635                 640

Gly Pro Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly Asp
                645                 650                 655

Lys Gln Thr Lys Asn Ala Thr Asn Ala Ser Gly Asn Ser Ser Ala Thr
            660                 665                 670

Val Val Phe Gly Ala Lys Arg Gln
        675                 680
```

<210> 140

<211> 570

<212> PRT

<213> Neisseria meningitidis

<400> 140

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

Gln His Asn Pro Gln Pro Glu Ala Pro Lys Tyr Gln Asp Glu Gln Thr
            20                  25                  30

Glu Lys Pro Ala Lys Pro Asp Glu Ala Ser Ala Ala Glu Asn Asp Arg
        35                  40                  45

Pro Ala Tyr Gly Phe Ala Val Lys Ile Pro Arg Arg Asn Val His Phe
    50                  55                  60

Asn Val Lys Gln Gly His Gln Pro Leu Ser Asp Ala Asp Trp Val Lys
65                  70                  75                  80

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

Asn Met Thr Gly Gly Thr Leu Asn Glu Ser Leu Gln Pro Gly Gly Asp
            100                 105                 110

Gly Lys Ser Arg Val Glu Gly Tyr Thr Asp Phe Lys Tyr Val Arg Ser
        115                 120                 125

Gly Tyr Ile Tyr Arg Asp Val Asn Lys Ile Asp Pro Lys Asn Asn Ile
    130                 135                 140

Ala Leu Phe Gly Pro Asp Gly Tyr Leu Phe Tyr Lys Gly Ser Asn Pro
145                 150                 155                 160

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

Tyr Val Thr Asp Ala Lys Met Glu Glu Lys Phe Pro Gln Leu Glu Asp
```

```
Tyr Val Thr Asp Ala Lys Met Gly Gln Lys Phe Pro Gln Leu Gly Asn
            180                 185                 190

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

Val Leu Arg Asn Lys Ser Glu Ala Pro Glu Gly His Thr Asp Phe Gly
    210                 215                 220

Leu Thr Ser Glu Phe Glu Val Asp Phe Ala Ala Lys Thr Met Thr Gly
225                 230                 235                 240

Ala Leu Tyr Arg Asn Asn Arg Ile Thr His Asn Glu Thr Glu Asn Lys
                245                 250                 255

Asp Lys Arg Ile Lys Arg Tyr Asp Ile Lys Ala Asp Leu His Gly Asn
            260                 265                 270

Arg Phe Lys Gly Lys Ala Leu Ala Ala Asp Lys Asp Ala Gly Asn Gly
        275                 280                 285

His Pro Phe Val Ser Asp Ser Asp Ser Leu Glu Gly Gly Phe Tyr Gly
    290                 295                 300

Pro Gln Gly Asp Glu Leu Gly Gly Lys Phe Leu Ala Asn Asp Lys Lys
305                 310                 315                 320

Val Leu Ala Val Phe Ser Ala Lys Gln Lys Asp Gly Ala Glu Lys Pro
                325                 330                 335

Leu Ala Glu Thr Phe Met Asp Ala Tyr Arg Ile Gly Ser Asp Phe Val
            340                 345                 350

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

Gly Val Glu Leu Ala Leu Val Pro Ser Glu Gly Thr Gln Thr Ala Phe
    370                 375                 380

Gln His Val Phe Lys Lys Asp Gly Val Lys Val Ser Ser Cys Cys Ser
385                 390                 395                 400

Asn Leu Asp Tyr Leu His Phe Gly Val Leu Glu His Gly Asp Ser His
                405                 410                 415

Asp Met Phe Leu Gln Gly Ser Arg Thr Pro Val Ser Asp Met Pro Val
            420                 425                 430

Thr Ala Gly Glu Ala Val Tyr Arg Gly Thr Trp Ser Gly Thr Ile Val
        435                 440                 445

Asn Gly Thr Ser Trp Ser Ala Glu Pro Ser Asp Lys Glu Gly Gly Asn
    450                 455                 460

Arg Ala Glu Phe Lys Val Asn Phe Ala Glu Arg Thr Leu Asn Gly Met
465                 470                 475                 480
```

```
Leu Thr Ala Lys Asn His Ile Ala Pro Val Phe Thr Ile Thr Ala Gln
                485                 490                 495

Ile Gln Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr Gly Glu Ser Gly
            500                 505                 510

Phe Ala Leu Asp Pro Lys Ser Thr Ile Asp Ser Val Tyr Thr Arg Ile
        515                 520                 525

Gln Ala Asp Val Ser Gly Gly Phe Tyr Gly Lys Asn Ala Ile Glu Met
    530                 535                 540

Gly Gly Ser Phe Ser Gly Asn Thr Leu Lys Gly Glu Ser Gly Lys Ala
545                 550                 555                 560

Ala Val Val Phe Gly Thr Lys Arg Gln Gln
                565                 570
```

<210> 141

<211> 660

<212> PRT

<213> Neisseria meningitidis

<400> 141

```
Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser Val Asp Thr Glu
1               5                   10                  15

Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser Ser Glu Thr Pro
            20                  25                  30

Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Phe Lys
        35                  40                  45

Arg Arg Asn Trp Tyr Pro Lys Asn Glu Glu Asp His Lys Ala Leu Ser
    50                  55                  60

Glu Ala Asp Trp Glu Lys Leu Gly Ala Gly Lys Pro Asp Glu Phe Pro
65                  70                  75                  80

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

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

Phe Gln Tyr Val Arg Ser Gly Tyr Ile Tyr Arg Asn Gly Ala Asn Lys
        115                 120                 125

Ile Asp Phe Gln Lys Lys Ile Ala Leu Ser Gly Pro Asp Gly Tyr Leu
    130                 135                 140

Phe Tyr Lys Gly Ser Asn Pro Ser Gln Ala Leu Pro Met Gly Lys Val
145                 150                 155                 160

Gly Tyr Lys Gly Thr Trp Asp Tyr Val Thr Asp Ala Lys Met Gly Gln
                165                 170                 175
```

```
Lys Phe Ser Gln Leu Ala Gly Phe Pro Ala Gly Asp Arg Tyr Gly Ala
            180                 185                 190

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

Gln Gly Gln Thr Asp Phe Gly Leu Thr Ser Glu Phe Glu Val Asp Phe
    210                 215                 220

Ala Ala Lys Thr Met Thr Gly Ala Leu Tyr Arg Asn Asn Arg Ile Thr
225                 230                 235                 240

Asn Asn Glu Thr Glu Asn Lys Ala Lys Gln Ile Lys Arg Tyr Asp Ile
                245                 250                 255

Gln Ala Asp Leu His Gly Asn Arg Phe Ser Gly Lys Ala Thr Ala Thr
            260                 265                 270

Asp Lys Pro Lys Asn Asp Glu Thr Lys Glu His Pro Phe Val Ser Asp
        275                 280                 285

Ser Ser Ser Leu Ser Gly Gly Phe Phe Gly Pro Lys Gly Glu Glu Leu
    290                 295                 300

Gly Phe Arg Phe Leu Ser Asp Asp Gln Lys Val Ala Val Val Gly Ser
305                 310                 315                 320

Ala Lys Thr Lys Asp Lys Leu Glu Asn Gly Ala Ala Ala Ser Gly Ser

                325                 330                 335

Thr Gly Ala Ala Ala Ser Gly Gly Ala Ala Asp Met Pro Ser Glu Asn
            340                 345                 350

Gly Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Lys Ser Gly Gly
        355                 360                 365

Lys Glu Val Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
    370                 375                 380

Val Asp Gly Ile Met Ile Pro Leu Leu Pro Lys Glu Ser Glu Ser Glu
385                 390                 395                 400

Ser Asn Gln Ala Asp Lys Gly Lys Asn Gly Gly Thr Ala Phe Thr Arg
                405                 410                 415

Lys Phe Glu His Thr Pro Glu Ser Asp Lys Lys Asp Thr Gln Ala Gly
            420                 425                 430

Thr Ala Glu Asn Gly Asn Pro Ala Ala Ser Asn Thr Ala Gly Asp Thr
        435                 440                 445

Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu
    450                 455                 460
```

```
Asn Tyr Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala
465                 470                 475                 480

Met Gln Ala Gly Glu Asn Gly Ser Gln Ala Asp Ala Lys Thr Glu Gln
                485                 490                 495

Val Glu Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu
            500                 505                 510

Ile Pro Lys Glu Gln Gln Asp Ile Val Tyr Arg Gly Ser Trp Tyr Gly
        515                 520                 525

His Ile Ala Asn Asp Thr Ser Trp Ser Gly Asn Ala Ser Asp Arg Glu
    530                 535                 540

Gly Gly Asn Arg Ala Asp Phe Thr Val Asn Phe Gly Thr Lys Lys Ile
545                 550                 555                 560

Asn Gly Thr Leu Thr Ala Glu Asn Arg Gln Glu Ala Thr Phe Thr Ile
                565                 570                 575

Val Gly Asp Ile Lys Asp Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala
            580                 585                 590

Asp Ser Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr Arg Thr Pro Lys
        595                 600                 605

Ala Tyr Ile Thr Asp Ala Lys Val Lys Gly Gly Phe Tyr Gly Pro Lys
    610                 615                 620

Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr
625                 630                 635                 640

Glu Lys Ala Thr Val Thr Ser Gly Asp Gly Asn Ser Ala Ser Ser Ala
                645                 650                 655

Thr Val Val Phe
            660
```

<210> 142

<211> 660

<212> PRT

<213> Neisseria meningitidis

<400> 142

```
Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser Val Asp Thr Glu
1               5                   10                  15

Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser Ser Glu Thr Pro
            20                  25                  30

Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Phe Lys
        35                  40                  45

Arg Arg Asn Trp His Pro Lys Asn Lys Glu Asp His Lys Ala Leu Ser
    50                  55                  60
```

```
50                  55                  60

Glu Ala Asp Trp Glu Lys Leu Gly Ala Gly Lys Pro Asp Glu Phe Pro
65                  70                  75                  80

Gln Lys Asn Glu Ile Ser Ala Met Asp Lys Gly Thr Leu Asn Glu Ser
                85                  90                  95

Ile Thr Pro Gly Asp Gly Lys Ser Arg Ala Glu Gly Tyr Thr Asp Phe
            100                 105                 110

Gln Tyr Val Arg Ser Gly Tyr Ile Tyr Arg Asn Gly Val Asn Lys Ile
        115                 120                 125

Asp Tyr Gln Asn Asn Ile Ala Leu Ser Gly Pro Asp Gly Tyr Leu Phe
    130                 135                 140

Tyr Lys Gly Ser Asn Pro Ser Gln Ala Leu Pro Thr Gly Lys Ala Ile
145                 150                 155                 160

Tyr Lys Gly Thr Trp Asp Tyr Val Thr Asp Ala Lys Glu Lys Gln Lys
                165                 170                 175

Phe Pro Gln Leu Gly Ser Phe Gln Ala Gly Asp Arg Tyr Gly Ala Leu
            180                 185                 190

Ser Ala Glu Glu Glu Asp Val Leu Arg Asn Lys Ser Glu Ala Lys Glu
        195                 200                 205

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

Ala Lys Thr Met Thr Gly Lys Leu Tyr Arg Asn Asn Arg Ile Thr Asn
225                 230                 235                 240

Asn Glu Thr Glu Asn Arg Asp Lys Gln Ile Lys Arg Tyr Asp Ile Gln
                245                 250                 255

Ala Asn Leu His Gly Asn Arg Phe Asn Gly Lys Ala Thr Ala Thr Asp
            260                 265                 270

Lys Pro Lys Glu Asn Glu Thr Lys Gln His Pro Phe Val Ser Asp Ser
        275                 280                 285

Ser Ser Leu Ser Gly Gly Phe Phe Gly Pro Gln Gly Glu Glu Leu Gly
    290                 295                 300

Phe Arg Phe Leu Ser Asn Asp Gln Lys Val Ala Val Val Gly Ser Ala
305                 310                 315                 320

Lys Thr Gln Asp Lys Ala Ala Asn Gly Asn Thr Ala Ala Ala Ser Gly
                325                 330                 335

Asp Ala Ser Val Ser Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu
            340                 345                 350

Asn Gly Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Leu Asn
        355                 360                 365
```

```
        355                 360                 365

Asp Lys Lys Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu
    370                 375                 380

Val Val Asp Gly Ile Met Ile Pro Leu Leu Pro Glu Thr Ser Glu Ser
385                 390                 395                 400

Gly Asn Asn Gln Ala Asp Lys Gly Lys Asn Gly Gly Thr Ala Phe Thr
                405                 410                 415

Arg Lys Phe Asp His Thr Pro Lys Ser Asp Glu Lys Asp Thr Gln Ala
            420                 425                 430

Gly Thr Ala Ala Asn Gly Ala Gln Thr Ala Ser Gly Thr Ala Gly Asp
        435                 440                 445

Thr Ser Gly Lys Thr Lys Thr Tyr Gln Val Glu Val Cys Cys Ser Asn
    450                 455                 460

Leu Asn Tyr Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Glu Ser
465                 470                 475                 480

Ala Met Gln Ala Gly Glu Ser Ser Ser Gln Thr Pro Ala Ala Gln Thr
                485                 490                 495

Ala Gln Gly Ala Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu
            500                 505                 510

Asn Lys Ile Pro Thr Asp Gln Asn Val Val Tyr Arg Gly Ser Trp Tyr
        515                 520                 525

Gly His Ile Ala Ser Ser Thr Ser Trp Ser Gly Asn Ala Ser Asn Ala
    530                 535                 540

Thr Ser Gly Asn Arg Ala Glu Phe Thr Val Asn Phe Asp Thr Lys Lys
545                 550                 555                 560

Ile Thr Gly Lys Leu Thr Ala Glu Asn Arg Gln Glu Ala Thr Phe Thr
                565                 570                 575

Ile Asp Gly Lys Ile Glu Gly Asn Gly Phe Glu Gly Thr Ala Lys Thr
            580                 585                 590

Ala Glu Leu Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr Gly Thr Pro
        595                 600                 605

Lys Ala Tyr Ile Thr Asn Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro
    610                 615                 620

Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln
625                 630                 635                 640

Thr Glu Asn Thr Thr Val Ala Ser Gly Asn Gly Asn Ser Ala Ser Ser
                645                 650                 655

Ala Thr Val Val
            660
```

<210> 143

<211> 670

<212> PRT

<213> Neisseria meningitidis

<400> 143

```
Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser Val Asp Thr Glu
1               5                   10                  15

Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser Ser Glu Thr Pro
            20                  25                  30

Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Phe Lys
        35                  40                  45

Arg Arg Asn Trp His Pro Arg Gly Asn Pro Lys Glu Asp Lys Ile Glu
    50                  55                  60

Leu Ser Glu Asn Asp Trp Glu Gln Thr Asp Asn Gly Asp Ile Lys Asn
65                  70                  75                  80

Pro Ser Lys Gln Lys Lys Ile Ile Asn Asp Leu Leu Gly Asn Gly Gly
                85                  90                  95

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

Thr Asp His His Asp Phe Gln Tyr Val Trp Ser Gly Phe Phe Tyr Lys
        115                 120                 125

Gln Ile Gln Thr Lys Phe Glu Thr Thr Asp Gly Lys Met Thr Val Arg
    130                 135                 140

Ser Gly Pro Asp Gly Tyr Ile Phe Tyr Lys Gly Lys Asp Pro Ser Arg
145                 150                 155                 160

Lys Leu Pro Val Ser Gly Glu Val Met Tyr Lys Gly Thr Trp Asp Phe
                165                 170                 175

Leu Thr Asp Val Lys Thr Ser Gln Lys Phe Thr Asp Leu Gly Asn Thr
            180                 185                 190

Ser Thr Arg Pro Gly Asp Arg Tyr Ser Ala Phe Ser Gly Glu Leu Asp
        195                 200                 205

Tyr Ile Val Asn Lys Asp Ser Asp Lys Lys Asp Glu His Val Gly Trp
    210                 215                 220

Gly Leu Thr Thr Glu Ile Thr Val Asp Phe Glu Lys Lys Thr Leu Ser
225                 230                 235                 240

Gly Lys Leu Ile Lys Asn Asn Arg Val Asn Asn Asp Asn Asp Lys His
                245                 250                 255
```

```
Thr Thr Gln Tyr Tyr Ser Leu Asp Ala Thr Leu Arg Gly Asn Arg Phe
            260                 265                 270

Asn Gly Lys Ala Thr Ala Thr Asp Lys Pro Lys Asn Asp Gly Glu Thr
        275                 280                 285

Lys Glu His Pro Phe Val Ser Asp Ser Ser Ser Leu Ser Gly Gly Phe
    290                 295                 300

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

Gln Lys Val Ala Val Val Gly Ser Ala Lys Thr Lys Asp Lys Pro Ala
                325                 330                 335

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

Asp Gly Ala Ala Gly Thr Ser Ser Lys Asn Gly Lys Leu Thr Thr Val
        355                 360                 365

Leu Asp Ala Val Glu Leu Lys Leu Gly Asp Lys Glu Val Gln Lys Leu
    370                 375                 380

Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met Ile
385                 390                 395                 400

Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly Asn Thr Asn Gln Gly Thr
                405                 410                 415

Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe Glu Gln Met Pro Glu Ser
            420                 425                 430

Asp Glu Lys Asp Thr Lys Ala Gln Thr Gly Thr Gly Gly Thr Gln Thr

        435                 440                 445

Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly Lys Thr Lys Thr Tyr Glu
    450                 455                 460

Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr Gly Met Leu
465                 470                 475                 480

Thr Arg Lys Asn Ser Lys Ser Ala Met Gln Ala Gly Glu Ser Ser Ser
                485                 490                 495

Gln Ala Asp Ala Lys Thr Glu Gln Val Gly Gln Ser Met Phe Leu Gln
            500                 505                 510

Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Asn Asp Gln Asn Val Val
        515                 520                 525

Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Asn Gly Thr Ser Trp Ser
    530                 535                 540

Gly Asn Ala Ser Asp Lys Glu Gly Gly Asn Arg Ala Asp Phe Thr Val
```

```
545                 550                 555                 560

Asn Phe Gly Thr Lys Lys Ile Asn Gly Thr Leu Thr Ala Asp Asn Arg
                565                 570                 575

Gln Ala Ala Thr Phe Thr Ile Val Gly Asp Ile Glu Gly Asn Gly Phe
            580                 585                 590

Ser Gly Thr Ala Lys Thr Ala Asp Ser Gly Phe Asp Leu Asp Gln Ser
        595                 600                 605

Asn Asn Thr Arg Thr Pro Lys Ala Tyr Ile Thr Asn Ala Lys Val Gln
    610                 615                 620

Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala
625                 630                 635                 640

Tyr Ser Asp Asp Lys Gln Thr Lys Asn Ala Thr Asp Ala Ser Gly Asn
                645                 650                 655

Gly Asn Ser Ala Ser Ser Ala Thr Val Val Phe Gly Ala Lys
            660                 665                 670
```

<210> 144

<211> 660

<212> PRT

<213> Neisseria meningitidis

<400> 144

```
Phe Asp Leu Asp Ser Val Asp Thr Glu Ala Pro Arg Pro Ala Pro Lys
1               5                   10                  15

Tyr Gln Asp Val Ser Ser Glu Lys Pro Gln Ala Gln Lys Asp Gln Gly
            20                  25                  30

Gly Tyr Gly Phe Ala Met Arg Leu Lys Arg Arg Asn Trp Tyr Arg Gln
        35                  40                  45

Ala Asn Pro Lys Glu Asp Glu Ile Lys Leu Ser Glu Asn Asp Trp Glu
    50                  55                  60

Gln Thr Asp Asn Gly Asp Ile Lys Asn Pro Ser Lys Gln Lys Asn Ile
65                  70                  75                  80

Ile Asn Ala Leu Thr Gly Asn Asn Gly Gly Ala Ser Leu Gln Asp Ser
                85                  90                  95

Ser Gln Glu Asn Gln Gly Ile Ser Lys Val Thr Gly His His Asn Phe
            100                 105                 110

Gln Tyr Val Trp Ser Gly Phe Phe Tyr Lys Gln Ile Gly Ser Thr Phe
        115                 120                 125

Glu Arg Lys Asp Ser Ser Ile Thr Ala Ala Arg Ser Gly Pro Asp Gly
    130                 135                 140
```

```
Tyr Ile Phe Tyr Lys Gly Lys Asp Pro Ser Arg Lys Leu Pro Val Ser
145                 150                 155                 160

Gly Glu Val Met Tyr Lys Gly Thr Trp Asp Phe Leu Thr Asp Val Lys
                165                 170                 175

Thr Ser Gln Lys Phe Thr Asp Leu Gly Asn Thr Ser Thr Arg Pro Gly
            180                 185                 190

Asp Arg Tyr Ser Ala Phe Ser Gly Gly Leu Asp Tyr Ile Val Asn Lys
        195                 200                 205

Asp Ser Asp Lys Lys Asp Glu His Val Gly Trp Gly Leu Thr Thr Glu
    210                 215                 220

Ile Thr Val Asp Phe Glu Lys Lys Thr Leu Ser Gly Lys Leu Ile Lys
225                 230                 235                 240

Asn Asn Arg Val Asn Asn Asp Asn Asp Lys His Thr Thr Gln Tyr Tyr
                245                 250                 255

Ser Leu Asp Ala Thr Leu Arg Gly Asn Arg Phe Ser Gly Lys Ala Glu
            260                 265                 270

Ala Thr Asp Lys Pro Lys Asn Asp Gly Glu Thr Lys Glu His Pro Phe
        275                 280                 285

Val Ser Asp Ser Ser Ser Leu Ser Gly Gly Phe Phe Gly Pro Lys Gly
    290                 295                 300

Glu Glu Leu Gly Phe Arg Phe Leu Ser Asp Asp Gln Lys Val Ala Val
305                 310                 315                 320

Val Gly Ser Ala Lys Thr Gln Asp Lys Pro Arg Asn Gly Ala Val Ala
                325                 330                 335

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

Ser Glu Asn Ser Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr
        355                 360                 365

Leu Asn Asp Lys Lys Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala
    370                 375                 380

Gln Leu Val Val Asp Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser
385                 390                 395                 400

Glu Ser Gly Lys Asn Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala
                405                 410                 415

Phe Thr Arg Lys Phe Asn His Thr Pro Lys Ser Asp Glu Lys Asp Thr
            420                 425                 430

Gln Ala Gly Thr Ala Glu Asn Gly Asn Pro Ala Ala Ser Asn Thr Ala
        435                 440                 445
```

```
Gly Asp Ala Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys
    450                 455                 460

Ser Asn Leu Asn Tyr Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser
465                 470                 475                 480

Lys Ser Ala Met Gln Ala Gly Glu Ser Ser Ser Gln Ala Asp Ala Lys
                485                 490                 495

Thr Glu Gln Val Gly Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp
            500                 505                 510

Glu Lys Glu Ile Pro Asn Asp Gln Asn Val Val Tyr Arg Gly Ser Trp
        515                 520                 525

Tyr Gly His Ile Ala Asn Gly Thr Ser Trp Ser Gly Asn Ala Ser Asp
    530                 535                 540

Lys Glu Gly Gly Asn Arg Ala Asp Phe Thr Val Asn Phe Gly Thr Lys
545                 550                 555                 560

Lys Ile Asn Gly Thr Leu Thr Ala Asp Asn Arg Gln Ala Ala Thr Phe
                565                 570                 575

Thr Ile Val Gly Asp Ile Glu Gly Asn Gly Phe Ser Gly Thr Ala Lys
            580                 585                 590

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

Pro Lys Ala Tyr Ile Thr Asn Ala Lys Val Gln Gly Gly Phe Tyr Gly
    610                 615                 620

Pro Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Ser Asp Asp Lys
625                 630                 635                 640

Gln Thr Lys Asn Ala Thr Asp Ala Ser Gly Asn Gly Asn Ser Ala Ser
                645                 650                 655

Ser Ala Thr Val
            660
```

<210> 145

<211> 690

<212> PRT

<213> Neisseria meningitidis

<400> 145

```
Cys Leu Gly Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser Val Asp Thr
1               5                   10                  15

Glu Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser Ser Glu Lys
            20                  25                  30
```

```
Pro Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Leu
        35                  40                  45

Lys Arg Arg Asn Trp Tyr Pro Ser Ala Lys Glu Asn Glu Val Lys Leu
    50                  55                  60

Asn Glu Ser Asp Trp Glu Thr Thr Gly Leu Pro Ser Asn Pro Lys Asn
65                  70                  75                  80

Leu Pro Glu Arg Gln Lys Ser Val Ile Asp Gln Val Glu Thr Asp Gly
                85                  90                  95

Asp Ser Asn Asn Ser Asn Ile Tyr Ser Ser Pro Tyr Leu Thr Gln Ser
            100                 105                 110

Asn His Gln Asn Gly Asn Thr Gly Asn Gly Val Asn Gln Pro Lys Asn
        115                 120                 125

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

Tyr Lys His Ala Lys Arg Glu Val Asn Leu Ala Val Glu Pro Lys Ser
145                 150                 155                 160

Ala Lys Asn Gly Asp Asp Gly Tyr Ile Phe Tyr His Gly Lys Asp Pro
                165                 170                 175

Ser Arg Gln Leu Pro Ala Ser Gly Lys Ile Thr Tyr Lys Gly Val Trp
            180                 185                 190

His Phe Ala Thr Asp Thr Lys Arg Gly Gln Lys Phe Arg Glu Ile Ile
        195                 200                 205

Gln Pro Ser Lys Asn Gln Gly Asp Arg Tyr Ser Gly Phe Ser Gly Asp
    210                 215                 220

Asp Asp Glu Gln Tyr Ser Asn Lys Asn Glu Ser Met Leu Lys Asp Gly
225                 230                 235                 240

His Glu Gly Tyr Gly Phe Thr Ser Asn Leu Glu Val Asp Phe Asp Asn
                245                 250                 255

Lys Lys Leu Thr Gly Lys Leu Ile Arg Asn Asn Ala Asn Gln Asn Asn
            260                 265                 270

Asn Thr Asn Asn Asp Lys His Thr Thr Gln Tyr Tyr Ser Leu Asp Ala
        275                 280                 285

Thr Leu Lys Gly Asn Arg Phe Ser Gly Lys Ala Glu Ala Thr Asp Lys
    290                 295                 300

Pro Lys Asn Asp Gly Glu Thr Lys Glu His Pro Phe Val Ser Asp Ser
305                 310                 315                 320

Ser Ser Leu Ser Gly Gly Phe Phe Gly Pro Gln Gly Glu Glu Leu Gly
                325                 330                 335

Phe Arg Phe Leu Ser Asn Asp Gln Lys Val Ala Val Val Gly Ser Ala
```

```
        340                 345                 350

Lys Thr Lys Asp Lys Pro Ala Asn Gly Asn Thr Ala Glu Ala Ser Gly
        355                 360                 365

Gly Thr Asp Ala Ala Ala Ser Gly Gly Ala Ala Gly Thr Ser Ser Glu
    370                 375                 380

Asn Ser Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr His Gly
385                 390                 395                 400

Gly Thr Ala Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu
                405                 410                 415

Val Val Asp Gly Ile Met Ile Pro Leu Leu Pro Gln Asn Ser Thr Gly
            420                 425                 430

Lys Asn Asn Gln Pro Asp Gln Gly Lys Asn Gly Gly Thr Ala Phe Ile
        435                 440                 445

Tyr Lys Thr Thr Tyr Thr Pro Lys Asn Asp Asp Lys Asp Thr Lys Ala
    450                 455                 460

Gln Thr Val Thr Gly Gly Thr Gln Thr Ala Ser Asn Thr Ala Gly Asp
465                 470                 475                 480

Ala Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn
                485                 490                 495

Leu Asn Tyr Leu Lys Tyr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn
            500                 505                 510

Thr Val Gly Ser Gly Asn Ser Ser Pro Thr Ala Ala Ala Gln Thr Asp
        515                 520                 525

Ala Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Asn Lys Ile
    530                 535                 540

Pro Ser Glu Gln Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile

545                 550                 555                 560

Ala Ser Ser Thr Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly
                565                 570                 575

Asn Arg Ala Glu Phe Thr Val Asn Phe Gly Glu Lys Lys Ile Thr Gly
            580                 585                 590

Thr Leu Thr Ala Glu Asn Arg Gln Glu Ala Thr Phe Thr Ile Asp Gly
        595                 600                 605

Lys Ile Glu Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala Glu Leu
    610                 615                 620

Gly Phe Asp Leu Asp Gln Lys Asn Thr Thr Arg Thr Pro Lys Ala Tyr
625                 630                 635                 640
```

Ile Thr Asp Ala Lys Val Lys Gly Gly Phe Tyr Gly Pro Lys Ala Glu
645 650 655

Glu Leu Gly Gly Trp Phe Ala Tyr Ser Asp Asp Lys Gln Thr Lys Asn
660 665 670

Ala Thr Asp Ala Ser Gly Asn Gly Asn Ser Ala Ser Ser Ala Thr Val
675 680 685

Val Phe
690

<210> 146

<211> 690

<212> PRT

<213> Neisseria meningitidis

<400> 146

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

Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser Ser Glu Lys Pro
20 25 30

Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Leu Lys
35 40 45

Arg Arg Asn Trp Tyr Pro Gln Ala Lys Glu Asp Glu Val Lys Leu Asn
50 55 60

Glu Ser Asp Trp Glu Ala Thr Gly Leu Pro Thr Glu Pro Lys Lys Leu
65 70 75 80

Pro Leu Lys Gln Glu Ser Val Ile Ser Lys Val Gln Ala Asn Asn Gly
85 90 95

Asp Asn Asn Ile Tyr Thr Ser Pro Tyr Leu Thr Gln Ser Asn His Gln
100 105 110

Asn Gly Asn Thr Gly Asn Gly Ala Asn Leu Pro Lys Asn Glu Val Thr
115 120 125

Asn Tyr Lys Asp Phe Lys Tyr Val Tyr Ser Gly Trp Phe Tyr Lys His
130 135 140

Ala Arg Asn Glu Ile Ile Arg Glu Asn Ser Ser Ile Lys Gly Ala Lys
145 150 155 160

Asn Gly Asp Asp Gly Tyr Ile Phe Tyr His Gly Lys Glu Pro Ser Arg
165 170 175

Gln Leu Pro Ala Ser Gly Thr Val Thr Tyr Lys Gly Met Trp His Phe
180 185 190

```
            ---                 ---                 ---

Ala Thr Asp Val Lys Lys Ser Gln Asn Phe Arg Asp Ile Ile Gln Pro
        195                 200                 205

Ser Lys Lys Gln Gly Asp Arg Tyr Ser Gly Phe Ser Gly Asp Asp Asp
    210                 215                 220

Glu Gln Tyr Ser Asn Lys Asn Glu Ser Met Leu Lys Asp Asp Gln Glu
225                 230                 235                 240

Gly Tyr Gly Phe Thr Ser Asn Leu Glu Val Asp Phe Asn Asn Lys Lys
                245                 250                 255

Leu Thr Gly Lys Leu Ile Arg Asn Asp Lys Val Thr Asn Ala Thr Thr
            260                 265                 270

Ser Gly Lys His Thr Thr Gln Tyr Tyr Ser Leu Glu Ala Gln Val Thr
        275                 280                 285

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

Gly Glu Thr Lys Gln His Pro Phe Val Ser Asp Ser Ser Ser Leu Ser
305                 310                 315                 320

Gly Gly Phe Phe Gly Pro Lys Gly Glu Glu Leu Gly Phe Arg Phe Leu
                325                 330                 335

Ser Asp Asp Lys Lys Val Ala Val Val Gly Ser Ala Lys Thr Lys Asp
            340                 345                 350

Lys Thr Glu Asn Gly Ala Ala Ala Ser Gly Gly Ala Gly Ala Ala Ala
        355                 360                 365

Ser Gly Gly Ala Ala Ala Met Pro Ser Glu Asn Gly Lys Leu Thr Thr
    370                 375                 380

Val Leu Asp Ala Val Glu Leu Thr His Gly Gly Thr Ala Ile Lys Asn
385                 390                 395                 400

Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met
                405                 410                 415

Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly His Asn Gln Ala Asn
            420                 425                 430

Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe Asp His Thr
        435                 440                 445

Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln Thr Asn Gly
    450                 455                 460

Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly Lys Thr Lys
465                 470                 475                 480

Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr
                485                 490                 495
```

```
                485                 490                 495

Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln Ala Gly Glu
            500                 505                 510

Asn Gly Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu Gln Ser Met
        515                 520                 525

Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Lys Glu Gln
    530                 535                 540

Gln Asp Ile Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Asn Asp
545                 550                 555                 560

Thr Ser Trp Ser Gly Asn Ala Ser Asp Arg Glu Gly Gly Asn Arg Ala
                565                 570                 575

Asp Phe Thr Val Asn Phe Gly Thr Lys Lys Ile Asn Gly Thr Leu Thr
            580                 585                 590

Ala Glu Asn Arg Gln Glu Ala Thr Phe Thr Ile Val Gly Asp Ile Lys
        595                 600                 605

Asp Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala Asp Ser Gly Phe Asp
    610                 615                 620

Leu Asp Gln Ser Asn Thr Thr Arg Thr Pro Lys Ala Tyr Ile Thr Asp
625                 630                 635                 640

Ala Lys Val Lys Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly
                645                 650                 655

Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Glu Lys Ala Thr Val
            660                 665                 670

Thr Ser Gly Asp Gly Asn Ser Ala Ser Ser Ala Thr Val Val Phe Gly
        675                 680                 685

Ala Lys
    690
```

<210> 147

<211> 690

<212> PRT

<213> Neisseria meningitidis

<400> 147

```
Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser Val Asp Thr Glu
1               5                   10                  15

Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser Ser Glu Lys Pro
            20                  25                  30

Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Phe Lys
        35                  40                  45
```

```
Arg Arg Asn Leu His Pro Met Ala Lys Glu Asn Glu Val Lys Leu Lys
     50                  55                  60

Asn Asp Asp Trp Glu Ala Thr Gly Leu Pro Thr Asn Pro Lys Glu Leu
65                  70                  75                  80

Pro Lys Arg Gln Glu Ser Val Ile Glu Gln Val Lys Thr Asp Asp Gly
                85                  90                  95

Ser Asn Ile Tyr Ser Ser Pro Tyr Leu Thr Gln Ser Asn His Pro Asn
            100                 105                 110

Gly Ser Ala Gly Asn Ser Val Asn Gln Pro Lys Asn Gln Ala Arg Asp
        115                 120                 125

Tyr Glu Asn Phe Gln Tyr Val Tyr Ser Gly Trp Phe Tyr Lys His Ala
    130                 135                 140

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

Gly Tyr Ile Phe Tyr His Gly Lys Glu Pro Ser Arg Gln Leu Pro Val
                165                 170                 175

Ser Glu Lys Ile Thr Tyr Lys Gly Val Trp His Phe Val Thr Asp Thr
            180                 185                 190

Lys Asn Gly Gln Lys Phe Tyr Asp Ile Ile Gln Ser Ser Lys Lys Gln
        195                 200                 205

Gly Asp Arg Tyr Ser Gly Phe Ser Gly Asp Glu Gly Glu Glu Tyr Ser
    210                 215                 220

Asn Lys Asn Glu Glu Thr Leu Lys Ser Asp His Glu Gly Tyr Gly Phe
225                 230                 235                 240

Thr Ser Asn Leu Glu Val Asp Phe Gly Asn Lys Lys Leu Thr Gly Lys
                245                 250                 255

Leu Ile Arg Asn Asn Ala Ser Leu Ser Asn Thr Asn Asn Asp Lys His
            260                 265                 270

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

Asn Gly Thr Ala Thr Ala Thr Asp Lys Pro Glu Gln Asp Gly Thr Lys
    290                 295                 300

Gln His Pro Phe Val Ser Asp Ser Ser Ser Leu Ser Gly Gly Phe Phe
305                 310                 315                 320

Gly Pro Gln Gly Glu Glu Leu Gly Phe Arg Phe Leu Ser Asn Asp Lys
                325                 330                 335

Lys Val Ala Val Val Gly Ser Ala Lys Thr Lys Asp Lys Pro Arg Asn
            340                 345                 350

Gly Ala Val Ala Ser Gly Gly Ala Gly Ala Ala Ala Ser Asp Gly Ala
```

```
Gly Ala Val Ala Ser Gly Gly Ala Gly Ala Ala Ala Ser Asn Gly Ala
        355                 360                 365

Ala Gly Thr Ser Ser Glu Asn Ser Lys Leu Thr Thr Val Leu Asp Ala
    370                 375                 380

Val Glu Leu Thr Leu Asn Asp Lys Lys Ile Lys Asn Leu Asp Asn Phe
385                 390                 395                 400

Ser Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met Ile Pro Leu Leu
                405                 410                 415

Pro Gln Asn Ser Thr Gly Glu Asn Asn Gln Pro Asp Gln Gly Lys Thr
            420                 425                 430

Gly Gly Thr Ala Phe Ile Tyr Lys Thr Thr Tyr Thr Pro Lys Asn Asp
        435                 440                 445

Asp Lys Asp Thr Lys Ala Gln Thr Gly Ala Ala Gly Ser Ser Gly Ala
    450                 455                 460

Gln Thr Ala Ser Gly Thr Glu Ser Val Thr Gly Gly Gln Ala Gly Thr
465                 470                 475                 480

Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys
                485                 490                 495

Tyr Gly Leu Leu Thr Arg Lys Thr Ala Ser Asn Thr Gly Glu Gly Gly
            500                 505                 510

Asn Gly Ser Gln Thr Ala Ala Gln Thr Ala Gln Gly Ala Gln Ser Met
        515                 520                 525

Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Asn Asp Gln
    530                 535                 540

Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly Tyr Ile Ala Asn Asp Thr
545                 550                 555                 560

Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly Asn Arg Ala Glu
                565                 570                 575

Phe Thr Val Asn Phe Gly Glu Lys Lys Ile Asn Gly Lys Leu Thr Ala
            580                 585                 590

Glu Asn Arg Gln Glu Ala Thr Phe Thr Ile Glu Gly Met Ile Gln Gly

        595                 600                 605

Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala Asp Leu Gly Phe Asp Leu
    610                 615                 620

Asp Gln Ser Asn Thr Thr Gly Thr Pro Lys Ala Tyr Ile Thr Asn Ala
625                 630                 635                 640

Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly
                645                 650                 655
```

645 650 655

Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Glu Asn Thr Thr Val Ala
660 665 670

Ser Gly Asn Gly Asn Ser Ala Ser Ser Ala Thr Val Val Phe Gly Ala
675 680 685

Lys Arg
690

<210> 148

<211> 575

<212> PRT

<213> Neisseria meningitidis

<400> 148

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

Gln Asp Met His Ser Lys Pro Lys Tyr Glu Asp Glu Lys Ser Gln Pro
20 25 30

Glu Ser Gln Gln Asp Val Ser Glu Asn Ser Gly Ala Ala Tyr Gly Phe
35 40 45

Ala Val Lys Leu Pro Arg Arg Asn Ala His Phe Asn Pro Lys Tyr Lys
50 55 60

Glu Lys His Lys Pro Leu Gly Ser Met Asp Trp Lys Lys Leu Gln Arg
65 70 75 80

Gly Glu Pro Asn Ser Phe Ser Glu Arg Asp Glu Leu Glu Lys Lys Arg
85 90 95

Gly Ser Ser Glu Leu Ile Glu Ser Lys Trp Glu Asp Gly Gln Ser Arg
100 105 110

Val Val Gly Tyr Thr Asn Phe Thr Tyr Val Arg Ser Gly Tyr Val Tyr
115 120 125

Leu Asn Lys Asn Asn Ile Asp Ile Lys Asn Asn Ile Val Leu Phe Gly
130 135 140

Pro Asp Gly Tyr Leu Tyr Tyr Lys Gly Lys Glu Pro Ser Lys Glu Leu
145 150 155 160

Pro Ser Glu Lys Ile Thr Tyr Lys Gly Thr Trp Asp Tyr Val Thr Asp
165 170 175

Ala Met Glu Lys Gln Arg Phe Glu Gly Leu Gly Ser Ala Ala Gly Gly
180 185 190

Asp Lys Ser Gly Ala Leu Ser Ala Leu Glu Glu Gly Val Leu Arg Asn

```
        195                 200                 205

Gln Ala Glu Ala Ser Ser Gly His Thr Asp Phe Gly Met Thr Ser Glu
    210                 215                 220

Phe Glu Val Asp Phe Ser Asp Lys Thr Ile Lys Gly Thr Leu Tyr Arg
225                 230                 235                 240

Asn Asn Arg Ile Thr Gln Asn Asn Ser Glu Asn Lys Gln Ile Lys Thr
                245                 250                 255

Thr Arg Tyr Thr Ile Gln Ala Thr Leu His Gly Asn Arg Phe Lys Gly
            260                 265                 270

Lys Ala Leu Ala Ala Asp Lys Gly Ala Thr Asn Gly Ser His Pro Phe
        275                 280                 285

Ile Ser Asp Ser Asp Ser Leu Glu Gly Gly Phe Tyr Gly Pro Lys Gly
    290                 295                 300

Glu Glu Leu Ala Gly Lys Phe Leu Ser Asn Asp Asn Lys Val Ala Ala
305                 310                 315                 320

Val Phe Gly Ala Lys Gln Lys Asp Lys Lys Asp Gly Glu Asn Ala Ala
                325                 330                 335

Gly Pro Ala Thr Glu Thr Val Ile Asp Ala Tyr Arg Ile Thr Gly Glu
            340                 345                 350

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

Leu Val Asp Gly Val Glu Leu Ser Leu Leu Pro Ser Glu Gly Asn Lys
    370                 375                 380

Ala Ala Phe Gln His Glu Ile Glu Gln Asn Gly Val Lys Ala Thr Val
385                 390                 395                 400

Cys Cys Ser Asn Leu Asp Tyr Met Ser Phe Gly Lys Leu Ser Lys Glu
                405                 410                 415

Asn Lys Asp Asp Met Phe Leu Gln Gly Val Arg Thr Pro Val Ser Asp
            420                 425                 430

Val Ala Ala Arg Thr Glu Ala Asn Ala Lys Tyr Arg Gly Thr Trp Tyr
        435                 440                 445

Gly Tyr Ile Ala Asn Gly Thr Ser Trp Ser Gly Glu Ala Ser Asn Gln
    450                 455                 460

Glu Gly Gly Asn Arg Ala Glu Phe Asp Val Asp Phe Ser Thr Lys Lys
465                 470                 475                 480

Ile Ser Gly Thr Leu Thr Ala Lys Asp Arg Thr Ser Pro Ala Phe Thr
                485                 490                 495
```

```
Ile Thr Ala Met Ile Lys Asp Asn Gly Phe Ser Gly Val Ala Lys Thr
            500                 505                 510

Gly Glu Asn Gly Phe Ala Leu Asp Pro Gln Asn Thr Gly Asn Ser His
        515                 520                 525

Tyr Thr His Ile Glu Ala Thr Val Ser Gly Gly Phe Tyr Gly Lys Asn
    530                 535                 540

Ala Ile Glu Met Gly Gly Ser Phe Ser Phe Pro Gly Asn Ala Pro Glu
545                 550                 555                 560

Gly Lys Gln Glu Lys Ala Ser Val Val Phe Gly Ala Lys Arg Gln
                565                 570                 575
```

<210> 149

<211> 1707

<212> DNA

<213> Neisseria meningitidis

<400> 149

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ggatcttctg aaaacagtaa gctgaccacg gttttggatg cggttgaatt gacactaaac       60

gacaagaaaa tcaaaaatct cgacaacttc agcaatgccg cccaactggt tgtcgacggc      120

attatgattc cgctcctgcc caaggattcc gaaagcggga acactcaggc agataaaggt      180

aaaaacggcg gaacagaatt tacccgcaaa tttgaacaca cgccggaaag tgataaaaaa      240

gacgcccaag caggtacgca gacgaatggg gcgcaaaccg cttcaaatac ggcaggtgat      300

accaatggca aaacaaaaac ctatgaagtc gaagtctgct gttccaacct caattatctg      360

aaatacggaa tgttgacgcg caaaaacagc aagtccgcga tgcaggcagg aggaaacagt      420

agtcaagctg atgctaaaac ggaacaagtt gaacaaagta tgttcctcca aggcgagcgt      480

accgatgaaa aagagattcc aaccgaccaa aacgtcgttt atcgggggtc ttggtacggg      540

catattgcca acggcacaag ctggagcggc aatgcttctg ataaagaggg cggcaacagg      600

gcggaattta ctgtgaattt tgccgataaa aaaattaccg gcaagttaac cgctgaaaac      660

aggcaggcgc aaacctttac cattgaggga atgattcagg gcaacggctt tgaaggtacg      720

gcgaaaactg ctgagtcagg ttttgatctc gatcaaaaaa ataccacccg cacgcctaag      780

gcatatatca cagatgccaa ggtaaagggc ggtttttacg ggcctaaagc cgaagagttg      840

ggcggatggt ttgcctatcc gggcgataaa caaacggaaa aggcaacagc tacatccagc      900

gatggaaatt cagcaagcag cgcgaccgtg gtattcggtg cgaaacgcca acagcctgtg      960

caaggggaaa acgcggcagg gcctgcaacg gaaaccgtga tagatgcata ccgtattacc     1020

ggcgaggagt ttaagaaaga gcaaatagac agttttggag atgtgaaaaa gctgctggtt     1080

gacggagtgg agctttcact gctgccgtct gagggcaata aggcggcatt tcagcacgag     1140

attgagcaaa acggcgtgaa ggcaacggtg tgttgttcca acttggatta catgagtttt     1200

gggaagctgt caaaagaaaa taaagacgat atgttcctgc aaggtgtccg cactccagta     1260

tccgatgtgg cggcaaggac ggaggcaaac gccaaatatc gcggtacttg gtacggatat     1320

...                                                                  1380
```

```
attgccaacg gcacaagctg gagcggcgaa gcctccaatc aggaaggtgg taatagggca     1380

gagtttgacg tggatttttc cactaaaaaa atcagtggca cactgacggc aaaagaccgt     1440

acgtctcctg cgtttactat tactgccatg attaaggaca acggtttttc aggtgtggcg     1500

aaaaccggtg aaaacggctt tgcgctggat ccgcaaaata ccggaaattc ccactatacg     1560

catattgaag ccactgtatc cggcggtttc tacggcaaaa acgccatcga gatgggcgga     1620

tcgttctcat ttccgggaaa tgcaccagag ggaaaacaag aaaaagcatc ggtggtattc     1680

ggtgcgaaac gccaacagct tgtgcaa                                         1707
```

<210> 150

<211> 569

<212> PRT

<213> Neisseria meningitidis

<400> 150

```
Gly Ser Ser Glu Asn Ser Lys Leu Thr Thr Val Leu Asp Ala Val Glu
1               5                  10                  15

Leu Thr Leu Asn Asp Lys Lys Ile Lys Asn Leu Asp Asn Phe Ser Asn
            20                  25                  30

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

Asp Ser Glu Ser Gly Asn Thr Gln Ala Asp Lys Gly Lys Asn Gly Gly
    50                  55                  60

Thr Glu Phe Thr Arg Lys Phe Glu His Thr Pro Glu Ser Asp Lys Lys
65                  70                  75                  80

Asp Ala Gln Ala Gly Thr Gln Thr Asn Gly Ala Gln Thr Ala Ser Asn
                85                  90                  95

Thr Ala Gly Asp Thr Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val
            100                 105                 110

Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr Gly Met Leu Thr Arg Lys
        115                 120                 125

Asn Ser Lys Ser Ala Met Gln Ala Gly Gly Asn Ser Ser Gln Ala Asp
    130                 135                 140

Ala Lys Thr Glu Gln Val Glu Gln Ser Met Phe Leu Gln Gly Glu Arg
145                 150                 155                 160

Thr Asp Glu Lys Glu Ile Pro Thr Asp Gln Asn Val Val Tyr Arg Gly
                165                 170                 175

Ser Trp Tyr Gly His Ile Ala Asn Gly Thr Ser Trp Ser Gly Asn Ala
            180                 185                 190

Ser Asp Lys Glu Gly Gly Asn Arg Ala Glu Phe Thr Val Asn Phe Ala
        195                 200                 205
```

```
Asp Lys Lys Ile Thr Gly Lys Leu Thr Ala Glu Asn Arg Gln Ala Gln
    210                 215                 220

Thr Phe Thr Ile Glu Gly Met Ile Gln Gly Asn Gly Phe Glu Gly Thr
225                 230                 235                 240

Ala Lys Thr Ala Glu Ser Gly Phe Asp Leu Asp Gln Lys Asn Thr Thr
                245                 250                 255

Arg Thr Pro Lys Ala Tyr Ile Thr Asp Ala Lys Val Lys Gly Gly Phe

            260                 265                 270

Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly
        275                 280                 285

Asp Lys Gln Thr Glu Lys Ala Thr Ala Thr Ser Ser Asp Gly Asn Ser
    290                 295                 300

Ala Ser Ser Ala Thr Val Val Phe Gly Ala Lys Arg Gln Gln Pro Val
305                 310                 315                 320

Gln Gly Glu Asn Ala Ala Gly Pro Ala Thr Glu Thr Val Ile Asp Ala
                325                 330                 335

Tyr Arg Ile Thr Gly Glu Glu Phe Lys Lys Glu Gln Ile Asp Ser Phe
            340                 345                 350

Gly Asp Val Lys Lys Leu Leu Val Asp Gly Val Glu Leu Ser Leu Leu
        355                 360                 365

Pro Ser Glu Gly Asn Lys Ala Ala Phe Gln His Glu Ile Glu Gln Asn
    370                 375                 380

Gly Val Lys Ala Thr Val Cys Cys Ser Asn Leu Asp Tyr Met Ser Phe
385                 390                 395                 400

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

Arg Thr Pro Val Ser Asp Val Ala Ala Arg Thr Glu Ala Asn Ala Lys
            420                 425                 430

Tyr Arg Gly Thr Trp Tyr Gly Tyr Ile Ala Asn Gly Thr Ser Trp Ser
        435                 440                 445

Gly Glu Ala Ser Asn Gln Glu Gly Gly Asn Arg Ala Glu Phe Asp Val
    450                 455                 460

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

Thr Ser Pro Ala Phe Thr Ile Thr Ala Met Ile Lys Asp Asn Gly Phe
                485                 490                 495

Ser Gly Val Ala Lys Thr Gly Glu Asn Gly Phe Ala Leu Asp Pro Gln
```

```
                500                 505                 510

Asn Thr Gly Asn Ser His Tyr Thr His Ile Glu Ala Thr Val Ser Gly
        515                 520                 525

Gly Phe Tyr Gly Lys Asn Ala Ile Glu Met Gly Gly Ser Phe Ser Phe
    530                 535                 540

Pro Gly Asn Ala Pro Glu Gly Lys Gln Glu Lys Ala Ser Val Val Phe
545                 550                 555                 560

Gly Ala Lys Arg Gln Gln Leu Val Gln
                565
```

<210> 151

<211> 2733

<212> DNA

<213> Neisseria meningitidis

<400> 151

```
atgcaacagc aacatttgtt ccgattaaat attttatgcc tgtcgctgat gactgcgctg       60
cctgcttatg cagaaaatgt gcaagccgga caagcacagg aaaaacagtt ggataccata      120
caggtaaaag ccaaaaaaca gaaaacccgc cgcgataacg aagtaaccgg tctgggcaaa      180
ttggtcaaaa ccgccgacac cctcagcaag gaacaggtac tcgatatccg cgacctgacg      240
cgttacgacc ccggcatcgc cgtggtcgaa caggggcgcg gcgcaagttc gggctactcg      300
atacgcggta tggacaaaaa ccgcgtttcc ttgacggtgg acggcttggc gcaaatacag      360
tcctacaccg cgcaggcggc attgggcggg acgaggacgg cgggcagcag cggcgcaatc      420
aatgaaatcg agtatgaaaa cgtcaaagct gtcgaaatca gcaaaggctc aaactcggtc      480
gaacaaggca gcggcgcatt ggcgggttcg gtcgcatttc aaaccaaaac cgccgacgat      540
gttatcgggg aaggcaggca gtggggcatt cagagtaaaa ccgcctattc cggcaaaaac      600
cgggggctta cccaatccat cgcgctggcg gggcgcatcg gcggtgcgga ggctttgctg      660
atccacaccg ggcggcgcgc gggggaaatc cgcgcacacg aagatgccgg acgcggcgtt      720
cagagcttta acaggctggt gccggttgaa gacagcagcg aatacgccta tttcatcgtt      780
gaagatgaat gcgaaggcaa aaattacgaa acgtgtaaaa gcaaaccgaa aaaagatgtt      840
gtcggcaaag acgaacgtca aacggtttcc acccgagact acacgggccc caaccgcttc      900
ctcgccgatc cgctttcata cgaaagccga tcgtggctgt tccgcccggg ttttcgtttt      960
gaaaacaaac ggcactacat cggcggcata ctcgaacaca cgcaacaaac tttcgacacg     1020
cgcgatatga cggttccggc attcctgacc aaggcggttt ttgatgcaaa ttcaaaacag     1080
gcgggttctt tgcccggcaa cggcaaatac gcgggcaacc acaaatacgg cggactgttt     1140
accaacggcg aaaacggtgc gctggtgggc gcggaatacg gtacgggcgt gttttacgac     1200
gagacgcaca ccaaaagccg ctacggtttg gaatatgtct ataccaatgc cgataaagac     1260
acttgggcgg attatgcccg cctctcttac gaccggcagg gcatcggttt ggacaatcat     1320
tttcagcaga cgcactgttc tgccgacggt tcggacaaat attgccgccc gagtgccgac     1380
```

```
aagccgtttt cctattacaa atccgaccgc gtgatttacg gggaaagcca caggctcttg     1440

caggcggcat tcaaaaaatc cttcgatacc gccaaaatcc gccacaacct gagcgtgaat     1500

ctcgggtttg accgctttga ctctaatctc cgccatcagg attattatta tcaacatgcc     1560

aaccgcgcct attcgtcgaa aacgcccccc aaaaccgcca accccaacgg cgacaagagc     1620

aaaccctatt gggtcagcat aggcgggggg aatgtggtta cggggcaaat ctgcctcttt     1680

ggcaacaata cttatacgga ctgcacgccg cgcagcatca acggcaaaag ctattacgcg     1740

gcagttcggg acaatgtccg tttgggcagg tgggcggatg tcggcgcggg gttgcgctac     1800

gactaccgca gcacgcattc ggacgacggc agcgtttcca ccggcacgca ccgcaccctg     1860

tcctggaacg ccggcatcgt cctcaaacct gccgactggc tggatttgac ttaccgcact     1920

tcaaccggct tccgcctgcc ctcgtttgcg gaaatgtacg gctggcggtc gggtgttcaa     1980

agcaaggcgg tcaaaatcga tccggaaaaa tcgttcaaca aagaagccgg catcgtgttt     2040

aaaggcgatt tcggcaactt ggaggcaagt tggttcaaca atgcctaccg cgatttgatt     2100

gtccggggtt atgaagcgca aattaaaaac ggcaaagaag aagccaaagg cgacccggct     2160

tacctcaatg cccaaagcgc gcggattacc ggcatcaata ttttgggcaa aatcgattgg     2220

aacggcgtat gggataaatt gcccgaaggt tggtattcta catttgccta taatcgtgtc     2280

catgtccgcg acatcaaaaa acgcgcagac cgcaccgata ttcaatcaca cctgtttgat     2340

gccatccaac cctcgcgcta tgtcgtcggc ttgggctatg accaaccgga aggcaaatgg     2400

ggtgtgaacg gtatgctgac ttattccaaa gccaaggaaa tcacagagtt gttgggcagc     2460

cgggctttgc tcaacggcaa cagccgcaat acaaaagcca ccgcgcgccg tacccgccct     2520

tggtatattg tggatgtgtc cggttattac acgattaaaa aacacttcac cctccgtgcg     2580

ggcgtgtaca acctcctcaa ctaccgctat gttacttggg aaaatgtgcg gcaaactgcc     2640

ggcggcgcag tcaaccaaca caaaaatgtc ggcgtttaca accgatatgc cgcccccggc     2700

cgaaactaca catttagctt ggaaatgaag ttt                                  2733
```

<210> 152

<211> 911

<212> PRT

<213> Neisseria meningitidis

<400> 152

```
Met Gln Gln Gln His Leu Phe Arg Leu Asn Ile Leu Cys Leu Ser Leu
1               5                  10                  15

Met Thr Ala Leu Pro Ala Tyr Ala Glu Asn Val Gln Ala Gly Gln Ala
            20                  25                  30

Gln Glu Lys Gln Leu Asp Thr Ile Gln Val Lys Ala Lys Lys Gln Lys
        35                  40                  45

Thr Arg Arg Asp Asn Glu Val Thr Gly Leu Gly Lys Leu Val Lys Thr
    50                  55                  60

Ala Asp Thr Leu Ser Lys Glu Gln Val Leu Asp Ile Arg Asp Leu Thr
65                  70                  75                  80
```

```
Arg Tyr Asp Pro Gly Ile Ala Val Val Glu Gln Gly Arg Gly Ala Ser
                85                  90                  95

Ser Gly Tyr Ser Ile Arg Gly Met Asp Lys Asn Arg Val Ser Leu Thr
            100                 105                 110

Val Asp Gly Leu Ala Gln Ile Gln Ser Tyr Thr Ala Gln Ala Ala Leu
        115                 120                 125

Gly Gly Thr Arg Thr Ala Gly Ser Ser Gly Ala Ile Asn Glu Ile Glu
    130                 135                 140

Tyr Glu Asn Val Lys Ala Val Glu Ile Ser Lys Gly Ser Asn Ser Val
145                 150                 155                 160

Glu Gln Gly Ser Gly Ala Leu Ala Gly Ser Val Ala Phe Gln Thr Lys
                165                 170                 175

Thr Ala Asp Asp Val Ile Gly Glu Gly Arg Gln Trp Gly Ile Gln Ser
            180                 185                 190

Lys Thr Ala Tyr Ser Gly Lys Asn Arg Gly Leu Thr Gln Ser Ile Ala
        195                 200                 205

Leu Ala Gly Arg Ile Gly Gly Ala Glu Ala Leu Leu Ile His Thr Gly
    210                 215                 220

Arg Arg Ala Gly Glu Ile Arg Ala His Glu Asp Ala Gly Arg Gly Val
225                 230                 235                 240

Gln Ser Phe Asn Arg Leu Val Pro Val Glu Asp Ser Ser Glu Tyr Ala
                245                 250                 255

Tyr Phe Ile Val Glu Asp Glu Cys Glu Gly Lys Asn Tyr Glu Thr Cys
            260                 265                 270

Lys Ser Lys Pro Lys Lys Asp Val Val Gly Lys Asp Glu Arg Gln Thr
        275                 280                 285

Val Ser Thr Arg Asp Tyr Thr Gly Pro Asn Arg Phe Leu Ala Asp Pro
    290                 295                 300

Leu Ser Tyr Glu Ser Arg Ser Trp Leu Phe Arg Pro Gly Phe Arg Phe
305                 310                 315                 320

Glu Asn Lys Arg His Tyr Ile Gly Gly Ile Leu Glu His Thr Gln Gln
                325                 330                 335

Thr Phe Asp Thr Arg Asp Met Thr Val Pro Ala Phe Leu Thr Lys Ala
            340                 345                 350

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

Lys Tyr Ala Gly Asn His Lys Tyr Gly Gly Leu Phe Thr Asn Gly Glu
    370                 375                 380
```

```
Asn Gly Ala Leu Val Gly Ala Glu Tyr Gly Thr Gly Val Phe Tyr Asp
385                 390                 395                 400

Glu Thr His Thr Lys Ser Arg Tyr Gly Leu Glu Tyr Val Tyr Thr Asn
                405                 410                 415

Ala Asp Lys Asp Thr Trp Ala Asp Tyr Ala Arg Leu Ser Tyr Asp Arg
            420                 425                 430

Gln Gly Ile Gly Leu Asp Asn His Phe Gln Gln Thr His Cys Ser Ala
        435                 440                 445

Asp Gly Ser Asp Lys Tyr Cys Arg Pro Ser Ala Asp Lys Pro Phe Ser
    450                 455                 460

Tyr Tyr Lys Ser Asp Arg Val Ile Tyr Gly Glu Ser His Arg Leu Leu
465                 470                 475                 480

Gln Ala Ala Phe Lys Lys Ser Phe Asp Thr Ala Lys Ile Arg His Asn
                485                 490                 495

Leu Ser Val Asn Leu Gly Phe Asp Arg Phe Asp Ser Asn Leu Arg His
            500                 505                 510

Gln Asp Tyr Tyr Tyr Gln His Ala Asn Arg Ala Tyr Ser Ser Lys Thr
        515                 520                 525

Pro Pro Lys Thr Ala Asn Pro Asn Gly Asp Lys Ser Lys Pro Tyr Trp
    530                 535                 540

Val Ser Ile Gly Gly Gly Asn Val Val Thr Gly Gln Ile Cys Leu Phe
545                 550                 555                 560

Gly Asn Asn Thr Tyr Thr Asp Cys Thr Pro Arg Ser Ile Asn Gly Lys
                565                 570                 575

Ser Tyr Tyr Ala Ala Val Arg Asp Asn Val Arg Leu Gly Arg Trp Ala
            580                 585                 590

Asp Val Gly Ala Gly Leu Arg Tyr Asp Tyr Arg Ser Thr His Ser Asp
        595                 600                 605

Asp Gly Ser Val Ser Thr Gly Thr His Arg Thr Leu Ser Trp Asn Ala
    610                 615                 620

Gly Ile Val Leu Lys Pro Ala Asp Trp Leu Asp Leu Thr Tyr Arg Thr
625                 630                 635                 640

Ser Thr Gly Phe Arg Leu Pro Ser Phe Ala Glu Met Tyr Gly Trp Arg
                645                 650                 655

Ser Gly Val Gln Ser Lys Ala Val Lys Ile Asp Pro Glu Lys Ser Phe
            660                 665                 670

Asn Lys Glu Ala Gly Ile Val Phe Lys Gly Asp Phe Gly Asn Leu Glu
        675                 680                 685
```

```
Ala Ser Trp Phe Asn Asn Ala Tyr Arg Asp Leu Ile Val Arg Gly Tyr
    690                 695                 700

Glu Ala Gln Ile Lys Asn Gly Lys Glu Glu Ala Lys Gly Asp Pro Ala
705                 710                 715                 720

Tyr Leu Asn Ala Gln Ser Ala Arg Ile Thr Gly Ile Asn Ile Leu Gly
                725                 730                 735

Lys Ile Asp Trp Asn Gly Val Trp Asp Lys Leu Pro Glu Gly Trp Tyr
            740                 745                 750

Ser Thr Phe Ala Tyr Asn Arg Val His Val Arg Asp Ile Lys Lys Arg
        755                 760                 765

Ala Asp Arg Thr Asp Ile Gln Ser His Leu Phe Asp Ala Ile Gln Pro

    770                 775                 780

Ser Arg Tyr Val Val Gly Leu Gly Tyr Asp Gln Pro Glu Gly Lys Trp
785                 790                 795                 800

Gly Val Asn Gly Met Leu Thr Tyr Ser Lys Ala Lys Glu Ile Thr Glu
                805                 810                 815

Leu Leu Gly Ser Arg Ala Leu Leu Asn Gly Asn Ser Arg Asn Thr Lys
            820                 825                 830

Ala Thr Ala Arg Arg Thr Arg Pro Trp Tyr Ile Val Asp Val Ser Gly
        835                 840                 845

Tyr Tyr Thr Ile Lys Lys His Phe Thr Leu Arg Ala Gly Val Tyr Asn
    850                 855                 860

Leu Leu Asn Tyr Arg Tyr Val Thr Trp Glu Asn Val Arg Gln Thr Ala
865                 870                 875                 880

Gly Gly Ala Val Asn Gln His Lys Asn Val Gly Val Tyr Asn Arg Tyr
                885                 890                 895

Ala Ala Pro Gly Arg Asn Tyr Thr Phe Ser Leu Glu Met Lys Phe
            900                 905                 910
```

<210> 153

<211> 760

<212> DNA

<213> Neisseria meningitidis

<400> 153

```
ggatcctcgt ctgaaaacag taagctgacc acggttttgg atgcggttga attgacacta      60

aacgacaaga aaatcaaaaa tctcgacaac ttcagcaatg ccgcccaact ggttgtcgac     120

ggcattatga ttgatctggc cggaacagaa tttacccgca aatttgaaca cacggccaag     180
```

```
gaaatcacag agttgttggg cagccgggct ttgctcaacg gcaacagccg caatacaaaa      240

gccaccgcgc gccgtacccg cacctatgaa gtcgaagtct gctgttccaa aacaaagtat      300

gttcctccaa ggcgagcgta ccgatgaaaa agagattcca accgaccaaa acgtcgttta      360

tcgggggtct tggtacgggc atattgccaa cggcacaagc tggagcggca atgcttctga      420

taaagagggc ggcaacaggg cggaatttac tgtgaatttt gccgataaaa aaattaccgg      480

caagttaacc gctgaaaaca ggcaggcgca aacctttacc attgagggaa tgattcaggg      540

caacggcttt gaaggtacgg cgaaaactgc tgagtcaggt tttgatctcg atcaaaaaaa      600

taccacccgc acgcctaagg catatatcac agatgccaag gtaaagggcg gtttttacgg      660

gcctaaagcc gaagagttgg gcggatggtt tgcctatcat aaaagcgata acggcagcgc      720

gaccgtggta ttcggtgcga aacgccaaca gcctgtgcaa                            760
```

<210> 154

<211> 270

<212> PRT

<213> Neisseria meningitidis

<400> 154

```
Gly Ser Ser Ser Glu Asn Ser Lys Leu Thr Thr Val Leu Asp Ala Val
1               5                  10                  15

Glu Leu Thr Leu Asn Asp Lys Lys Ile Lys Asn Leu Asp Asn Phe Ser
            20                  25                  30

Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met Ile Asp Leu Ala Gly
        35                  40                  45

Thr Glu Phe Thr Arg Lys Phe Glu His Thr Ala Lys Glu Ile Thr Glu
    50                  55                  60

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

Ala Thr Ala Arg Arg Thr Arg Thr Tyr Glu Val Glu Val Cys Cys Ser
                85                  90                  95

Asn Leu Asn Tyr Leu Lys Tyr Gly Met Leu Thr Arg Lys Gly Lys Gln
            100                 105                 110

Val Glu Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu
        115                 120                 125

Ile Pro Thr Asp Gln Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His
    130                 135                 140

Ile Ala Asn Gly Thr Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly
145                 150                 155                 160

Gly Asn Arg Ala Glu Phe Thr Val Asn Phe Ala Asp Lys Lys Ile Thr
                165                 170                 175
```

```
Gly Lys Leu Thr Ala Glu Asn Arg Gln Ala Gln Thr Phe Thr Ile Glu
            180                 185                 190

Gly Met Ile Gln Gly Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala Glu
        195                 200                 205

Ser Gly Phe Asp Leu Asp Gln Lys Asn Thr Thr Arg Thr Pro Lys Ala
    210                 215                 220

Tyr Ile Thr Asp Ala Lys Val Lys Gly Gly Phe Tyr Gly Pro Lys Ala
225                 230                 235                 240

Glu Glu Leu Gly Gly Trp Phe Ala Tyr His Lys Ser Asp Asn Gly Ser
                245                 250                 255

Ala Thr Val Val Phe Gly Ala Lys Arg Gln Gln Pro Val Gln
            260                 265                 270
```

<210> 155

<211> 807

<212> DNA

<213> Neisseria meningitidis

<400> 155

```
ggatcctcgt ctgaaaacag taagctgacc acggttttgg atgcggttga attgacacta       60

aacgacaaga aaatcaaaaa tctcgacaac ttcagcaatg ccgcccaact ggttgtcgac      120

ggcattatga ttgatctggc cggaacagaa tttacccgca aatttgaaca cacgattaac      180

ggcaaaacct atgaagtcga agtctgctgt tccaacctca attatctgaa atacggaatg      240

ttgacgcgca aagttacttg ggaaaatgtg cggcaaactg ccggcggcgc agtcaaccaa      300

cacaaaaatg tcggcgttta caaccgatat gccgttgaac aaagtatgtt cctccaaggc      360

gagcgtaccg atgaaaaaga gattccaacc gaccaaaacg tcgtttatcg ggggtcttgg      420

tacgggcata ttgccaacgg cacaagctgg agcggcaatg cttctgataa agagggcggc      480

aacagggcgg aatttactgt gaattttgcc gataaaaaaa ttaccggcaa gttaaccgct      540

gaaaacaggc aggcgcaaac ctttaccatt gagggaatga ttcagggcaa cggctttgaa      600

ggtacggcga aaactgctga gtcaggtttt gatctcgatc aaaaaaatac cacccgcacg      660

cctaaggcat atatcacaga tgccaaggta aagggcggtt tttacgggcc taaagccgaa      720

gagttgggcg gatggtttgc ctatcataaa agcgataacg gcagcgcgac cgtggtattc      780

ggtgcgaaac gccaacagcc tgtgcaa                                          807
```

<210> 156

<211> 269

<212> PRT

<213> Neisseria meningitidis

<400> 156

```
Gly Ser Ser Ser Glu Asn Ser Lys Leu Thr Thr Val Leu Asp Ala Val
1               5                   10                  15
```

```
Glu Leu Thr Leu Asn Asp Lys Lys Ile Lys Asn Leu Asp Asn Phe Ser
            20                  25                  30

Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met Ile Asp Leu Ala Gly
        35                  40                  45

Thr Glu Phe Thr Arg Lys Phe Glu His Thr Ile Asn Gly Lys Thr Tyr
    50                  55                  60

Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr Gly Met
65                  70                  75                  80

Leu Thr Arg Lys Val Thr Trp Glu Asn Val Arg Gln Thr Ala Gly Gly
                85                  90                  95

Ala Val Asn Gln His Lys Asn Val Gly Val Tyr Asn Arg Tyr Ala Val
            100                 105                 110

Glu Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile
        115                 120                 125

Pro Thr Asp Gln Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile
    130                 135                 140

Ala Asn Gly Thr Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly
145                 150                 155                 160

Asn Arg Ala Glu Phe Thr Val Asn Phe Ala Asp Lys Lys Ile Thr Gly
                165                 170                 175

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

Met Ile Gln Gly Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala Glu Ser
        195                 200                 205

Gly Phe Asp Leu Asp Gln Lys Asn Thr Thr Arg Thr Pro Lys Ala Tyr
    210                 215                 220

Ile Thr Asp Ala Lys Val Lys Gly Gly Phe Tyr Gly Pro Lys Ala Glu
225                 230                 235                 240

Glu Leu Gly Gly Trp Phe Ala Tyr His Lys Ser Asp Asn Gly Ser Ala
                245                 250                 255

Thr Val Val Phe Gly Ala Lys Arg Gln Gln Pro Val Gln
            260                 265
```

<210> 157

<211> 759

<212> DNA

<213> Neisseria meningitidis

<400> 157

```
ggatcctcgt ctgaaaacag taagctgacc acggttttgg atgcggttga attgacacta       60

aacgacaaga aaatcaaaaa tctcgacaac ttcagcaatg ccgcccaact ggttgtcgac      120
```

```
ggcattatga ttgatctggc cggaacagaa tttacccgca aatttgaaca cacgattaac      180

ggcaaaacct atgaagtcga agtctgctgt tccaacctca attatctgaa atacggaatg      240

ttgacgcgca aaggcaaaca ggttgaacaa agtatgttcc tccaaggcga gcgtaccgat      300

gaaaaagaga ttccaaccga ccaaaacgtc gtttatcggg ggtcttggta cgggcatatt      360

gccaacggca caagctggag cggcaatgct tctgataaag agggcggcaa cagggcggaa      420

tttactgtga attttgccga taaaaaaatt accggcaagt taaccgctga aaacaggcag      480

gcgcaaacct ttaccattga gggaatgatt cagggcaacg gctttgaagg tacggcgaaa      540

actgctgagt caggttttga tctcgatcaa aaaaatacca cccgcacgcc taaggcatat      600

atcacagatg ccaaggtaaa gggcggtttt tacgggccta aagccgaaga gttgggcgga      660

tggtttgcct ataccgcgca ggcggcattg ggcgggacga ggacggcggg cagcagcgcg      720

accgtggtat tcggtgcgaa acgccaacag cctgtgcaa                              759
```

<210> 158

<211> 253

<212> PRT

<213> Neisseria meningitidis

<400> 158

```
Gly Ser Ser Ser Glu Asn Ser Lys Leu Thr Thr Val Leu Asp Ala Val
1               5                   10                  15

Glu Leu Thr Leu Asn Asp Lys Lys Ile Lys Asn Leu Asp Asn Phe Ser
            20                  25                  30

Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met Ile Asp Leu Ala Gly
        35                  40                  45

Thr Glu Phe Thr Arg Lys Phe Glu His Thr Ile Asn Gly Lys Thr Tyr
    50                  55                  60

Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr Gly Met
65                  70                  75                  80

Leu Thr Arg Lys Gly Lys Gln Val Glu Gln Ser Met Phe Leu Gln Gly
                85                  90                  95

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

Arg Gly Ser Trp Tyr Gly His Ile Ala Asn Gly Thr Ser Trp Ser Gly
        115                 120                 125

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

Phe Ala Asp Lys Lys Ile Thr Gly Lys Leu Thr Ala Glu Asn Arg Gln
145                 150                 155                 160

Ala Gln Thr Phe Thr Ile Glu Gly Met Ile Gln Gly Asn Gly Phe Glu
```

```
                165                 170                 175

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

Thr Thr Arg Thr Pro Lys Ala Tyr Ile Thr Asp Ala Lys Val Lys Gly
        195                 200                 205

Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr
    210                 215                 220

Thr Ala Gln Ala Ala Leu Gly Gly Thr Arg Thr Ala Gly Ser Ser Ala
225                 230                 235                 240

Thr Val Val Phe Gly Ala Lys Arg Gln Gln Pro Val Gln
                245                 250
```

<210> 159

<211> 774

<212> DNA

<213> Neisseria meningitidis

<400> 159

```
ggatcctcgt ctgaaaacag taagctgacc acggttttgg atgcggttga attgacacta       60

aacgacaaga aaatcaaaaa tctcgacaac ttcagcaatg ccgcccaact ggttgtcgac      120

ggcattatga ttccactcct cccagccaca aaagccgtct ttgatgagaa ccgcaaatac      180

ggcccggaat ttacccgcaa atttgaacac acgattaacg gcaaaaccta tgaagtcgaa      240

gtctgctgtt ccaacctcaa ttatctgaaa tacggaatgt tgacgcgcaa aggcaaacag      300

gttgaacaaa gtatgttcct ccaaggcgag cgtaccgatg aaaaagagat tccaaccgac      360

caaaacgtcg tttatcgggg gtcttggtac gggcatattg ccaacggcac aagctggagc      420

ggcaatgctt ctgataaaga gggcggcaac agggcggaat ttactgtgaa ttttgccgat      480

aaaaaaatta ccggcaagtt aaccgctgaa aacaggcagg cgcaaacctt taccattgag      540

ggaatgattc agggcaacgg ctttgaaggt acggcgaaaa ctgctgagtc aggttttgat      600

ctcgatcaaa aaaataccac ccgcacgcct aaggcatata tcacagatgc caaggtaaag      660

ggcggttttt acgggcctaa agccgaagag ttgggcggat ggtttgccta tcataaaagc      720

gataacggca gcgcgaccgt ggtattcggt gcgaaacgcc aacagcctgt gcaa            774
```

<210> 160

<211> 258

<212> PRT

<213> Neisseria meningitidis

<400> 160

```
Gly Ser Ser Ser Glu Asn Ser Lys Leu Thr Thr Val Leu Asp Ala Val
1               5                   10                  15

Glu Leu Thr Leu Asn Asp Lys Lys Ile Lys Asn Leu Asp Asn Phe Ser
            20                  25                  30
```

```
Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met Ile Pro Leu Leu Pro
        35                  40                  45

Ala Thr Lys Ala Val Phe Asp Glu Asn Arg Lys Tyr Gly Pro Glu Phe
    50                  55                  60

Thr Arg Lys Phe Glu His Thr Ile Asn Gly Lys Thr Tyr Glu Val Glu
65                  70                  75                  80

Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr Gly Met Leu Thr Arg
                85                  90                  95

Lys Gly Lys Gln Val Glu Gln Ser Met Phe Leu Gln Gly Glu Arg Thr
            100                 105                 110

Asp Glu Lys Glu Ile Pro Thr Asp Gln Asn Val Val Tyr Arg Gly Ser
        115                 120                 125

Trp Tyr Gly His Ile Ala Asn Gly Thr Ser Trp Ser Gly Asn Ala Ser
    130                 135                 140

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

Lys Lys Ile Thr Gly Lys Leu Thr Ala Glu Asn Arg Gln Ala Gln Thr
                165                 170                 175

Phe Thr Ile Glu Gly Met Ile Gln Gly Asn Gly Phe Glu Gly Thr Ala
            180                 185                 190

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

Thr Pro Lys Ala Tyr Ile Thr Asp Ala Lys Val Lys Gly Gly Phe Tyr
    210                 215                 220

Gly Pro Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr His Lys Ser
225                 230                 235                 240

Asp Asn Gly Ser Ala Thr Val Val Phe Gly Ala Lys Arg Gln Gln Pro
                245                 250                 255

Val Gln
```

<210> 161

<211> 2832

<212> DNA

<213> Neisseria meningitidis

<400> 161

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atgaataaga aacacggttt tccgctgact ctgactgcct tggccattgc aaccgctttt       60

ccggcttatg ctgcccaagc ggggggggcg acacctgatg ccgcgcagac ccaatccctg      120

aaagagatta ccgtccgtgc cgccaaagtg ggacggcgat cgaaagaggc gaccggtttg      180
```

ggcaaaatcg tcaaaacgtc ggaaacgttg aacaaagaac aggtactcgg tatccgcgac 240

ctgacgcgct acgatccggg cgtggcggtt gtcgaacagg gcaacggcgc gagcggcggc 300

tactcgatac gcggcgtgga taaaaaccgt gtggcggttt cggtcgacgg tgttgcccaa 360

atacaggcgt ttaccgtgca gggatcgttg agcggatacg gcggacgcgg cggcagcggt 420

gcaatcaacg aaatcgaata tgaaaacatc agcacggtgg aaatcgacaa aggtgccggt 480

tcgtccgatc acggcagcgg cgcactcggc ggcgcggtcg ccttccgcac caaagaggcg 540

gcagacctga tttcagacgg caaaagttgg gggatacagg caaaaaccgc ctacggcagt 600

aaaaaccgcc aatttatgaa gtcgctcggc gcggggttca gcaaagacgg ttgggaaggg 660

ctgttaatcc gaaccgaacg ccaagggcgg gaaacgcgcc cgcacggcga tattgcggac 720

ggggtggaat acggcataga ccgtttggac gcgttccgtc agacatacga tattaaacgc 780

aagacaagag agccattttt ctcagtagag ggcgagcgtg aatccaagcc cgtggcaaaa 840

ttggcgggct acgggaaata tttgaacaac cagctcaacc gctgggtaaa agaacgtatt 900

gaacaaaatc agcctttaag tgctgaagaa gaggcgcagg tgcgggaggc gcaggcgcgc 960

cacgaaaatc tgtccgccca agcttacacg ggcggcggca ggatattgcc cgatccgatg 1020

gattaccgca gcggctcttg gcttgccaag ctgggctacc gcttcggcgg caggcattat 1080

gtcggcggcg tgtttgagga taccaaacag cgttacgata tccgcgatat gacggaaaaa 1140

cagtattacg gtacggacga ggcggaaaag tttagagaca agagcggggt gtacgacggc 1200

gacgatttcc gcgacggctt gtattttgtg ccgaatatag aagagtggaa gggcgataaa 1260

aatttggtca ggggcatagg tttgaaatat tcccgcacca aatttattga cgaacatcac 1320

cgccgccgcc gtatgggttt gctgtatcgt tatgaaaacg aagcgtattc tgacaattgg 1380

gcggataagg cggtgttgtc gtttgacaaa cagggcgtgg caaccgataa caacacgctg 1440

aagctgaatt gcgccgtgta tcctgctgtg gacaaatcct gccgcgcgtc ggcggacaaa 1500

ccgtattcct acgacagcag cgaccgtttc cactaccgcg aacagcacaa tgttttgaat 1560

gcctcgtttg agaaatcgct gaaaaacaaa tggacgaaac accatctgac tttgggcttc 1620

ggttacgatg cttccaaagc gatttcccgc cccgaacagc tttcccacaa tgcggcaagg 1680

atttcggaat ccacgggatt cgatgaaaac aatcaagata agtatctttt gggtaagccc 1740

gaagtcgtcg aagggtcggt ctgcggctac atcgaaaccc tgcgttcccg caaatgcgtg 1800

ccaagaaaaa tcaacggcag caatatccat atttctttga acgaccgttt ttcaatcggc 1860

aaatatttcg atttcagctt gggcggcagg tacgaccgga aaaacttcac cacgtcggaa 1920

gaactcgtcc gcagcgggcg gtatgttgac cgttcgtgga acagcggcat cttgttcaaa 1980

ccgaaccggc atttttccgt gtcttaccgt gcctccagcg gcttcagaac gccctcattc 2040

caagaacttt tcgggataga catttatcac gattatccga aaggctggca gcgtcccgcc 2100

ctgaaatcgg aaaaggcagc caaccgggaa atcggtttgc agtggaaggg cgatttcggc 2160

tttttggaaa tcagcagctt ccgcaaccgt tataccgata tgattgccgt tgccgatcac 2220

aaaaccaaat tgccgaatca ggcaggacaa ttgacagaga ttgatatacg cgattattac 2280

aatgcccaaa atatgtcgct tcaaggcgtt aatatattgg gaaaaatcga ctggaacggc 2340

```
gtgtatggca aactgcccga aggtttgtac accacattgg cgtacaaccg catcaaaccg     2400

aaatcggtat ccaaccggcc gggactgtcc ctccgcagct atgctttgga tgcggtacag     2460

ccgtcgcgtt atgttttggg gttcggatac gaccagcctg aggggaaatg gggcgcaaac     2520

attatgctga cctattccaa agggaaaaac cctgacgagc ttgcttatct ggcaggcgat     2580

caaaaacgat attcgacaaa aagagcgtcg tcttcttggt cgacggcaga cgtttccgcc     2640

tatctgaatc tgaaaaaacg gctgaccttg agggcggcta tctacaatat cggcaactac     2700

cgctacgtta cttgggaatc cttgcgccag actgcggaaa gcacggcaaa ccggcacggc     2760

ggcgacagca actatggaag gtatgccgca ccgggcagga acttcagtct cgcgctcgaa     2820

atgaagtttt aa                                                         2832
```

<210> 162

<211> 943

<212> PRT

<213> Neisseria meningitidis

<400> 162

```
Met Asn Lys Lys His Gly Phe Pro Leu Thr Leu Thr Ala Leu Ala Ile
1               5                  10                  15

Ala Thr Ala Phe Pro Ala Tyr Ala Ala Gln Ala Gly Gly Ala Thr Pro
            20                  25                  30

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

Lys Val Gly Arg Arg Ser Lys Glu Ala Thr Gly Leu Gly Lys Ile Val
    50                  55                  60

Lys Thr Ser Glu Thr Leu Asn Lys Glu Gln Val Leu Gly Ile Arg Asp
65                  70                  75                  80

Leu Thr Arg Tyr Asp Pro Gly Val Ala Val Val Glu Gln Gly Asn Gly
                85                  90                  95

Ala Ser Gly Gly Tyr Ser Ile Arg Gly Val Asp Lys Asn Arg Val Ala
            100                 105                 110

Val Ser Val Asp Gly Val Ala Gln Ile Gln Ala Phe Thr Val Gln Gly
        115                 120                 125

Ser Leu Ser Gly Tyr Gly Gly Arg Gly Gly Ser Gly Ala Ile Asn Glu
    130                 135                 140

Ile Glu Tyr Glu Asn Ile Ser Thr Val Glu Ile Asp Lys Gly Ala Gly
145                 150                 155                 160

Ser Ser Asp His Gly Ser Gly Ala Leu Gly Gly Ala Val Ala Phe Arg
                165                 170                 175

Thr Lys Glu Ala Ala Asp Leu Ile Ser Asp Gly Lys Ser Trp Gly Ile
            180                 185                 190
```

```
Gln Ala Lys Thr Ala Tyr Gly Ser Lys Asn Arg Gln Phe Met Lys Ser
        195                 200                 205

Leu Gly Ala Gly Phe Ser Lys Asp Gly Trp Glu Gly Leu Leu Ile Arg
    210                 215                 220

Thr Glu Arg Gln Gly Arg Glu Thr Arg Pro His Gly Asp Ile Ala Asp
225                 230                 235                 240

Gly Val Glu Tyr Gly Ile Asp Arg Leu Asp Ala Phe Arg Gln Thr Tyr
                245                 250                 255

Asp Ile Lys Arg Lys Thr Arg Glu Pro Phe Phe Ser Val Glu Gly Glu
            260                 265                 270

Arg Glu Ser Lys Pro Val Ala Lys Leu Ala Gly Tyr Gly Lys Tyr Leu
        275                 280                 285

Asn Asn Gln Leu Asn Arg Trp Val Lys Glu Arg Ile Glu Gln Asn Gln
    290                 295                 300

Pro Leu Ser Ala Glu Glu Glu Ala Gln Val Arg Glu Ala Gln Ala Arg
305                 310                 315                 320

His Glu Asn Leu Ser Ala Gln Ala Tyr Thr Gly Gly Gly Arg Ile Leu
                325                 330                 335

Pro Asp Pro Met Asp Tyr Arg Ser Gly Ser Trp Leu Ala Lys Leu Gly
            340                 345                 350

Tyr Arg Phe Gly Gly Arg His Tyr Val Gly Gly Val Phe Glu Asp Thr
        355                 360                 365

Lys Gln Arg Tyr Asp Ile Arg Asp Met Thr Glu Lys Gln Tyr Tyr Gly
    370                 375                 380

Thr Asp Glu Ala Glu Lys Phe Arg Asp Lys Ser Gly Val Tyr Asp Gly
385                 390                 395                 400

Asp Asp Phe Arg Asp Gly Leu Tyr Phe Val Pro Asn Ile Glu Glu Trp
                405                 410                 415

Lys Gly Asp Lys Asn Leu Val Arg Gly Ile Gly Leu Lys Tyr Ser Arg
            420                 425                 430

Thr Lys Phe Ile Asp Glu His His Arg Arg Arg Arg Met Gly Leu Leu
        435                 440                 445

Tyr Arg Tyr Glu Asn Glu Ala Tyr Ser Asp Asn Trp Ala Asp Lys Ala
    450                 455                 460

Val Leu Ser Phe Asp Lys Gln Gly Val Ala Thr Asp Asn Asn Thr Leu
465                 470                 475                 480

Lys Leu Asn Cys Ala Val Tyr Pro Ala Val Asp Lys Ser Cys Arg Ala
                485                 490                 495
```

```
Ser Ala Asp Lys Pro Tyr Ser Tyr Asp Ser Ser Asp Arg Phe His Tyr
            500                 505                 510

Arg Glu Gln His Asn Val Leu Asn Ala Ser Phe Glu Lys Ser Leu Lys
        515                 520                 525

Asn Lys Trp Thr Lys His His Leu Thr Leu Gly Phe Gly Tyr Asp Ala
    530                 535                 540

Ser Lys Ala Ile Ser Arg Pro Glu Gln Leu Ser His Asn Ala Ala Arg
545                 550                 555                 560

Ile Ser Glu Ser Thr Gly Phe Asp Glu Asn Asn Gln Asp Lys Tyr Leu
                565                 570                 575

Leu Gly Lys Pro Glu Val Val Glu Gly Ser Val Cys Gly Tyr Ile Glu
            580                 585                 590

Thr Leu Arg Ser Arg Lys Cys Val Pro Arg Lys Ile Asn Gly Ser Asn
        595                 600                 605

Ile His Ile Ser Leu Asn Asp Arg Phe Ser Ile Gly Lys Tyr Phe Asp
    610                 615                 620

Phe Ser Leu Gly Gly Arg Tyr Asp Arg Lys Asn Phe Thr Thr Ser Glu
625                 630                 635                 640

Glu Leu Val Arg Ser Gly Arg Tyr Val Asp Arg Ser Trp Asn Ser Gly
                645                 650                 655

Ile Leu Phe Lys Pro Asn Arg His Phe Ser Val Ser Tyr Arg Ala Ser
            660                 665                 670

Ser Gly Phe Arg Thr Pro Ser Phe Gln Glu Leu Phe Gly Ile Asp Ile
        675                 680                 685

Tyr His Asp Tyr Pro Lys Gly Trp Gln Arg Pro Ala Leu Lys Ser Glu
    690                 695                 700

Lys Ala Ala Asn Arg Glu Ile Gly Leu Gln Trp Lys Gly Asp Phe Gly
705                 710                 715                 720

Phe Leu Glu Ile Ser Ser Phe Arg Asn Arg Tyr Thr Asp Met Ile Ala

                725                 730                 735

Val Ala Asp His Lys Thr Lys Leu Pro Asn Gln Ala Gly Gln Leu Thr
            740                 745                 750

Glu Ile Asp Ile Arg Asp Tyr Tyr Asn Ala Gln Asn Met Ser Leu Gln
        755                 760                 765

Gly Val Asn Ile Leu Gly Lys Ile Asp Trp Asn Gly Val Tyr Gly Lys
    770                 775                 780

Leu Pro Glu Glu Leu Tyr Thr Thr Leu Ala Tyr Asn Arg Ile Lys Pro
```

```
Leu Pro Glu Gly Leu Tyr Thr Thr Leu Ala Tyr Asn Arg Ile Lys Pro
785                 790                 795                 800

Lys Ser Val Ser Asn Arg Pro Gly Leu Ser Leu Arg Ser Tyr Ala Leu
                805                 810                 815

Asp Ala Val Gln Pro Ser Arg Tyr Val Leu Gly Phe Gly Tyr Asp Gln
            820                 825                 830

Pro Glu Gly Lys Trp Gly Ala Asn Ile Met Leu Thr Tyr Ser Lys Gly
        835                 840                 845

Lys Asn Pro Asp Glu Leu Ala Tyr Leu Ala Gly Asp Gln Lys Arg Tyr
    850                 855                 860

Ser Thr Lys Arg Ala Ser Ser Ser Trp Ser Thr Ala Asp Val Ser Ala
865                 870                 875                 880

Tyr Leu Asn Leu Lys Lys Arg Leu Thr Leu Arg Ala Ala Ile Tyr Asn
                885                 890                 895

Ile Gly Asn Tyr Arg Tyr Val Thr Trp Glu Ser Leu Arg Gln Thr Ala
            900                 905                 910

Glu Ser Thr Ala Asn Arg His Gly Gly Asp Ser Asn Tyr Gly Arg Tyr
        915                 920                 925

Ala Ala Pro Gly Arg Asn Phe Ser Leu Ala Leu Glu Met Lys Phe
    930                 935                 940
```

<210> 163

<211> 768

<212> DNA

<213> Neisseria meningitidis

<400> 163

```
ggatcctcgt ctgaaaacag taagctgacc acggttttgg atgcggttga attgacacta       60

aacgacaaga aaatcaaaaa tctcgacaac ttcagcaatg ccgcccaact ggttgtcgac      120

ggcattatga ttgatctggc cggaacagaa tttacccgca aatttgaaca cacgctcaac      180

cgctgggtaa aagaacgtat tgaacaaaat cagcctttaa cctatgaagt cgaagtctgc      240

tgttccaacc tcaattatct gaaatacgga atgttgacgc gcaaaggcaa acaggttgaa      300

caaagtatgt tcctccaagg cgagcgtacc gatgaaaaag agattccaac cgaccaaaac      360

gtcgtttatc gggggtcttg gtacgggcat attgccaacg gcacaagctg gagcggcaat      420

gcttctgata aagagggcgg caacagggcg gaatttactg tgaattttgc cgataaaaaa      480

attaccggca agttaaccgc tgaaaacagg caggcgcaaa cctttaccat tgagggaatg      540

attcagggca acggctttga aggtacggcg aaaactgctg agtcaggttt tgatctcgat      600

caaaaaaata ccacccgcac gcctaaggca tatatcacag atgccaaggt aaagggcggt      660

ttttacgggc ctaaagccga agagttgggc ggatggtttg cctatcataa aagcgataac      720

ggcaggcgcg ccgtggtatt cggtgccgaa cgccaacagc ctgtgcaa                   768
```

ggcagcgcga ccgtggtatt cggtgcgaaa cgccaacagc ctgtgcaa 768

<210> 164

<211> 256

<212> PRT

<213> Neisseria meningitidis

<400> 164

```
Gly Ser Ser Ser Glu Asn Ser Lys Leu Thr Thr Val Leu Asp Ala Val
1               5                  10                  15

Glu Leu Thr Leu Asn Asp Lys Lys Ile Lys Asn Leu Asp Asn Phe Ser
            20                  25                  30

Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met Ile Asp Leu Ala Gly
        35                  40                  45

Thr Glu Phe Thr Arg Lys Phe Glu His Thr Leu Asn Arg Trp Val Lys
    50                  55                  60

Glu Arg Ile Glu Gln Asn Gln Pro Leu Thr Tyr Glu Val Glu Val Cys
65                  70                  75                  80

Cys Ser Asn Leu Asn Tyr Leu Lys Tyr Gly Met Leu Thr Arg Lys Gly
                85                  90                  95

Lys Gln Val Glu Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu
            100                 105                 110

Lys Glu Ile Pro Thr Asp Gln Asn Val Val Tyr Arg Gly Ser Trp Tyr
        115                 120                 125

Gly His Ile Ala Asn Gly Thr Ser Trp Ser Gly Asn Ala Ser Asp Lys
    130                 135                 140

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

Ile Thr Gly Lys Leu Thr Ala Glu Asn Arg Gln Ala Gln Thr Phe Thr
                165                 170                 175

Ile Glu Gly Met Ile Gln Gly Asn Gly Phe Glu Gly Thr Ala Lys Thr
            180                 185                 190

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

Lys Ala Tyr Ile Thr Asp Ala Lys Val Lys Gly Gly Phe Tyr Gly Pro
    210                 215                 220

Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr His Lys Ser Asp Asn
225                 230                 235                 240

Gly Ser Ala Thr Val Val Phe Gly Ala Lys Arg Gln Gln Pro Val Gln
                245                 250                 255
```

<210> 165
<211> 777
<212> DNA
<213> Neisseria meningitidis

<400> 165
ggatcctcgt ctgaaaacag taagctgacc acggttttgg atgcggttga attgacacta 60

aacgacaaga aaatcaaaaa tctcgacaac ttcagcaatg ccgcccaact ggttgtcgac 120

ggcattatga ttccactcct cccatacggt acggacgagg cggaaaagtt tagagacaag 180

agcggggtgg aatttacccg caaatttgaa cacacgatta acggcaaaac ctatgaagtc 240

gaagtctgct gttccaacct caattatctg aaatacggaa tgttgacgcg caaaggcaaa 300

caggttgaac aaagtatgtt cctccaaggc gagcgtaccg atgaaaaaga gattccaacc 360

gaccaaaacg tcgtttatcg ggggtcttgg tacgggcata ttgccaacgg cacaagctgg 420

agcggcaatg cttctgataa agagggcggc aacagggcgg aatttactgt gaattttgcc 480

gataaaaaaa ttaccggcaa gttaaccgct gaaaacaggc aggcgcaaac ctttaccatt 540

gagggaatga ttcagggcaa cggctttgaa ggtacggcga aaactgctga gtcaggtttt 600

gatctcgatc aaaaaaatac cacccgcacg cctaaggcat atatcacaga tgccaaggta 660

aagggcggtt tttacgggcc taaagccgaa gagttgggcg gatggtttgc ctatcataaa 720

agcgataacg gcagcgcgac cgtggtattc ggtgcgaaac gccaacagcc tgtgcaa 777

<210> 166
<211> 259
<212> PRT
<213> Neisseria meningitidis

<400> 166
Gly Ser Ser Ser Glu Asn Ser Lys Leu Thr Thr Val Leu Asp Ala Val
1 5 10 15

Glu Leu Thr Leu Asn Asp Lys Lys Ile Lys Asn Leu Asp Asn Phe Ser
20 25 30

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

Tyr Gly Thr Asp Glu Ala Glu Lys Phe Arg Asp Lys Ser Gly Val Glu
50 55 60

Phe Thr Arg Lys Phe Glu His Thr Ile Asn Gly Lys Thr Tyr Glu Val
65 70 75 80

Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr Gly Met Leu Thr
85 90 95

Arg Lys Gly Lys Gln Val Glu Gln Ser Met Phe Leu Gln Gly Glu Arg
100 105 110

```
Thr Asp Glu Lys Glu Ile Pro Thr Asp Gln Asn Val Val Tyr Arg Gly
        115                 120                 125

Ser Trp Tyr Gly His Ile Ala Asn Gly Thr Ser Trp Ser Gly Asn Ala
    130                 135                 140

Ser Asp Lys Glu Gly Gly Asn Arg Ala Glu Phe Thr Val Asn Phe Ala
145                 150                 155                 160

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

Thr Phe Thr Ile Glu Gly Met Ile Gln Gly Asn Gly Phe Glu Gly Thr
            180                 185                 190

Ala Lys Thr Ala Glu Ser Gly Phe Asp Leu Asp Gln Lys Asn Thr Thr
        195                 200                 205

Arg Thr Pro Lys Ala Tyr Ile Thr Asp Ala Lys Val Lys Gly Gly Phe

    210                 215                 220

Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr His Lys
225                 230                 235                 240

Ser Asp Asn Gly Ser Ala Thr Val Val Phe Gly Ala Lys Arg Gln Gln
                245                 250                 255

Pro Val Gln
```

<210> 167

<211> 1062

<212> DNA

<213> Haemophilus influenzae

<400> 167

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ggatccgcga ccaccagcac caccgcgaac gcgaaaaccg atgcgaccac caacgcggaa       60

aactttacca ccaaagatat tagcagcttt ggcgaagcgg attatctgct gattgataac      120

tatccggtgc cgctgctgcc ggaaaccgaa aacagcggcg attttgcgac cagcaaacat      180

tatgaagtgc gcgataaaac ctataaagtg gaagcgtgct gcaaaaacct gagctatgtg      240

aaatttggca tgtattatga aaccaaacgc ccggcggcga aaccgaaagc gcagaaaaaa      300

aaacgcaaaa aaaaaaaaac cggcgtgaaa agcgtgaaaa aaggcaaaaa aaaaattaaa      360

aaaaaaaaag gcaccaaaaa agcggcggtg aaaaaaaaag gcagcaaaaa aaaagcggtg      420

aaaggcaaaa aaaaagcgaa aaaaccgaaa aaaaaaagcc cgaccaaaaa aggcggcagc      480

ggcagcaaag gcattctgcc ggcgccgaaa gcgccgaaag gccgcaacat taaatatcat      540

cagtttctgc tgggcctgcg caccgcgagc agcaaaattc cgaccaccgg caacgtgaaa      600

tatcgcggca gctggtttgg ctatattagc gatggcgaaa ccagctatag caccaccggc      660

gataaacgcc aggataaaaa cgcggtggcg gaatttgatg tgaactttgc ggaaaaaacc      720
```

```
ctgaaaggca gcctgaaacg cgcggatagc cagaacccgg tgtttagcat tgaagcgaac      780

tttaaaaacg gcggcaacgc gtttaccggc accgcgaccg cgaaagatct ggtgattgat      840

ggcaaaaaca gccagaccaa aaacaccccg attaacatta ccaccaaagt gaacggcgcg      900

ttttatggcc cgaacgcgag cgaactgggc ggctatttta cctataacgg caaaaacccg      960

accgataaaa acagcccgac cgcgagcagc ccgagcaaca gcgaaaaagc gcgcgcggcg     1020

gtggtgtttg gcgcgaaaaa acaggtggaa accaacaaca aa                        1062
```

<210> 168

<211> 354

<212> PRT

<213> Haemophilus influenzae

<400> 168

```
Gly Ser Ala Thr Thr Ser Thr Thr Ala Asn Ala Lys Thr Asp Ala Thr
1               5                  10                  15

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

Ala Asp Tyr Leu Leu Ile Asp Asn Tyr Pro Val Pro Leu Leu Pro Glu
        35                  40                  45

Thr Glu Asn Ser Gly Asp Phe Ala Thr Ser Lys His Tyr Glu Val Arg
    50                  55                  60

Asp Lys Thr Tyr Lys Val Glu Ala Cys Cys Lys Asn Leu Ser Tyr Val
65                  70                  75                  80

Lys Phe Gly Met Tyr Tyr Glu Thr Lys Arg Pro Ala Ala Lys Pro Lys
                85                  90                  95

Ala Gln Lys Lys Lys Arg Lys Lys Lys Lys Thr Gly Val Lys Ser Val
            100                 105                 110

Lys Lys Gly Lys Lys Lys Ile Lys Lys Lys Lys Gly Thr Lys Lys Ala
        115                 120                 125

Ala Val Lys Lys Lys Gly Ser Lys Lys Lys Ala Val Lys Gly Lys Lys
    130                 135                 140

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

Gly Ser Lys Gly Ile Leu Pro Ala Pro Lys Ala Pro Lys Gly Arg Asn
                165                 170                 175

Ile Lys Tyr His Gln Phe Leu Leu Gly Leu Arg Thr Ala Ser Ser Lys
            180                 185                 190

Ile Pro Thr Thr Gly Asn Val Lys Tyr Arg Gly Ser Trp Phe Gly Tyr
        195                 200                 205

Ile Ser Asp Gly Glu Thr Ser Tyr Ser Thr Thr Gly Asp Lys Arg Gln
```

```
    210                 215                 220

Asp Lys Asn Ala Val Ala Glu Phe Asp Val Asn Phe Ala Glu Lys Thr
225                 230                 235                 240

Leu Lys Gly Ser Leu Lys Arg Ala Asp Ser Gln Asn Pro Val Phe Ser

                245                 250                 255

Ile Glu Ala Asn Phe Lys Asn Gly Gly Asn Ala Phe Thr Gly Thr Ala
            260                 265                 270

Thr Ala Lys Asp Leu Val Ile Asp Gly Lys Asn Ser Gln Thr Lys Asn
        275                 280                 285

Thr Pro Ile Asn Ile Thr Thr Lys Val Asn Gly Ala Phe Tyr Gly Pro
    290                 295                 300

Asn Ala Ser Glu Leu Gly Gly Tyr Phe Thr Tyr Asn Gly Lys Asn Pro
305                 310                 315                 320

Thr Asp Lys Asn Ser Pro Thr Ala Ser Ser Pro Ser Asn Ser Glu Lys
                325                 330                 335

Ala Arg Ala Ala Val Val Phe Gly Ala Lys Lys Gln Val Glu Thr Asn
            340                 345                 350

Asn Lys
```

<210> 169

<211> 1614

<212> DNA

<213> Haemophilus parasuis

<400> 169

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tgttctggcg gaaaaggaag ttttgattta gaagatgttc agcctaataa gacaacgggc       60

gtgtctaaag aagagtataa ggatgtggaa acggataaga aagtaaaaga acagttaggg      120

gaattgatgg aacctgcttt ggggtatgtt gtaaaagttc cagtgagtca aagtggagta      180

aaaagaacgg aaatctcaaa tccagaagca attactgatg aagatcttaa taaaatacca      240

aattacgaga ttatcaaagg tgtagcttat ccaaatgcgg gcgagctagt agataaaaca      300

gcagctgaga cgatgaaata tgttcgttct ggttatgtaa ttgatgtata tcattctggt      360

actcgtgata aaggttatgt gttttataaa ggtattactc cctcaaaaga attaccgcag      420

gggccagccc ttacctacca aggtgaatgg gattttacct cagatgctaa tttaaataat      480

gaagagggaa gacctactta tttaaacgac gattattata ctacatggat aggtaaacgg      540

gcgggcttgg tttcgggaga tgcgaaacct tcaaagcata aatacacaag ccagtttaaa      600

gttgattttg caactaaaaa aatgacaggt aagttatccg ataaagagaa aacgatttat      660

acagtcaatg ctgatattag aggtaatcgt tttacgggtt ctgctacagc aagtgataaa      720

gacaaaggga aaggtgcatc atataacttc tttagtgtcg attctcagtc tttagaaggc      780
```

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ggcttctatg gtccaaaagc ggaagaaatg gcaggtaaat ttgtagccga cgacaaatct      840

ctttttgccg ttttttcagc aaaacacaat gcttctaatg ttaacaccgt tcgtattatt      900

gatgcctcaa aaattgattt aactaatttc agcatttcag aacttaccaa ttttggcgat      960

gcttctgttt taattattga tgggaaaaaa atggagctag ctggtagcga gtttacaaat     1020

aagcacacta ttgatatcaa tggtaaaaaa atggtagctg tagcctgctg tagtaatttg     1080

gaatatatga aatttggtca attatggcag caaacagagg gcgaaaaaca agttaaagat     1140

aatagtttat tcctacaagg cgaacgtact gcaacagata agatgccaaa agacggaaac     1200

tataaatata ttggtacttg ggatgctcag gtttcaaaag aaaataatta ctgggttgct     1260

acggcagatg atgatagaaa agctggctac cgcacagaat ttgatgttga ttttggcagc     1320

aaaaatttaa gtggtaagtt atttgataaa aacggtgtaa atcctgtgtt taccgtaaat     1380

gcaaaaattg atggtaatgg ttttactggc gaagctaaaa cctcagatgc tggcttcgtt     1440

ctagatccag gtagtttacg tcatgacaat gtgaaattta gcgatgtagc agttagtggt     1500

ggcttctatg gtccaacggc agcagagctt ggcggacaat tccgttatca atcagacaat     1560

ggcagtgtag gtgtaggtgc tgtctttggt gcaaaacaac aagtaaaaaa ataa           1614
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<210> 170

<211> 537

<212> PRT

<213> Haemophilus parasuis

<400> 170

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Cys Ser Gly Gly Lys Gly Ser Phe Asp Leu Glu Asp Val Gln Pro Asn
1               5                  10                  15

Lys Thr Thr Gly Val Ser Lys Glu Glu Tyr Lys Asp Val Glu Thr Asp
            20                  25                  30

Lys Lys Val Lys Glu Gln Leu Gly Glu Leu Met Glu Pro Ala Leu Gly
        35                  40                  45

Tyr Val Val Lys Val Pro Val Ser Gln Ser Gly Val Lys Arg Thr Glu
    50                  55                  60

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

Asn Tyr Glu Ile Ile Lys Gly Val Ala Tyr Pro Asn Ala Gly Glu Leu
                85                  90                  95

Val Asp Lys Thr Ala Ala Glu Thr Met Lys Tyr Val Arg Ser Gly Tyr
            100                 105                 110

Val Ile Asp Val Tyr His Ser Gly Thr Arg Asp Lys Gly Tyr Val Phe
        115                 120                 125

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

```
Thr Tyr Gln Gly Glu Trp Asp Phe Thr Ser Asp Ala Asn Leu Asn Asn
145                 150                 155                 160

Glu Glu Gly Arg Pro Thr Tyr Leu Asn Asp Asp Tyr Tyr Thr Thr Trp
                165                 170                 175

Ile Gly Lys Arg Ala Gly Leu Val Ser Gly Asp Ala Lys Pro Ser Lys
            180                 185                 190

His Lys Tyr Thr Ser Gln Phe Lys Val Asp Phe Ala Thr Lys Lys Met
        195                 200                 205

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

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

Asp Lys Gly Lys Gly Ala Ser Tyr Asn Phe Phe Ser Val Asp Ser Gln
                245                 250                 255

Ser Leu Glu Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Met Ala Gly
            260                 265                 270

Lys Phe Val Ala Asp Asp Lys Ser Leu Phe Ala Val Phe Ser Ala Lys
        275                 280                 285

His Asn Ala Ser Asn Val Asn Thr Val Arg Ile Ile Asp Ala Ser Lys
    290                 295                 300

Ile Asp Leu Thr Asn Phe Ser Ile Ser Glu Leu Thr Asn Phe Gly Asp
305                 310                 315                 320

Ala Ser Val Leu Ile Ile Asp Gly Lys Lys Met Glu Leu Ala Gly Ser
                325                 330                 335

Glu Phe Thr Asn Lys His Thr Ile Asp Ile Asn Gly Lys Lys Met Val
            340                 345                 350

Ala Val Ala Cys Cys Ser Asn Leu Glu Tyr Met Lys Phe Gly Gln Leu
        355                 360                 365

Trp Gln Gln Thr Glu Gly Glu Lys Gln Val Lys Asp Asn Ser Leu Phe
    370                 375                 380

Leu Gln Gly Glu Arg Thr Ala Thr Asp Lys Met Pro Lys Asp Gly Asn
385                 390                 395                 400

Tyr Lys Tyr Ile Gly Thr Trp Asp Ala Gln Val Ser Lys Glu Asn Asn
                405                 410                 415

Tyr Trp Val Ala Thr Ala Asp Asp Asp Arg Lys Ala Gly Tyr Arg Thr
            420                 425                 430

Glu Phe Asp Val Asp Phe Gly Ser Lys Asn Leu Ser Gly Lys Leu Phe
        435                 440                 445
```

```
Asp Lys Asn Gly Val Asn Pro Val Phe Thr Val Asn Ala Lys Ile Asp
    450                 455                 460

Gly Asn Gly Phe Thr Gly Glu Ala Lys Thr Ser Asp Ala Gly Phe Val
465                 470                 475                 480

Leu Asp Pro Gly Ser Leu Arg His Asp Asn Val Lys Phe Ser Asp Val
                485                 490                 495

Ala Val Ser Gly Gly Phe Tyr Gly Pro Thr Ala Ala Glu Leu Gly Gly
            500                 505                 510

Gln Phe Arg Tyr Gln Ser Asp Asn Gly Ser Val Gly Val Gly Ala Val
        515                 520                 525

Phe Gly Ala Lys Gln Gln Val Lys Lys
    530                 535
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<210> 171

<211> 1614

<212> DNA

<213> Haemophilus parasuis

<400> 171

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tgttctggcg gaaaaggaag ttttgattta gaagatgttc agcctaataa gacaacgggc       60

gtgtctaaag aagagtataa ggatgtggaa acggataaga aagtaaaaga acagttaggg      120

gaattgatgg aacctgcttt ggggtatgtt gtaaaagttc cagtgagtca aagtggagta      180

aaaagaacgg aaatctcaaa tccagaagca attactgatg aagatcttaa taaaatacca      240

aattacgaga ttatcaaagg tgtagcttat ccaaattatg gcgagctagt agataaaaca      300

gcagctgaga cgatgaaata tgttcgttct ggttatgtaa ttgatgtata tcattctggt      360

actcgtgata aaggttatgt gttttataaa ggtattactc cctcaaaaga attaccgcag      420

gggccagccc ttacctacca aggtgaatgg gattttacct cagatgctaa tttaaataat      480

gaagagggaa gacctactta tttaaacgac gattattata ctacatggat aggtaaacgg      540

gcgggcttgg tttcgggaga tgcgaaacct tcaaagcata aatacacaag ccagtttaaa      600

gttgattttg caactaaaaa aatgacaggt aagttatccg ataaagagaa aacgatttat      660

acagtcaatg ctgatattag aggtaatcgt tttacgggtt ctgctacagc aagtgataaa      720

gacaaaggga aaggtgcatc atataacttc tttagtgtcg attctcagtc tttagaaggc      780

ggcttctatg gtccaaaagc ggaagaaatg gcaggtaaat ttgtagccga cgacaaatct      840

ctttttgccg ttttttcagc aaaacacaat gcttctaatg ttaacaccgt tcgtattatt      900

gatgcctcaa aaattgattt aactaatttc agcatttcag aacttaccaa ttttggcgat      960

gcttctgttt taattattga tgggaaaaaa atggagctag ctggtagcga gtttacaaat     1020

aagcacacta ttgatatcaa tggtaaaaaa atggtagctg tagcctgctg tagtaatttg     1080

gaatatatga aatttggtca attatggcag caaacagagg gcgaaaaaca agttaaagat     1140

aatagtttat tcctacaagg cgaacgtact gcaacagata agatgccaaa agacggaaac     1200
```

tataaatata ttggtacttg ggatgctcag gtttcaaaag aaaataatta ctgggttgct 1260

acggcagatg atgatagaaa agctggctac cgcacagaat ttgatgttga ttttggcagc 1320

aaaaatttaa gtggtaagtt atttgataaa aacggtgtaa atcctgtgtt taccgtaaat 1380

gcaaaaattg atggtaatgg ttttactggc gaagctaaaa cctcagatgc tggcttcgtt 1440

ctagatccag gtagtttacg tcatgacaat gtgaaattta gcgatgtagc agttagtggt 1500

ggcttctatg gtccaacggc agcagagctt ggcggacaat tccgttatca atcagacaat 1560

ggcagtgtag gtgtaggtgc tgtctttggt gcaaaacaac aagtaaaaaa ataa 1614

<210> 172

<211> 537

<212> PRT

<213> Haemophilus parasuis

<400> 172

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Cys Ser Gly Gly Lys Gly Ser Phe Asp Leu Glu Asp Val Gln Pro Asn
1               5                   10                  15

Lys Thr Thr Gly Val Ser Lys Glu Glu Tyr Lys Asp Val Glu Thr Asp
            20                  25                  30

Lys Lys Val Lys Glu Gln Leu Gly Glu Leu Met Glu Pro Ala Leu Gly
        35                  40                  45

Tyr Val Val Lys Val Pro Val Ser Gln Ser Gly Val Lys Arg Thr Glu
    50                  55                  60

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

Asn Tyr Glu Ile Ile Lys Gly Val Ala Tyr Pro Asn Tyr Gly Glu Leu
                85                  90                  95

Val Asp Lys Thr Ala Ala Glu Thr Met Lys Tyr Val Arg Ser Gly Tyr
            100                 105                 110

Val Ile Asp Val Ala His Ser Gly Thr Arg Asp Lys Gly Tyr Val Phe
        115                 120                 125

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

Thr Tyr Gln Gly Glu Trp Asp Phe Thr Ser Asp Ala Asn Leu Asn Asn
145                 150                 155                 160

Glu Glu Gly Arg Pro Thr Tyr Leu Asn Asp Asp Tyr Tyr Thr Thr Trp
                165                 170                 175

Ile Gly Lys Arg Ala Gly Leu Val Ser Gly Asp Ala Lys Pro Ser Lys
            180                 185                 190

His Lys Tyr Thr Ser Gln Phe Lys Val Asp Phe Ala Thr Lys Lys Met
        195                 200                 205
```

```
Thr Gly Lys Leu Ser Asp Lys Glu Lys Thr Ile Tyr Thr Val Asn Ala
    210                 215                 220

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

Asp Lys Gly Lys Gly Ala Ser Tyr Asn Phe Phe Ser Val Asp Ser Gln
                245                 250                 255

Ser Leu Glu Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Met Ala Gly
            260                 265                 270

Lys Phe Val Ala Asp Asp Lys Ser Leu Phe Ala Val Phe Ser Ala Lys
        275                 280                 285

His Asn Ala Ser Asn Val Asn Thr Val Arg Ile Ile Asp Ala Ser Lys
    290                 295                 300

Ile Asp Leu Thr Asn Phe Ser Ile Ser Glu Leu Thr Asn Phe Gly Asp
305                 310                 315                 320

Ala Ser Val Leu Ile Ile Asp Gly Lys Lys Met Glu Leu Ala Gly Ser
                325                 330                 335

Glu Phe Thr Asn Lys His Thr Ile Asp Ile Asn Gly Lys Lys Met Val
            340                 345                 350

Ala Val Ala Cys Cys Ser Asn Leu Glu Tyr Met Lys Phe Gly Gln Leu
        355                 360                 365

Trp Gln Gln Thr Glu Gly Glu Lys Gln Val Lys Asp Asn Ser Leu Phe
    370                 375                 380

Leu Gln Gly Glu Arg Thr Ala Thr Asp Lys Met Pro Lys Asp Gly Asn
385                 390                 395                 400

Tyr Lys Tyr Ile Gly Thr Trp Asp Ala Gln Val Ser Lys Glu Asn Asn
                405                 410                 415

Tyr Trp Val Ala Thr Ala Asp Asp Asp Arg Lys Ala Gly Tyr Arg Thr
            420                 425                 430

Glu Phe Asp Val Asp Phe Gly Ser Lys Asn Leu Ser Gly Lys Leu Phe
        435                 440                 445

Asp Lys Asn Gly Val Asn Pro Val Phe Thr Val Asn Ala Lys Ile Asp
    450                 455                 460

Gly Asn Gly Phe Thr Gly Glu Ala Lys Thr Ser Asp Ala Gly Phe Val
465                 470                 475                 480

Leu Asp Pro Gly Ser Leu Arg His Asp Asn Val Lys Phe Ser Asp Val
                485                 490                 495

Ala Val Ser Gly Gly Phe Tyr Gly Pro Thr Ala Ala Glu Leu Gly Gly
            500                 505                 510
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Gln Phe Arg Tyr Gln Ser Asp Asn Gly Ser Val Gly Val Gly Ala Val
515 520 525

Phe Gly Ala Lys Gln Gln Val Lys Lys
530 535

<210> 173

<211> 1614

<212> DNA

<213> Haemophilus parasuis

<400> 173

tgttctggcg gaaaaggaag ttttgattta gaagatgttc agcctaataa gacaacgggc 60

gtgtctaaag aagagtataa ggatgtggaa acggataaga aagtaaaaga acagttaggg 120

gaattgatgg aacctgcttt ggggtatgtt gtaaaagttc cagtgagtca aagtggagta 180

aaaagaacgg aaatctcaaa tccagaagca attactgatg aagatcttaa taaaatacca 240

aattacgaga ttatcaaagg tgtagcttat ccaaattatg gcgagctagt agataaaaca 300

gcagctgaga cgatgaaata tgttcgttct ggttatgtaa ttgatgtata tcattctggt 360

actcgtgata aaggttatgt gttttataaa ggtattactc cctcaaaaga attaccgcag 420

gggccagccc ttacctacca aggtgaatgg gattttacct cagatgctaa tttaaataat 480

gaagagggaa gacctactta tttaaacgac gattattata ctacatggat aggtaaacgg 540

gcgggcttgg tttcgggaga tgcgaaacct tcaaagcata aatacacaag ccagtttaaa 600

gttgattttg caactaaaaa aatgacaggt aagttatccg ataaagagaa aacgatttat 660

acagtcaatg ctgatattag aggtaatcgt tttacgggtt ctgctacagc aagtgataaa 720

gacaaaggga aaggtgcatc atataacttc tttagtgtcg attctcagtc tttagaaggc 780

ggcttctatg gtccaaaagc ggaagaaatg gcaggtaaat ttgtagccga cgacaaatct 840

ctttttgccg ttttttcagc aaaacacaat gcttctaatg ttaacaccgt tcgtattatt 900

gatgcctcaa aaattgattt aactaatttc agcatttcag aacttaccaa ttttggcgat 960

gcttctgttt taattattga tgggaaaaaa atggagctag ctggtagcga gtttacaaat 1020

aagcacacta ttgatatcaa tggtaaaaaa atggtagctg tagcctgctg tagtaatttg 1080

gaatatatga aatttggtca attatggcag caaacagagg gcgaaaaaca agttaaagat 1140

aatagtttat tcctacaagg cgaacgtact gcaacagata agatgccaaa agacggaaac 1200

tataaatata ttggtacttg ggatgctcag gtttcaaaag aaaataatta ctgggttgct 1260

acggcagatg atgatagaaa agctggctac cgcacagaat ttgatgttga ttttggcagc 1320

aaaaatttaa gtggtaagtt atttgataaa aacggtgtaa atcctgtgtt taccgtaaat 1380

gcaaaaattg atggtaatgg ttttactggc gaagctaaaa cctcagatgc tggcttcgtt 1440

ctagatccag gtagtttacg tcatgacaat gtgaaattta gcgatgtagc agttagtggt 1500

ggcttctatg gtccaacggc agcagagctt ggcggacaat tccgttatca atcagacaat 1560

ggcagtgtag gtgtaggtgc tgtctttggt gcaaaacaac aagtaaaaaa ataa 1614

<210> 174

<211> 537

<212> PRT

<213> Haemophilus parasuis

<400> 174

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Cys Ser Gly Gly Lys Gly Ser Phe Asp Leu Glu Asp Val Gln Pro Asn
1               5                   10                  15

Lys Thr Thr Gly Val Ser Lys Glu Glu Tyr Lys Asp Val Glu Thr Asp
            20                  25                  30

Lys Lys Val Lys Glu Gln Leu Gly Glu Leu Met Glu Pro Ala Leu Gly
        35                  40                  45

Tyr Val Val Lys Val Pro Val Ser Gln Ser Gly Val Lys Arg Thr Glu
    50                  55                  60

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

Asn Tyr Glu Ile Ile Lys Gly Val Ala Tyr Pro Asn Tyr Gly Glu Leu
                85                  90                  95

Val Asp Lys Thr Ala Ala Glu Thr Met Lys Tyr Val Arg Ser Gly Tyr
            100                 105                 110

Val Ile Asp Val Tyr His Ser Gly Thr Arg Asp Lys Gly Tyr Val Phe
        115                 120                 125

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

Thr Tyr Gln Gly Glu Trp Asp Phe Thr Ser Asp Ala Asn Leu Asn Asn
145                 150                 155                 160

Glu Glu Gly Arg Pro Thr Ala Leu Asn Asp Asp Tyr Tyr Thr Thr Trp
                165                 170                 175

Ile Gly Lys Arg Ala Gly Leu Val Ser Gly Asp Ala Lys Pro Ser Lys
            180                 185                 190

His Lys Tyr Thr Ser Gln Phe Lys Val Asp Phe Ala Thr Lys Lys Met
        195                 200                 205

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

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

Asp Lys Gly Lys Gly Ala Ser Tyr Asn Phe Phe Ser Val Asp Ser Gln
                245                 250                 255

Ser Leu Glu Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Met Ala Gly
```

```
            260                 265                 270

Lys Phe Val Ala Asp Asp Lys Ser Leu Phe Ala Val Phe Ser Ala Lys
        275                 280                 285

His Asn Ala Ser Asn Val Asn Thr Val Arg Ile Ile Asp Ala Ser Lys
    290                 295                 300

Ile Asp Leu Thr Asn Phe Ser Ile Ser Glu Leu Thr Asn Phe Gly Asp
305                 310                 315                 320

Ala Ser Val Leu Ile Ile Asp Gly Lys Lys Met Glu Leu Ala Gly Ser
                325                 330                 335

Glu Phe Thr Asn Lys His Thr Ile Asp Ile Asn Gly Lys Lys Met Val
            340                 345                 350

Ala Val Ala Cys Cys Ser Asn Leu Glu Tyr Met Lys Phe Gly Gln Leu
        355                 360                 365

Trp Gln Gln Thr Glu Gly Glu Lys Gln Val Lys Asp Asn Ser Leu Phe
    370                 375                 380

Leu Gln Gly Glu Arg Thr Ala Thr Asp Lys Met Pro Lys Asp Gly Asn
385                 390                 395                 400

Tyr Lys Tyr Ile Gly Thr Trp Asp Ala Gln Val Ser Lys Glu Asn Asn
                405                 410                 415

Tyr Trp Val Ala Thr Ala Asp Asp Asp Arg Lys Ala Gly Tyr Arg Thr
            420                 425                 430

Glu Phe Asp Val Asp Phe Gly Ser Lys Asn Leu Ser Gly Lys Leu Phe
        435                 440                 445

Asp Lys Asn Gly Val Asn Pro Val Phe Thr Val Asn Ala Lys Ile Asp
    450                 455                 460

Gly Asn Gly Phe Thr Gly Glu Ala Lys Thr Ser Asp Ala Gly Phe Val
465                 470                 475                 480

Leu Asp Pro Gly Ser Leu Arg His Asp Asn Val Lys Phe Ser Asp Val
                485                 490                 495

Ala Val Ser Gly Gly Phe Tyr Gly Pro Thr Ala Ala Glu Leu Gly Gly
            500                 505                 510

Gln Phe Arg Tyr Gln Ser Asp Asn Gly Ser Val Gly Val Gly Ala Val
        515                 520                 525

Phe Gly Ala Lys Gln Gln Val Lys Lys
    530                 535
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<210> 175

<211> 1614

<212> DNA

<213> Haemophilus parasuis

<400> 175

tgttctggcg gaaaaggaag ttttgattta gaagatgttc agcctaataa gacaacgggc 60

gtgtctaaag aagagtataa ggatgtggaa acggataaga aagtaaaaga acagttaggg 120

gaattgatgg aacctgcttt ggggtatgtt gtaaaagttc cagtgagtca aagtggagta 180

aaaagaacgg aaatctcaaa tccagaagca attactgatg aagatcttaa taaaatacca 240

aattacgaga ttatcaaagg tgtagcttat ccaaattatg gcgagctagt agataaaaca 300

gcagctgaga cgatgaaata tgttcgttct ggttatgtaa ttgatgtata tcattctggt 360

actcgtgata aaggttatgt gttttataaa ggtattactc cctcaaaaga attaccgcag 420

gggccagccc ttacctacca aggtgaatgg gattttacct cagatgctaa tttaaataat 480

gaagagggaa gacctactta tttaaacgac gattattata ctacatggat aggtaaacgg 540

gcgggcttgg tttcgggaga tgcgaaacct tcaaagcata aatacacaag ccagtttaaa 600

gttgattttg caactaaaaa aatgacaggt aagttatccg ataaagagaa aacgatttat 660

acagtcaatg ctgatattag aggtaatcgt tttacgggtt ctgctacagc aagtgataaa 720

gacaaaggga aaggtgcatc atataacttc tttagtgtcg attctcagtc tttagaaggc 780

ggcttctatg gtccaaaagc ggaagaaatg gcaggtaaat ttgtagccga cgacaaatct 840

ctttttgccg ttttttcagc aaaacacaat gcttctaatg ttaacaccgt tcgtattatt 900

gatgcctcaa aaattgattt aactaatttc agcatttcag aacttaccaa ttttggcgat 960

gcttctgttt taattattga tgggaaaaaa atggagctag ctggtagcga gtttacaaat 1020

aagcacacta ttgatatcaa tggtaaaaaa atggtagctg tagcctgctg tagtaatttg 1080

gaatatatga aatttggtca attatggcag caaacagagg gcgaaaaaca agttaaagat 1140

aatagtttat tcctacaagg cgaacgtact gcaacagata agatgccaaa agacggaaac 1200

tataaatata ttggtacttg ggatgctcag gtttcaaaag aaaataatta ctgggttgct 1260

acggcagatg atgatagaaa agctggctac cgcacagaat ttgatgttga ttttggcagc 1320

aaaaatttaa gtggtaagtt atttgataaa aacggtgtaa atcctgtgtt taccgtaaat 1380

gcaaaaattg atggtaatgg ttttactggc gaagctaaaa cctcagatgc tggcttcgtt 1440

ctagatccag gtagtttacg tcatgacaat gtgaaattta gcgatgtagc agttagtggt 1500

ggcttctatg gtccaacggc agcagagctt ggcggacaat tccgttatca atcagacaat 1560

ggcagtgtag gtgtaggtgc tgtctttggt gcaaaacaac aagtaaaaaa ataa 1614

<210> 176

<211> 537

<212> PRT

<213> Haemophilus parasuis

<400> 176

Cys Ser Gly Gly Lys Gly Ser Phe Asp Leu Glu Asp Val Gln Pro Asn
1 5 10 15

Lys Thr Thr Gly Val Ser Lys Glu Glu Tyr Lys Asp Val Glu Thr Asp

```
            20                  25                  30

Lys Lys Val Lys Glu Gln Leu Gly Glu Leu Met Glu Pro Ala Leu Gly
        35                  40                  45

Tyr Val Val Lys Val Pro Val Ser Gln Ser Gly Val Lys Arg Thr Glu
    50                  55                  60

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

Asn Tyr Glu Ile Ile Lys Gly Val Ala Tyr Pro Asn Ala Gly Glu Leu
                85                  90                  95

Val Asp Lys Thr Ala Ala Glu Thr Met Lys Tyr Val Arg Ser Gly Tyr
            100                 105                 110

Val Ile Asp Val Tyr His Ser Gly Thr Arg Asp Lys Gly Tyr Val Phe
        115                 120                 125

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

Thr Tyr Gln Gly Glu Trp Asp Phe Thr Ser Asp Ala Asn Leu Asn Asn
145                 150                 155                 160

Glu Glu Gly Arg Pro Thr Tyr Leu Asn Asp Asp Tyr Tyr Thr Thr Ala
                165                 170                 175

Ile Gly Lys Arg Ala Gly Leu Val Ser Gly Asp Ala Lys Pro Ser Lys

            180                 185                 190

His Lys Tyr Thr Ser Gln Phe Lys Val Asp Phe Ala Thr Lys Lys Met
        195                 200                 205

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

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

Asp Lys Gly Lys Gly Ala Ser Tyr Asn Phe Phe Ser Val Asp Ser Gln
                245                 250                 255

Ser Leu Glu Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Met Ala Gly
            260                 265                 270

Lys Phe Val Ala Asp Asp Lys Ser Leu Phe Ala Val Phe Ser Ala Lys
        275                 280                 285

His Asn Ala Ser Asn Val Asn Thr Val Arg Ile Ile Asp Ala Ser Lys
    290                 295                 300

Ile Asp Leu Thr Asn Phe Ser Ile Ser Glu Leu Thr Asn Phe Gly Asp
305                 310                 315                 320
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305                 310                 315                 320

Ala Ser Val Leu Ile Ile Asp Gly Lys Lys Met Glu Leu Ala Gly Ser
                325                 330                 335

Glu Phe Thr Asn Lys His Thr Ile Asp Ile Asn Gly Lys Lys Met Val
            340                 345                 350

Ala Val Ala Cys Cys Ser Asn Leu Glu Tyr Met Lys Phe Gly Gln Leu
        355                 360                 365

Trp Gln Gln Thr Glu Gly Glu Lys Gln Val Lys Asp Asn Ser Leu Phe
    370                 375                 380

Leu Gln Gly Glu Arg Thr Ala Thr Asp Lys Met Pro Lys Asp Gly Asn
385                 390                 395                 400

Tyr Lys Tyr Ile Gly Thr Trp Asp Ala Gln Val Ser Lys Glu Asn Asn
                405                 410                 415

Tyr Trp Val Ala Thr Ala Asp Asp Asp Arg Lys Ala Gly Tyr Arg Thr
            420                 425                 430

Glu Phe Asp Val Asp Phe Gly Ser Lys Asn Leu Ser Gly Lys Leu Phe
        435                 440                 445

Asp Lys Asn Gly Val Asn Pro Val Phe Thr Val Asn Ala Lys Ile Asp
    450                 455                 460

Gly Asn Gly Phe Thr Gly Glu Ala Lys Thr Ser Asp Ala Gly Phe Val
465                 470                 475                 480

Leu Asp Pro Gly Ser Leu Arg His Asp Asn Val Lys Phe Ser Asp Val
                485                 490                 495

Ala Val Ser Gly Gly Phe Tyr Gly Pro Thr Ala Ala Glu Leu Gly Gly
            500                 505                 510

Gln Phe Arg Tyr Gln Ser Asp Asn Gly Ser Val Gly Val Gly Ala Val
        515                 520                 525

Phe Gly Ala Lys Gln Gln Val Lys Lys
    530                 535
```

<210> 177

<211> 670

<212> PRT

<213> Neisseria meningitidis

<400> 177

```
Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser Val Asp Thr Glu
1               5                   10                  15

Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser Ser Glu Lys Pro
            20                  25                  30
```

```
Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Leu Lys
        35                  40                  45

Arg Arg Asn Trp Tyr Arg Gln Ala Asn Pro Lys Glu Asp Glu Ile Lys
    50                  55                  60

Leu Ser Glu Asn Asp Trp Glu Gln Thr Asp Asn Gly Asp Ile Lys Asn
65                  70                  75                  80

Pro Ser Lys Gln Lys Asn Ile Ile Asn Ala Leu Thr Gly Asn Asn Gly
                85                  90                  95

Gly Ala Ser Leu Gln Asp Ser Ser Gln Glu Asn Gln Gly Ile Ser Lys
            100                 105                 110

Val Thr Gly His His Asn Phe Gln Tyr Val Trp Ser Gly Phe Phe Tyr
        115                 120                 125

Lys Gln Ile Gly Ser Thr Phe Glu Arg Lys Asp Ser Ser Ile Thr Ala
    130                 135                 140

Ala Arg Ser Gly Pro Asp Gly Tyr Ile Phe Tyr Lys Gly Lys Asp Pro
145                 150                 155                 160

Ser Arg Lys Leu Pro Val Ser Gly Glu Val Met Tyr Lys Gly Thr Trp
                165                 170                 175

Asp Phe Leu Thr Asp Val Lys Thr Ser Gln Lys Phe Thr Asp Leu Gly
            180                 185                 190

Asn Thr Ser Thr Arg Pro Gly Asp Arg Tyr Ser Ala Phe Ser Gly Glu
        195                 200                 205

Leu Asp Tyr Ile Val Asn Lys Asp Ser Asp Lys Lys Asp Glu His Val
    210                 215                 220

Gly Trp Gly Leu Thr Thr Glu Ile Thr Val Asp Phe Glu Lys Lys Thr
225                 230                 235                 240

Leu Ser Gly Lys Leu Ile Lys Asn Asn Arg Val Asn Asn Asp Asn Asp
                245                 250                 255

Lys His Thr Thr Gln Tyr Tyr Ser Leu Asp Ala Thr Leu Arg Gly Asn
            260                 265                 270

Arg Phe Ser Gly Lys Ala Glu Ala Thr Asp Lys Pro Lys Asn Asp Gly
        275                 280                 285

Glu Thr Lys Glu His Pro Phe Val Ser Asp Ser Ser Ser Leu Ser Gly
    290                 295                 300

Gly Phe Phe Gly Pro Lys Gly Glu Glu Leu Gly Phe Arg Phe Leu Ser
305                 310                 315                 320

Asp Asp Gln Lys Val Ala Val Val Gly Ser Ala Lys Thr Gln Asp Lys
                325                 330                 335
```

```
Pro Arg Asn Gly Ala Val Ala Ser Gly Gly Ala Gly Ala Ala Ala Ser
            340                 345                 350

Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys Leu Thr Thr Val
        355                 360                 365

Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys Ile Lys Asn Leu
    370                 375                 380

Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met Ile
385                 390                 395                 400

Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly Lys Asn Gln Ala Asn Gln
                405                 410                 415

Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe Asn His Thr Pro
            420                 425                 430

Lys Ser Asp Glu Lys Asp Thr Gln Ala Gly Thr Ala Glu Asn Gly Asn
        435                 440                 445

Pro Ala Ala Ser Asn Thr Ala Gly Asp Ala Asn Gly Lys Thr Lys Thr
    450                 455                 460

Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr Gly
465                 470                 475                 480

Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln Ala Gly Glu Ser
                485                 490                 495

Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Gly Gln Ser Met Phe
            500                 505                 510

Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Asn Asp Gln Asn
        515                 520                 525

Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Asn Gly Thr Ser
    530                 535                 540

Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly Asn Arg Ala Asp Phe
545                 550                 555                 560

Thr Val Asn Phe Gly Thr Lys Lys Ile Asn Gly Thr Leu Thr Ala Asp
                565                 570                 575

Asn Arg Gln Ala Ala Thr Phe Thr Ile Val Gly Asp Ile Glu Gly Asn
            580                 585                 590

Gly Phe Ser Gly Thr Ala Lys Thr Ala Asp Ser Gly Phe Asp Leu Asp
        595                 600                 605

Gln Ser Asn Asn Thr Arg Thr Pro Lys Ala Tyr Ile Thr Asn Ala Lys
    610                 615                 620

Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly Trp
625                 630                 635                 640
```

```
Phe Ala Tyr Ser Asp Asp Lys Gln Thr Lys Asn Ala Thr Asp Ala Ser
                645                 650                 655

Gly Asn Gly Asn Ser Ala Ser Ser Ala Thr Val Val Phe Gly
            660                 665                 670
```

<210> 178

<211> 680

<212> PRT

<213> Neisseria meningitidis

<400> 178

```
Cys Leu Gly Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser Val Asp Thr
1               5                  10                  15

Glu Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser Ser Glu Lys
            20                  25                  30

Pro Gln Ala Pro Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Phe
        35                  40                  45

Lys Arg Arg Asn Trp Tyr Pro Ser Ala Lys Glu Asn Glu Val Lys Leu
    50                  55                  60

Asn Glu Gly Asp Trp Glu Ala Thr Gly Leu Pro Thr Glu Pro Lys Glu
65                  70                  75                  80

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

Asp Ser Asn Ile Tyr Ser Ser Pro Tyr Leu Thr Pro Ser Asn His Gln
            100                 105                 110

Ser Gly Ser Ala Gly Asn Gly Val Asn Gln Pro Lys Asn Lys Ala Thr
        115                 120                 125

Asp His Glu Asn Phe Gln Tyr Val Tyr Ser Gly Trp Phe Tyr Lys His
    130                 135                 140

Ala Lys Gln His Arg Asp Leu Ala Asn Lys Ile Val Gln Gln Gly Asp
145                 150                 155                 160

Asp Gly Tyr Ile Phe Tyr His Gly Lys Glu Pro Ser Arg Gln Leu Pro
                165                 170                 175

Ala Ser Gly Lys Ile Thr Tyr Lys Gly Val Trp His Phe Ala Thr Asp
            180                 185                 190

Val Lys Lys Ser Gln Asn Phe Arg Glu Ile Ile Gln Pro Ser Lys Ser
        195                 200                 205

Gln Gly Asp Arg Tyr Ser Gly Phe Ser Gly Asp Asp Gly Glu Glu Tyr
    210                 215                 220

Ser Asn Lys Asn Glu Thr Thr Leu Gln Ser Gly His Glu Gly Tyr Gly
225                 230                 235                 240
```

```
Phe Thr Ser Asn Leu Glu Val Asp Phe Asp Asn Lys Lys Leu Thr Gly
               245                 250                 255

Lys Leu Ile Arg Asn Asn Ala Asn Thr Ser Asn Asn Gln Ala Thr Thr
           260                 265                 270

Gln Tyr Tyr Ser Leu Asp Ala Gln Ile Thr Gly Asn Arg Phe Asn Gly
       275                 280                 285

Lys Ala Met Ala Thr Asp Lys Pro Gly Thr Gly Glu Thr Lys Leu His
   290                 295                 300

Pro Phe Val Ser Asp Ser Ser Ser Leu Ser Gly Gly Phe Phe Gly Pro
305                 310                 315                 320

Lys Gly Glu Glu Leu Gly Phe Arg Phe Leu Ser Asp Asp Gln Lys Val
               325                 330                 335

Ala Val Val Gly Ser Ala Lys Thr Gln Asp Lys Pro Gly Asn Gly Ala
           340                 345                 350

Ala Ala Ser Gly Gly Thr Gly Ala Ala Ala Ser Gly Gly Ala Ala Asp
       355                 360                 365

Met Pro Ser Glu Asn Ser Lys Leu Thr Thr Val Leu Asp Ala Val Glu
   370                 375                 380

Leu Thr His Gly Gly Thr Ala Ile Lys Asn Leu Asp Asn Phe Ser Asn
385                 390                 395                 400

Ala Ala Gln Leu Val Val Asp Gly Ile Met Ile Pro Leu Leu Pro Glu
               405                 410                 415

Ala Ser Glu Ser Gly His Asn Gln Ala Asn Gln Gly Thr Asn Gly Gly

           420                 425                 430

Thr Ala Phe Thr Arg Lys Phe Asn His Thr Pro Thr Ser Asp Glu Lys
       435                 440                 445

Asp Thr Gln Ala Gly Thr Ala Ala Asn Gly Asn Gln Ala Ala Ser Asn
   450                 455                 460

Thr Ala Gly Asp Ala Asn Gly Lys Thr Lys Thr Tyr Ala Val Glu Val
465                 470                 475                 480

Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr Gly Leu Leu Thr Arg Lys
               485                 490                 495

Thr Ala Gly Asn Thr Gly Glu Gly Gly Asn Gly Ser Gln Thr Ala Ala
           500                 505                 510

Gln Thr Asp Ala Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu
       515                 520                 525
```

```
Asn Lys Ile Pro Thr Asp Gln Asn Val Val Tyr Arg Gly Ser Trp Tyr
    530                 535                 540

Gly His Ile Ala Asn Gly Thr Ser Trp Ser Gly Asn Ala Ser Asp Lys
545                 550                 555                 560

Glu Gly Gly Asn Arg Ala Glu Phe Thr Val Asn Phe Gly Glu Lys Lys
                565                 570                 575

Ile Asn Gly Thr Leu Thr Ala Glu Asn Arg Gln Ala Ala Thr Phe Thr
            580                 585                 590

Ile Glu Gly Asp Ile Lys Asp Asn Gly Phe Glu Gly Thr Ala Lys Thr
        595                 600                 605

Ala Asp Leu Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr Gly Thr Pro
    610                 615                 620

Lys Ala Tyr Ile Thr Asn Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro
625                 630                 635                 640

Lys Ala Asp Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly Asp Asn Gln
                645                 650                 655

Ala Gln Pro Ser Ala Ser Gly Ser Gly Ala Ser Ala Ala Asn Ser Ala
            660                 665                 670

Thr Val Val Phe Gly Ala Lys Arg
        675                 680
```

<210> 179

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 179

```
Thr Gln Asp Lys Pro Arg Asn Gly Ala Val Ala Ser Gly Gly Ala Gly
1               5                   10                  15

Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys
            20                  25                  30

Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys
        35                  40                  45

Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
    50                  55                  60

Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly Lys Asn
65                  70                  75                  80

Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
                85                  90                  95

Asn His Thr Pro Lys Ser Asp Glu Lys Asp Thr Gln Ala Gly Thr Ala
```

```
            100                 105                 110

Glu Asn Gly Asn Pro Ala Ala Ser Asn Thr Ala Gly Asp Ala Asn Gly
        115                 120                 125

Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
    130                 135                 140

Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln
145                 150                 155                 160

Ala Gly Glu Ser Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Gly
                165                 170                 175

Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro
            180                 185                 190

Asn Asp Gln Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala
        195                 200                 205

Asn Gly Thr Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly Asn
    210                 215                 220

Arg Ala Asp Phe Thr Val Asn Phe Gly Thr Lys Lys Ile Asn Gly Thr
225                 230                 235                 240

Leu Thr Ala Asp Asn Arg Gln Ala Ala Thr Phe Thr Ile Val Gly Asp
                245                 250                 255

Ile Glu Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala Asp Ser Gly
            260                 265                 270

Phe Asp Leu Asp Gln Ser Asn Asn Thr Arg Thr Pro Lys Ala Tyr Ile
        275                 280                 285

Thr Asn Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu
    290                 295                 300

Leu Gly Gly Trp Phe Ala Tyr Ser Asp Asp Lys Gln Thr Lys Asn Ala
305                 310                 315                 320

Thr Asp Ala Ser Gly Asn Gly Asn Ser Ala Ser Ser Ala Thr Val Val
                325                 330                 335

Phe Gly Ala Lys
            340
```

<210> 180

<211> 330

<212> PRT

<213> Neisseria meningitidis

<400> 180

```
Thr Gln Asp Lys Pro Gly Asn Gly Ala Ala Ala Ser Gly Gly Thr Gly
1               5                   10                  15
```

```
Ala Ala Ala Ser Gly Gly Ala Ala Asp Met Pro Ser Glu Asn Ser Lys
            20                  25                  30

Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr His Gly Gly Thr Ala
        35                  40                  45

Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
    50                  55                  60

Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly His Asn
65                  70                  75                  80

Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
                85                  90                  95

Asn His Thr Pro Thr Ser Asp Glu Lys Asp Thr Gln Ala Gly Thr Ala
            100                 105                 110

Ala Asn Gly Asn Gln Ala Ala Ser Asn Thr Ala Gly Asp Ala Asn Gly
        115                 120                 125

Lys Thr Lys Thr Tyr Ala Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
    130                 135                 140

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

Gly Gly Asn Gly Ser Gln Thr Ala Ala Gln Thr Asp Ala Gln Ser Met
                165                 170                 175

Phe Leu Gln Gly Glu Arg Thr Asp Glu Asn Lys Ile Pro Thr Asp Gln
            180                 185                 190

Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Asn Gly Thr
        195                 200                 205

Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly Asn Arg Ala Glu
    210                 215                 220

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

Glu Asn Arg Gln Ala Ala Thr Phe Thr Ile Glu Gly Asp Ile Lys Asp
                245                 250                 255

Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala Asp Leu Gly Phe Asp Leu
            260                 265                 270

Asp Gln Ser Asn Thr Thr Gly Thr Pro Lys Ala Tyr Ile Thr Asn Ala
        275                 280                 285

Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Asp Glu Leu Gly Gly
    290                 295                 300

Trp Phe Ala Tyr Pro Gly Asp Asn Gln Ala Gln Pro Ser Ala Ser Gly
305                 310                 315                 320
```

```
Ser Gly Ala Ser Ala Ala Asn Ser Ala Thr
                325                 330
```

<210> 181

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 181

```
Thr Lys Asp Lys Ala Glu Ser Gly Asn Gly Asn Gly Asn Gly Thr Ser
1               5                   10                  15

Gly Gly Ala Ser Val Ser Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser
            20                  25                  30

Glu Asn Ser Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Lys Ser
        35                  40                  45

Gly Asp Lys Glu Val Lys Lys Leu Asp Asn Phe Ser Asn Ala Ala Gln
    50                  55                  60

Leu Val Val Asp Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu
65                  70                  75                  80

Ser Gly Ser Asn Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe
                85                  90                  95

Thr Arg Lys Phe Asn His Thr Pro Lys Ser Asp Glu Lys Asp Thr Gln
            100                 105                 110

Ala Gly Thr Ala Glu Asn Gly Asn Pro Ala Ala Ser Asn Thr Ala Gly
        115                 120                 125

Asp Ala Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser
    130                 135                 140

Asn Leu Asn Tyr Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys
145                 150                 155                 160

Ser Ala Met Gln Ala Gly Glu Ser Ser Ser Gln Ala Asp Ala Lys Thr
                165                 170                 175

Glu Gln Val Glu Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu
            180                 185                 190

Lys Glu Ile Pro Asn Asp Gln Asn Val Val Tyr Arg Gly Ser Trp Tyr
        195                 200                 205

Gly His Ile Ala Asn Gly Thr Ser Trp Ser Gly Asn Ala Ser Asp Lys
    210                 215                 220

Glu Gly Gly Asn Arg Ala Asp Phe Thr Val Asn Phe Gly Thr Lys Lys
225                 230                 235                 240
```

```
Ile Asn Gly Thr Leu Thr Ala Asp Asn Arg Gln Ala Ala Thr Phe Thr
                245                 250                 255

Ile Val Gly Asp Ile Glu Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr
            260                 265                 270

Ala Asp Ser Gly Phe Asp Leu Asp Gln Ser Asn Asn Thr Arg Thr Pro
        275                 280                 285

Lys Ala Tyr Ile Thr Asn Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro
    290                 295                 300

Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Ser Asp Asp Lys Gln
305                 310                 315                 320

Thr Lys Asn Ala Thr Asp Ala Ser Gly Asn Gly Asn Ser Ala Ser Ser
                325                 330                 335

Ala Thr Val Val
            340
```

<210> 182

<211> 330

<212> PRT

<213> Neisseria meningitidis

<400> 182

```
Thr Lys Asp Lys Pro Gly Asn Gly Ala Ala Ala Pro Gly Gly Thr Asp
1               5                   10                  15

Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys
            20                  25                  30

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

Val Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
    50                  55                  60

Gly Ile Met Ile Pro Leu Leu Pro Lys Asp Ser Glu Ser Gly Asn Thr
65                  70                  75                  80

Gln Ala Asp Lys Gly Lys Asn Gly Gly Thr Glu Phe Thr Arg Lys Phe
                85                  90                  95

Glu His Thr Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Ala
            100                 105                 110

Glu Asn Gly Asn Pro Ala Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly
        115                 120                 125

Lys Thr Lys Thr Tyr Ala Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
    130                 135                 140

Leu Lys Tyr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn Thr Gly Glu
145                 150                 155                 160
```

```
Gly Gly Asn Gly Ala Ala Gln Thr Asp Ala Gln Ser Met Phe Leu Gln
                165                 170                 175

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

Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Asn Gly Thr Ser Trp Ser
        195                 200                 205

Gly Asn Ala Ser Asp Lys Glu Gly Gly Asn Arg Ala Glu Phe Thr Val
    210                 215                 220

Asn Phe Ala Asp Lys Lys Leu Asn Gly Thr Leu Thr Ala Gly Glu Arg
225                 230                 235                 240

Thr Ser Pro Thr Phe Thr Ile Thr Ala Thr Ile Gln Gly Asn Gly Phe
                245                 250                 255

Glu Gly Thr Ala Lys Thr Gly Asp Asp Gly Phe Ala Leu Asp Thr Lys
            260                 265                 270

Asn Thr Val Asp Thr His Lys Ala His Ile Thr Asp Ala Asn Val Gln
        275                 280                 285

Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala
    290                 295                 300

Tyr Pro Gly Asp Arg Gln Ala Gln Pro Ser Ala Ser Gly Ser Gly Thr
305                 310                 315                 320

Ser Ala Ala Asn Ser Ala Thr Val Val Phe
                325                 330
```

<210> 183

<211> 320

<212> PRT

<213> Neisseria meningitidis

<400> 183

```
Thr Lys Asp Lys Pro Ala Asn Gly Asn Thr Ala Ala Ala Ser Gly Gly
1               5                   10                  15

Thr Asp Ala Ala Ala Ser Gly Gly Thr Ala Gly Thr Pro Ser Glu Ser
            20                  25                  30

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

Lys Glu Val Lys Lys Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
    50                  55                  60

Val Asp Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly
65                  70                  75                  80
```

```
Asn Asn Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg
                85                  90                  95

Lys Phe Asn His Thr Pro Lys Ser Asp Glu Lys Asp Thr Gln Ala Gly
            100                 105                 110

Thr Ala Glu Asn Gly Asn Pro Ala Ala Ser Asn Thr Ala Gly Asp Ala
        115                 120                 125

Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu
    130                 135                 140

Asn Tyr Leu Lys Tyr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn Thr
145                 150                 155                 160

Gly Glu Gly Gly Asn Gly Ser Pro Thr Ala Ala Gln Thr Asp Ala Gln
                165                 170                 175

Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Lys
            180                 185                 190

Glu Gln Gln Asp Ile Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala
        195                 200                 205

Asn Gly Thr Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly Asn
    210                 215                 220

Arg Ala Glu Phe Thr Val Asn Phe Gly Asp Lys Lys Ile Thr Gly Thr
225                 230                 235                 240

Leu Thr Ala Asp Asn Arg Gln Ala Ala Thr Phe Thr Ile Glu Gly Asp
                245                 250                 255

Ile Glu Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr Asp Asn Leu Gly
            260                 265                 270

Phe Asp Leu Asp Gln Ser Asp Asn Thr Arg Thr Pro Lys Ala Tyr Ile
        275                 280                 285

Thr Asp Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu
    290                 295                 300

Leu Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Glu Lys Ala
305                 310                 315                 320
```

<210> 184

<211> 350

<212> PRT

<213> Neisseria meningitidis

<400> 184

```
Thr Gln Asp Lys Ala Ala Asn Gly Asn Thr Ala Ala Ala Ser Gly Gly
1               5                   10                  15

Thr Asp Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn
```

```
                20                  25                  30

Ser Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp
        35                  40                  45

Lys Lys Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
    50                  55                  60

Val Asp Gly Ile Met Ile Pro Leu Leu Pro Glu Thr Ser Glu Ser Gly
65                  70                  75                  80

Ser Asn Gln Ala Asp Lys Gly Lys Lys Gly Lys Asn Gly Lys Asn Gly
                85                  90                  95

Gly Thr Asp Phe Thr Tyr Lys Thr Thr Tyr Thr Pro Lys Asn Asp Asp
            100                 105                 110

Lys Asp Thr Lys Ala Gln Thr Gly Ala Ala Gly Ser Ser Gly Ala Gln
        115                 120                 125

Thr Asp Leu Gly Lys Ala Asp Val Asn Gly Gly Lys Ala Glu Thr Lys
    130                 135                 140

Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr
145                 150                 155                 160

Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln Ala Gly Gly
                165                 170                 175

Asn Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu Gln Ser Met
            180                 185                 190

Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Asn Asp Gln
        195                 200                 205

Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Ser Ser Thr
    210                 215                 220

Ser Trp Ser Gly Asn Ala Ser Asn Ala Thr Ser Gly Asn Arg Ala Glu
225                 230                 235                 240

Phe Thr Val Asn Phe Asp Thr Lys Lys Ile Asn Gly Thr Leu Thr Ala
                245                 250                 255

Glu Asn Arg Gln Glu Ala Thr Phe Thr Ile Asp Gly Lys Ile Glu Gly
            260                 265                 270

Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala Asp Leu Gly Phe Asp Leu
        275                 280                 285

Asp Gln Ser Asn Thr Thr Gly Thr Pro Lys Ala Tyr Ile Thr Asp Ala
    290                 295                 300

Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly
305                 310                 315                 320
```

```
Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Glu Lys Ala Thr Val Ala
                325                 330                 335

Ser Gly Asp Gly Asn Ser Ala Ser Ser Ala Thr Val Val Phe
            340                 345                 350
```

<210> 185

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 185

```
Thr Lys Asp Lys Pro Ala Asn Gly Asn Thr Ala Ala Ala Ser Gly Gly
1               5                  10                  15

Thr Asp Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn
            20                  25                  30

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

Lys Glu Val Gln Lys Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
    50                  55                  60

Val Asp Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly
65                  70                  75                  80

Asn Asn Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg
                85                  90                  95

Lys Phe Asp His Thr Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly
            100                 105                 110

Thr Gln Thr Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr
        115                 120                 125

Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu
    130                 135                 140

Asn Tyr Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala
145                 150                 155                 160

Met Gln Ala Gly Glu Ser Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln
                165                 170                 175

Val Glu Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu
            180                 185                 190

Ile Pro Ser Glu Gln Asn Ile Val Tyr Arg Gly Ser Trp Tyr Gly Tyr
        195                 200                 205

Ile Ala Asn Asp Lys Ser Thr Ser Trp Ser Gly Asn Ala Ser Asn Ala
    210                 215                 220

Thr Ser Gly Asn Arg Ala Glu Phe Thr Val Asn Phe Ala Asp Lys Lys
```

```
225                 230                 235                 240

Ile Thr Gly Thr Leu Thr Ala Asp Asn Arg Gln Glu Ala Thr Phe Thr
                245                 250                 255

Ile Asp Gly Asn Ile Lys Asp Asn Gly Phe Glu Gly Thr Ala Lys Thr

            260                 265                 270

Ala Glu Ser Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr Arg Thr Pro
        275                 280                 285

Lys Ala Tyr Ile Thr Asp Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro
    290                 295                 300

Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln
305                 310                 315                 320

Thr Lys Asn Ala Thr Asn Ala Ser Gly Asn Ser Ser Ala Thr Val Val
                325                 330                 335

Phe Gly Ala Lys
            340
```

<210> 186

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 186

```
Thr Lys Asp Lys Pro Ala Asn Gly Asn Thr Ala Ala Ala Ser Gly Gly
1               5                   10                  15

Thr Asp Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn
            20                  25                  30

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

Lys Glu Val Gln Lys Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
    50                  55                  60

Val Asp Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly
65                  70                  75                  80

Asn Asn Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg
                85                  90                  95

Lys Phe Asp His Thr Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly
            100                 105                 110

Thr Gln Thr Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr
        115                 120                 125

Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu
```

```
Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu
    130                 135                 140

Asn Tyr Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala
145                 150                 155                 160

Met Gln Ala Gly Glu Ser Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln
                165                 170                 175

Val Glu Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu
            180                 185                 190

Ile Pro Ser Glu Gln Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His
        195                 200                 205

Ile Ala Asn Gly Thr Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly
    210                 215                 220

Gly Asn Arg Ala Glu Phe Thr Val Asp Phe Gly Ala Lys Lys Ile Asn
225                 230                 235                 240

Gly Lys Leu Thr Ala Glu Asn Arg Gln Ala Ala Thr Phe Thr Ile Glu
                245                 250                 255

Gly Asp Ile Glu Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala Glu
            260                 265                 270

Ser Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr Arg Thr Pro Lys Ala
        275                 280                 285

Tyr Ile Thr Asp Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala
    290                 295                 300

Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Lys
305                 310                 315                 320

Asn Ala Thr Asn Ala Ser Gly Asn Ser Ser Ala Thr Val Val Phe Gly
                325                 330                 335

Ala Lys Arg Gln
            340
```

<210> 187

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 187

```
Thr Lys Asp Lys Ala Glu Ser Gly Lys Thr Val Ala Ala Ser Gly Gly
1               5                   10                  15

Thr Gly Ala Ala Ala Ser Gly Gly Ala Ala Asp Met Pro Ser Glu Asn
            20                  25                  30
```

```
Gly Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp
        35                  40                  45

Lys Lys Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
    50                  55                  60

Val Asp Gly Ile Met Ile Pro Leu Leu Pro Lys Asp Ser Glu Ser Gly
65                  70                  75                  80

Asn Asn Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Tyr
                85                  90                  95

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

Thr Ala Ala Asn Gly Asn Gln Ala Ala Ser Asn Thr Ala Gly Asp Thr
        115                 120                 125

Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu
    130                 135                 140

Asn Tyr Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala
145                 150                 155                 160

Met Gln Ala Gly Glu Asn Gly Ser Gln Ala Asp Ala Lys Thr Glu Gln
                165                 170                 175

Val Glu Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu
            180                 185                 190

Ile Pro Lys Glu Gln Gln Asp Ile Val Tyr Arg Gly Ser Trp Tyr Gly
        195                 200                 205

His Ile Ala Gly Ser Thr Ser Trp Ser Gly Asn Ala Ser Asn Ala Thr
    210                 215                 220

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

Asn Gly Lys Leu Thr Ala Glu Asn Arg Gln Ala Ala Thr Phe Thr Ile
                245                 250                 255

Val Gly Asp Ile Lys Asp Asn Gly Phe Glu Gly Thr Ala Lys Thr Asp
            260                 265                 270

Asn Leu Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr Gly Thr Pro Lys
        275                 280                 285

Ala Tyr Ile Thr Asn Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys
    290                 295                 300

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

Lys Asn Ala Thr Asp Ala Ser Gly Asn Gly Asn Ser Ala Ser Ser Ala
```

```
                325                 330                 335

Thr Val Val Phe
            340
```

<210> 188

<211> 330

<212> PRT

<213> Neisseria meningitidis

<400> 188

```
Thr Lys Asp Lys Asn Ala Asn Gly Asn Thr Pro Ala Ala Ser Ser Gly
1               5                  10                  15

Ala Gly Ala Ala Thr Met Pro Ser Glu Thr Arg Leu Thr Thr Val Leu
            20                  25                  30

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

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

Leu Leu Pro Glu Ala Ser Glu Ser Gly Lys Asn Gln Ala Asp Lys Gly
65                  70                  75                  80

Lys Asn Gly Gly Thr Ala Phe Thr Tyr Thr Ile Thr Tyr Thr Pro Glu
                85                  90                  95

Ser Asp Lys Lys Asp Thr Gln Ala Gly Thr Pro Thr Asn Gly Ala Gln
            100                 105                 110

Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly Lys Thr Lys Thr Tyr
        115                 120                 125

Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr Gly Met
    130                 135                 140

Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln Ala Gly Glu Ser Ser
145                 150                 155                 160

Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu Gln Ser Met Phe Leu
                165                 170                 175

Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Ser Glu Gln Asn Ile
            180                 185                 190

Val Tyr Arg Gly Ser Trp Tyr Gly Tyr Ile Ala Asn Asp Lys Ser Thr
        195                 200                 205

Ser Trp Ser Gly Asn Ala Ser Asn Ala Thr Ser Gly Asn Arg Ala Glu
    210                 215                 220

Phe Thr Val Asn Phe Ala Asp Lys Lys Ile Thr Gly Thr Leu Thr Ala
225                 230                 235                 240
```

```
Asp Asn Arg Gln Glu Ala Thr Phe Thr Ile Asp Gly Asn Ile Lys Asp
                245                 250                 255

Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala Glu Ser Gly Phe Asp Leu
            260                 265                 270

Asp Gln Ser Asn Thr Thr Arg Thr Pro Lys Ala Tyr Ile Thr Asp Ala
        275                 280                 285

Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly
    290                 295                 300

Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Lys Asn Ala Thr Asn Ala
305                 310                 315                 320

Ser Gly Asn Ser Ser Ala Thr Val Val Phe
                325                 330
```

<210> 189

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 189

```
Thr Lys Asp Lys Leu Glu Asn Gly Ala Ala Ala Ser Gly Ser Thr Gly
1               5                   10                  15

Ala Ala Ala Ser Gly Gly Ala Ala Asp Met Pro Ser Glu Asn Gly Lys
            20                  25                  30

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

Val Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
    50                  55                  60

Gly Ile Met Ile Pro Leu Leu Pro Lys Glu Ser Glu Ser Glu Ser Asn
65                  70                  75                  80

Gln Ala Asp Lys Gly Lys Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
                85                  90                  95

Glu His Thr Pro Glu Ser Asp Lys Lys Asp Thr Gln Ala Gly Thr Ala
            100                 105                 110

Glu Asn Gly Asn Pro Ala Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly
        115                 120                 125

Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
    130                 135                 140

Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln
145                 150                 155                 160

Ala Gly Glu Asn Gly Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu
                165                 170                 175
```

```
                165                 170                 175

Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro
            180                 185                 190

Lys Glu Gln Gln Asp Ile Val Tyr Arg Gly Ser Trp Tyr Gly His Ile
        195                 200                 205

Ala Asn Asp Thr Ser Trp Ser Gly Asn Ala Ser Asp Arg Glu Gly Gly
    210                 215                 220

Asn Arg Ala Asp Phe Thr Val Asn Phe Gly Thr Lys Lys Ile Asn Gly
225                 230                 235                 240

Thr Leu Thr Ala Glu Asn Arg Gln Glu Ala Thr Phe Thr Ile Val Gly
                245                 250                 255

Asp Ile Lys Asp Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala Asp Ser
            260                 265                 270

Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr Arg Thr Pro Lys Ala Tyr
        275                 280                 285

Ile Thr Asp Ala Lys Val Lys Gly Gly Phe Tyr Gly Pro Lys Ala Glu
    290                 295                 300

Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Glu Lys
305                 310                 315                 320

Ala Thr Val Thr Ser Gly Asp Gly Asn Ser Ala Ser Ser Ala Thr Val
                325                 330                 335

Val Phe Gly Ala
            340
```

<210> 190

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 190

```
Thr Gln Asp Lys Ala Ala Asn Gly Asn Thr Ala Ala Ala Ser Gly Asp
1               5                   10                  15

Ala Ser Val Ser Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn
            20                  25                  30

Gly Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp
        35                  40                  45

Lys Lys Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
    50                  55                  60

Val Asp Gly Ile Met Ile Pro Leu Leu Pro Glu Thr Ser Glu Ser Gly
65                  70                  75                  80
```

```
Asn Asn Gln Ala Asp Lys Gly Lys Asn Gly Gly Thr Ala Phe Thr Arg
                85                  90                  95

Lys Phe Asp His Thr Pro Lys Ser Asp Glu Lys Asp Thr Gln Ala Gly
            100                 105                 110

Thr Ala Ala Asn Gly Ala Gln Thr Ala Ser Gly Thr Ala Gly Asp Thr
        115                 120                 125

Ser Gly Lys Thr Lys Thr Tyr Gln Val Glu Val Cys Cys Ser Asn Leu
    130                 135                 140

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

Met Gln Ala Gly Glu Ser Ser Ser Gln Thr Pro Ala Ala Gln Thr Ala
                165                 170                 175

Gln Gly Ala Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Asn
            180                 185                 190

Lys Ile Pro Thr Asp Gln Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly
        195                 200                 205

His Ile Ala Ser Ser Thr Ser Trp Ser Gly Asn Ala Ser Asn Ala Thr
    210                 215                 220

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

Thr Gly Lys Leu Thr Ala Glu Asn Arg Gln Glu Ala Thr Phe Thr Ile
                245                 250                 255

Asp Gly Lys Ile Glu Gly Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala
            260                 265                 270

Glu Leu Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr Gly Thr Pro Lys
        275                 280                 285

Ala Tyr Ile Thr Asn Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys
    290                 295                 300

Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr
305                 310                 315                 320

Glu Asn Thr Thr Val Ala Ser Gly Asn Gly Asn Ser Ala Ser Ser Ala
                325                 330                 335

Thr Val Val Phe
            340
```

<210> 191

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 191

```
Thr Lys Asp Lys Pro Ala Asn Gly Asn Thr Ala Glu Ala Ser Gly Gly
1               5                  10                  15

Thr Gly Ala Ala Ala Ser Asp Gly Ala Ala Gly Thr Ser Ser Lys Asn
            20                  25                  30

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

Lys Glu Val Gln Lys Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
    50                  55                  60

Val Asp Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly
65                  70                  75                  80

Asn Thr Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
                85                  90                  95

Glu Gln Met Pro Glu Ser Asp Glu Lys Asp Thr Lys Ala Gln Thr Gly
            100                 105                 110

Thr Gly Gly Thr Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly
        115                 120                 125

Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
    130                 135                 140

Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln
145                 150                 155                 160

Ala Gly Glu Ser Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Gly
                165                 170                 175

Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro
            180                 185                 190

Asn Asp Gln Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala
        195                 200                 205

Asn Gly Thr Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly Asn
    210                 215                 220

Arg Ala Asp Phe Thr Val Asn Phe Gly Thr Lys Lys Ile Asn Gly Thr
225                 230                 235                 240

Leu Thr Ala Asp Asn Arg Gln Ala Ala Thr Phe Thr Ile Val Gly Asp
                245                 250                 255

Ile Glu Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala Asp Ser Gly
            260                 265                 270

Phe Asp Leu Asp Gln Ser Asn Asn Thr Arg Thr Pro Lys Ala Tyr Ile
        275                 280                 285

Thr Asn Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu
    290                 295                 300
```

```
Leu Gly Gly Trp Phe Ala Tyr Ser Asp Asp Lys Gln Thr Lys Asn Ala
305                 310                 315                 320

Thr Asp Ala Ser Gly Asn Gly Asn Ser Ala Ser Ser Ala Thr Val Val
                325                 330                 335

Phe Gly Ala Lys
            340
```

<210> 192

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 192

```
Thr Gln Asp Lys Pro Arg Asn Gly Ala Val Ala Ser Gly Gly Ala Gly
1               5                   10                  15

Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys
            20                  25                  30

Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys
        35                  40                  45

Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
    50                  55                  60

Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly Lys Asn
65                  70                  75                  80

Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
                85                  90                  95

Asn His Thr Pro Lys Ser Asp Glu Lys Asp Thr Gln Ala Gly Thr Ala
            100                 105                 110

Glu Asn Gly Asn Pro Ala Ala Ser Asn Thr Ala Gly Asp Ala Asn Gly
        115                 120                 125

Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
    130                 135                 140

Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln
145                 150                 155                 160

Ala Gly Glu Ser Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Gly
                165                 170                 175

Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro
            180                 185                 190

Asn Asp Gln Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala
        195                 200                 205
```

```
Asn Gly Thr Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly Asn
    210                 215                 220

Arg Ala Asp Phe Thr Val Asn Phe Gly Thr Lys Lys Ile Asn Gly Thr
225                 230                 235                 240

Leu Thr Ala Asp Asn Arg Gln Ala Ala Thr Phe Thr Ile Val Gly Asp
                245                 250                 255

Ile Glu Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala Asp Ser Gly
            260                 265                 270

Phe Asp Leu Asp Gln Ser Asn Asn Thr Arg Thr Pro Lys Ala Tyr Ile
        275                 280                 285

Thr Asn Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu
    290                 295                 300

Leu Gly Gly Trp Phe Ala Tyr Ser Asp Asp Lys Gln Thr Lys Asn Ala
305                 310                 315                 320

Thr Asp Ala Ser Gly Asn Gly Asn Ser Ala Ser Ser Ala Thr Val Val
                325                 330                 335

Phe Gly Ala Lys
            340
```

<210> 193

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 193

```
Thr Lys Asp Lys Pro Ala Asn Gly Asn Thr Ala Glu Ala Ser Gly Gly
1               5                   10                  15

Thr Asp Ala Ala Ala Ser Gly Gly Ala Ala Gly Thr Ser Ser Glu Asn
            20                  25                  30

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

Thr Ala Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
    50                  55                  60

Val Asp Gly Ile Met Ile Pro Leu Leu Pro Gln Asn Ser Thr Gly Lys
65                  70                  75                  80

Asn Asn Gln Pro Asp Gln Gly Lys Asn Gly Gly Thr Ala Phe Ile Tyr
                85                  90                  95

Lys Thr Thr Tyr Thr Pro Lys Asn Asp Asp Lys Asp Thr Lys Ala Gln
            100                 105                 110

Thr Val Thr Gly Gly Thr Gln Thr Ala Ser Asn Thr Ala Gly Asp Ala
```

```
        115                 120                 125

Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu
    130                 135                 140

Asn Tyr Leu Lys Tyr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn Thr
145                 150                 155                 160

Val Gly Ser Gly Asn Ser Ser Pro Thr Ala Ala Ala Gln Thr Asp Ala
                165                 170                 175

Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Asn Lys Ile Pro
            180                 185                 190

Ser Glu Gln Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala
        195                 200                 205

Ser Ser Thr Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly Asn
    210                 215                 220

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

Leu Thr Ala Glu Asn Arg Gln Glu Ala Thr Phe Thr Ile Asp Gly Lys
                245                 250                 255

Ile Glu Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala Glu Leu Gly

            260                 265                 270

Phe Asp Leu Asp Gln Lys Asn Thr Thr Arg Thr Pro Lys Ala Tyr Ile
        275                 280                 285

Thr Asp Ala Lys Val Lys Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu
    290                 295                 300

Leu Gly Gly Trp Phe Ala Tyr Ser Asp Asp Lys Gln Thr Lys Asn Ala
305                 310                 315                 320

Thr Asp Ala Ser Gly Asn Gly Asn Ser Ala Ser Ser Ala Thr Val Val
                325                 330                 335

Phe Gly Ala Lys
            340
```

<210> 194

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 194

```
Thr Lys Asp Lys Thr Glu Asn Gly Ala Ala Ala Ser Gly Gly Ala Gly
1               5                   10                  15

Ala Ala Ala Ser Gly Gly Ala Ala Ala Met Pro Ser Glu Asn Gly Lys
```

```
            20                  25                  30

Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr His Gly Gly Thr Ala
        35                  40                  45

Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
    50                  55                  60

Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly His Asn
65                  70                  75                  80

Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
                85                  90                  95

Asp His Thr Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln
            100                 105                 110

Thr Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly
        115                 120                 125

Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr

    130                 135                 140

Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln
145                 150                 155                 160

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

Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro
            180                 185                 190

Lys Glu Gln Gln Asp Ile Val Tyr Arg Gly Ser Trp Tyr Gly His Ile
        195                 200                 205

Ala Asn Asp Thr Ser Trp Ser Gly Asn Ala Ser Asp Arg Glu Gly Gly
    210                 215                 220

Asn Arg Ala Asp Phe Thr Val Asn Phe Gly Thr Lys Lys Ile Asn Gly
225                 230                 235                 240

Thr Leu Thr Ala Glu Asn Arg Gln Glu Ala Thr Phe Thr Ile Val Gly
                245                 250                 255

Asp Ile Lys Asp Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala Asp Ser
            260                 265                 270

Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr Arg Thr Pro Lys Ala Tyr
        275                 280                 285

Ile Thr Asp Ala Lys Val Lys Gly Gly Phe Tyr Gly Pro Lys Ala Glu
    290                 295                 300

Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Glu Lys
```

```
305                 310                 315                 320

Ala Thr Val Thr Ser Gly Asp Gly Asn Ser Ala Ser Ser Ala Thr Val
                325                 330                 335

Val Phe Gly Ala
            340
```

<210> 195

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 195

```
Thr Lys Asp Lys Pro Arg Asn Gly Ala Val Ala Ser Gly Gly Ala Gly

1               5                   10                  15

Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys
            20                  25                  30

Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys
        35                  40                  45

Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
    50                  55                  60

Gly Ile Met Ile Pro Leu Leu Pro Gln Asn Ser Thr Gly Glu Asn Asn
65                  70                  75                  80

Gln Pro Asp Gln Gly Lys Thr Gly Gly Thr Ala Phe Ile Tyr Lys Thr
                85                  90                  95

Thr Tyr Thr Pro Lys Asn Asp Asp Lys Asp Thr Lys Ala Gln Thr Gly
            100                 105                 110

Ala Ala Gly Ser Ser Gly Ala Gln Thr Ala Ser Gly Thr Glu Ser Val
        115                 120                 125

Thr Gly Gly Gln Ala Gly Thr Lys Thr Tyr Glu Val Glu Val Cys Cys
    130                 135                 140

Ser Asn Leu Asn Tyr Leu Lys Tyr Gly Leu Leu Thr Arg Lys Thr Ala
145                 150                 155                 160

Ser Asn Thr Gly Glu Gly Gly Asn Gly Ser Gln Thr Ala Ala Gln Thr
                165                 170                 175

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

Lys Glu Ile Pro Asn Asp Gln Asn Val Val Tyr Arg Gly Ser Trp Tyr
        195                 200                 205

Gly Tyr Ile Ala Asn Asp Thr Ser Trp Ser Gly Asn Ala Ser Asp Lys
```

```
    210                 215                 220

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

Ile Asn Gly Lys Leu Thr Ala Glu Asn Arg Gln Glu Ala Thr Phe Thr
                245                 250                 255

Ile Glu Gly Met Ile Gln Gly Asn Gly Phe Glu Gly Thr Ala Lys Thr
            260                 265                 270

Ala Asp Leu Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr Gly Thr Pro
        275                 280                 285

Lys Ala Tyr Ile Thr Asn Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro
    290                 295                 300

Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln
305                 310                 315                 320

Thr Glu Asn Thr Thr Val Ala Ser Gly Asn Gly Asn Ser Ala Ser Ser
                325                 330                 335

Ala Thr Val Val
            340
```

<210> 196

<211> 620

<212> PRT

<213> Haemophilus influenzae

<400> 196

```
Cys Ser Gly Gly Gly Ser Phe Asp Val Asp Asn Val Ser Asn Thr Pro
1               5                   10                  15

Ser Ser Lys Pro Arg Tyr Gln Asp Asp Thr Ser Ser Ser Arg Thr Lys
            20                  25                  30

Ser Lys Leu Glu Lys Leu Ser Ile Pro Ser Leu Gly Gly Gly Met Lys
        35                  40                  45

Leu Val Ala Leu Asn Leu Phe Asp Arg Asn Lys Pro Ser Leu Leu Asn
    50                  55                  60

Glu Asp Ser Tyr Met Ile Phe Ser Ser Arg Ser Thr Ile Glu Glu Asp
65                  70                  75                  80

Val Lys Asn Asn Asn Gln Asn Gly Glu His Pro Ile Asp Ser Ile Val
                85                  90                  95

Asp Pro Arg Ala Pro Asn Ser Asn Glu Asn Arg His Gly Gln Lys Tyr
            100                 105                 110

Val Tyr Ser Gly Leu Tyr Tyr Ile Gln Ser Trp Ser Leu Arg Asp Leu
        115                 120                 125
```

```
Pro Asn Lys Lys Phe Tyr Ser Gly Tyr Tyr Gly Tyr Ala Tyr Tyr Phe
    130                 135                 140

Gly Asn Thr Thr Ala Ser Ala Leu Pro Val Gly Gly Val Ala Thr Tyr
145                 150                 155                 160

Lys Gly Thr Trp Ser Phe Ile Thr Ala Ala Glu Asn Gly Lys Asn Tyr
                165                 170                 175

Glu Leu Leu Arg Asn Ser Gly Gly Gly Gln Ala Tyr Ser Arg Arg Ser
            180                 185                 190

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

Glu Phe Thr Val Asn Phe Gly Thr Lys Lys Leu Thr Gly Gly Leu Tyr
    210                 215                 220

Tyr Asn Leu Arg Glu Thr Asp Ala Asn Lys Ser Gln Asn Arg Thr His
225                 230                 235                 240

Lys Leu Tyr Asp Leu Glu Ala Asp Val His Ser Asn Arg Phe Arg Gly
                245                 250                 255

Lys Val Lys Pro Thr Lys Lys Glu Ser Ser Glu Glu His Pro Phe Thr
            260                 265                 270

Ser Glu Gly Thr Leu Glu Gly Gly Phe Tyr Gly Pro Glu Gly Gln Glu
        275                 280                 285

Leu Gly Gly Lys Phe Leu Ala His Asp Lys Lys Val Phe Gly Val Phe
    290                 295                 300

Ser Ala Lys Glu Gln Gln Glu Thr Ser Glu Asn Lys Lys Leu Pro Lys
305                 310                 315                 320

Glu Thr Leu Ile Asp Gly Lys Leu Thr Thr Phe Lys Thr Thr Asn Ala
                325                 330                 335

Thr Ala Asn Ala Thr Thr Asp Ala Thr Thr Ser Thr Thr Ala Ser Thr
            340                 345                 350

Lys Thr Asp Thr Thr Thr Asn Ala Thr Ala Asn Thr Glu Asn Phe Thr
        355                 360                 365

Thr Lys Asp Ile Pro Ser Phe Gly Glu Ala Asp Tyr Leu Leu Ile Asp
    370                 375                 380

Asn Tyr Pro Val Pro Leu Phe Pro Glu Ser Gly Asp Phe Ile Ser Ser
385                 390                 395                 400

Lys His His Thr Val Gly Lys Lys Thr Tyr Gln Val Glu Ala Cys Cys
                405                 410                 415

Ser Asn Leu Ser Tyr Val Lys Phe Gly Met Tyr Tyr Glu Ala Pro Pro
            420                 425                 430
```

```
Lys Glu Glu Glu Lys Glu Lys Asp Lys Asp Lys Asp Lys Asp Lys Glu
        435                 440                 445

Lys Glu Lys Gln Ala Thr Thr Ser Ile Lys Thr Tyr Tyr Gln Phe Leu
    450                 455                 460

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

Lys Tyr His Gly Asn Trp Phe Gly Tyr Ile Ser Asp Gly Glu Thr Ser
                485                 490                 495

Tyr Ser Ala Ser Gly Asp Lys Glu Arg Ser Lys Asn Ala Val Ala Glu
            500                 505                 510

Phe Asn Val Asn Phe Ala Glu Lys Thr Leu Thr Gly Glu Leu Lys Arg
        515                 520                 525

His Asp Thr Gln Asn Pro Val Phe Lys Ile Asn Ala Thr Phe Gln Ser
    530                 535                 540

Gly Lys Asn Asp Phe Thr Gly Thr Ala Thr Ala Lys Asp Leu Ala Ile
545                 550                 555                 560

Asp Gly Lys Asn Thr Gln Gly Thr Ser Lys Val Asn Phe Thr Ala Thr
                565                 570                 575

Val Asn Gly Ala Phe Tyr Gly Pro His Ala Thr Glu Leu Gly Gly Tyr
            580                 585                 590

Phe Thr Tyr Asn Gly Asn Asn Pro Thr Asp Lys Asn Ser Ser Ser Asn
        595                 600                 605

Ser Glu Lys Ala Arg Ala Ala Val Val Leu Glu Leu
    610                 615                 620
```

<210> 197

<211> 630

<212> PRT

<213> Haemophilus influenzae

<400> 197

```
Cys Ser Gly Gly Gly Gly Ser Phe Asp Val Asp Asp Val Ser Asn Pro
1               5                   10                  15

Ser Ser Ser Lys Pro Arg Tyr Gln Asp Asp Thr Ser Ser Ser Arg Thr
            20                  25                  30

Lys Ser Lys Leu Glu Asn Leu Ser Ile Pro Ser Leu Gly Gly Gly Met
        35                  40                  45

Lys Leu Val Ala Gln Asn Leu Arg Asp Arg Thr Lys Pro Ser Leu Leu
    50                  55                  60

Asn Glu Asp Asp Tyr Met Ile Phe Ser Ser Leu Ser Thr Ile Lys Ala
```

```
65                  70                  75                  80

Asp Val Glu Lys Glu Asn Lys His Tyr Thr Ser Pro Val Gly Ser Ile
                85                  90                  95

Asp Glu Pro Ser Thr Thr Asn Pro Lys Glu Asn Asp His Gly Gln Arg
            100                 105                 110

Tyr Val Tyr Ser Gly Leu Tyr Tyr Ile Pro Ser Trp Asn Leu Asn Asp
        115                 120                 125

Leu Lys Asn Asn Lys Tyr Tyr Tyr Ser Gly Tyr Tyr Gly Tyr Ala Tyr
    130                 135                 140

Tyr Phe Gly Lys Gln Thr Ala Thr Thr Leu Pro Val Asn Gly Lys Val
145                 150                 155                 160

Thr Tyr Lys Gly Thr Trp Ser Phe Ile Thr Ala Ala Glu Asn Gly Lys
                165                 170                 175

Arg Tyr Pro Leu Leu Ser Asn Gly Ser Gln Ala Tyr Phe Arg Arg Ser
            180                 185                 190

Ala Ile Pro Glu Asp Ile Asp Leu Glu Val Lys Asn Asp Glu Asn Arg
        195                 200                 205

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

Leu Thr Gly Gly Leu Phe Tyr Thr Lys Arg Gln Thr His Ile Gln Asn
225                 230                 235                 240

His Glu Lys Lys Lys Leu Tyr Asp Ile Asp Ala His Ile Tyr Ser Asn
                245                 250                 255

Arg Phe Arg Gly Lys Val Asn Pro Thr Gln Lys Asp Ser Lys Glu His
            260                 265                 270

Pro Phe Thr Ser Glu Gly Thr Leu Glu Gly Gly Phe Tyr Gly Pro Glu
        275                 280                 285

Gly Gln Glu Leu Gly Gly Lys Phe Leu Ala Gly Asp Lys Lys Val Phe
    290                 295                 300

Gly Val Phe Ser Ala Lys Gly Thr Glu Glu Asn Lys Lys Leu Pro Lys
305                 310                 315                 320

Glu Thr Leu Ile Asp Gly Lys Leu Thr Thr Phe Ser Thr Lys Thr Thr
                325                 330                 335

Asp Ala Lys Thr Asn Ala Thr Ala Asn Ala Thr Thr Ser Thr Ala Ala
            340                 345                 350

Asn Thr Thr Thr Asp Thr Thr Ala Asn Thr Ile Thr Asp Ala Glu Asn
        355                 360                 365
```

```
Phe Lys Thr Lys Asp Ile Ser Ser Phe Gly Glu Ala Asp Tyr Leu Leu
    370                 375                 380

Ile Asp Asn Tyr Pro Val Pro Leu Leu Pro Glu Ser Gly Asp Phe Ile
385                 390                 395                 400

Ser Ser Lys His His Thr Val Gly Lys Lys Thr Tyr Gln Val Lys Ala
                405                 410                 415

Cys Cys Ser Asn Leu Ser Tyr Val Lys Phe Gly Met Tyr Tyr Glu Val
            420                 425                 430

Pro Pro Lys Glu Glu Glu Lys Asp Lys Glu Lys Lys Glu Lys Glu Lys
        435                 440                 445

Glu Lys Gln Ala Thr Asn Leu Ser Asn Thr Tyr Tyr Gln Phe Leu Leu
    450                 455                 460

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

Tyr Leu Gly Ser Trp Phe Gly Tyr Leu Ser Asp Gly Ser Thr Ser Tyr

                485                 490                 495

Ser Pro Ser Gly Asp Lys Lys Arg Glu Asn Asn Ala Leu Ala Glu Phe
            500                 505                 510

Asn Val Asn Phe Val Asp Lys Thr Leu Lys Gly Gln Leu Ile Arg His
        515                 520                 525

Asp Asn Gln Asn Thr Val Phe Thr Ile Asp Ala Thr Phe Lys Gly Gly
    530                 535                 540

Lys Asn Asn Phe Thr Gly Thr Ala Thr Ala Asn Asn Val Ala Ile Asp
545                 550                 555                 560

Pro Gln Ser Thr Gln Gly Thr Ser Asn Val Asn Phe Thr Ala Thr Val
                565                 570                 575

Asn Gly Ala Phe Tyr Gly Pro Asn Ala Thr Glu Leu Gly Gly Tyr Phe
            580                 585                 590

Thr Tyr Asn Gly Asn Pro Thr Asp Lys Ser Ser Ser Thr Val Pro Ser
        595                 600                 605

Ser Ser Asn Ser Lys Asn Ala Arg Ala Ala Val Val Phe Gly Ala Arg
    610                 615                 620

Gln Gln Val Glu Thr Thr
625                 630
```

<210> 198

<211> 599

<212> PRT

<213> Haemophilus influenzae

<400> 198

```
Cys Ser Gly Gly Gly Gly Ser Phe Asp Val Asp Asp Val Ser Asn Pro
1               5                  10                  15

Ser Ser Ser Lys Pro Arg Tyr Gln Asp Asp Thr Ser Asn Gln Arg Lys
            20                  25                  30

Lys Ser Asn Leu Glu Lys Leu Ser Ile Pro Ser Leu Gly Gly Gly Met
        35                  40                  45

Lys Leu Val Ala Gln Asn Leu Arg Gly Arg Glu Pro Ser Leu Leu Asn
    50                  55                  60

Glu Asp Gly Tyr Ile Ile Phe Ser Ser Leu Ser Lys Ile Glu Asp Asp

65                  70                  75                  80

Phe Lys Lys Glu Asn Gln Ser Gln Glu Pro Thr Ile Gly Ser Ile Asp
                85                  90                  95

Glu Pro Ser Glu Thr Asn Ser Pro Gln Asn His His Gly Gln Gln Tyr
            100                 105                 110

Val Tyr Ser Gly Leu Tyr Tyr Ile Gln Ser Trp Arg Asn Phe Ser Asn
        115                 120                 125

Gly Lys Phe Tyr Ser Gly Tyr Tyr Gly Tyr Ala Tyr Tyr Phe Gly Lys
    130                 135                 140

Gln Thr Ala Thr Thr Leu Pro Val Asn Gly Glu Ala Thr Tyr Lys Gly
145                 150                 155                 160

Thr Trp Ser Phe Ile Thr Ala Thr Glu Arg Gly Lys Asn Tyr Ser Leu
                165                 170                 175

Phe Ser Asn Ser Ser Gly Gln Gly Tyr Ser Arg Arg Ser Ala Ile Ser
            180                 185                 190

Glu Asp Ile Asp Leu Glu Asn Asp Gln Asn Asn Gly Glu Thr Gly Leu
        195                 200                 205

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

Leu Phe Tyr Thr Lys Arg Lys Thr Asn Asn Gln Asn Tyr Glu Lys Lys
225                 230                 235                 240

Lys Leu Tyr Asp Ile Asp Ala Asn Ile Tyr Ser Asn Arg Phe Arg Gly
                245                 250                 255

Lys Val Lys Pro Thr Glu Lys Asp Ser Glu Glu His Pro Phe Thr Arg
            260                 265                 270
```

```
Glu Gly Thr Leu Glu Gly Gly Phe Tyr Gly Pro Asn Gly Glu Glu Leu
        275                 280                 285

Gly Gly Lys Leu Ala Gly Asp Lys Lys Val Phe Gly Val Phe Ser Ala
    290                 295                 300

Lys Glu Thr Glu Glu Thr Lys Gln Lys Thr Leu Pro Lys Glu Thr Leu
305                 310                 315                 320

Ile Asp Gly Lys Leu Thr Thr Phe Ser Thr Lys Lys Pro Asp Ala Thr
                325                 330                 335

Thr Ser Thr Thr Ala Asn Ala Lys Thr Asp Ala Thr Thr Asn Ala Glu
            340                 345                 350

Asn Phe Thr Thr Lys Asp Ile Ser Ser Phe Gly Glu Ala Asp Tyr Leu
        355                 360                 365

Leu Ile Asp Asn Tyr Pro Val Pro Leu Leu Pro Glu Thr Glu Asn Ser
    370                 375                 380

Gly Asp Phe Ala Thr Ser Lys His Tyr Glu Val Arg Asp Lys Thr Tyr
385                 390                 395                 400

Lys Val Glu Ala Cys Cys Lys Asn Leu Ser Tyr Val Lys Phe Gly Met
                405                 410                 415

Tyr Tyr Glu Asp Asn Lys Lys Asn Asn Lys Asn Glu Thr Glu Gln Tyr
            420                 425                 430

His Gln Phe Leu Leu Gly Leu Arg Thr Ala Ser Ser Lys Ile Pro Thr
        435                 440                 445

Thr Gly Asn Val Lys Tyr Arg Gly Ser Trp Phe Gly Tyr Ile Ser Asp
    450                 455                 460

Gly Glu Thr Ser Tyr Ser Thr Thr Gly Asp Lys Arg Gln Asp Lys Asn
465                 470                 475                 480

Ala Val Ala Glu Phe Asp Val Asn Phe Ala Glu Lys Thr Leu Lys Gly
                485                 490                 495

Ser Leu Lys Arg Ala Asp Ser Gln Asn Pro Val Phe Ser Ile Glu Ala
            500                 505                 510

Asn Phe Lys Asn Gly Gly Asn Ala Phe Thr Gly Thr Ala Thr Ala Lys
        515                 520                 525

Asp Leu Val Ile Asp Gly Lys Asn Ser Gln Thr Lys Asn Thr Pro Ile
    530                 535                 540

Asn Ile Thr Thr Lys Val Asn Gly Ala Phe Tyr Gly Pro Asn Ala Ser
545                 550                 555                 560

Glu Leu Gly Gly Tyr Phe Thr Tyr Asn Gly Lys Asn Pro Thr Asp Lys
                565                 570                 575

Asn Ser Pro Thr Ala Ser Ser Pro Ser Asn Ser Glu Lys Ala Arg Ala
```

```
            580                 585                 590

Ala Val Val Phe Gly Ala Lys
        595
```

<210> 199

<211> 630

<212> PRT

<213> Haemophilus influenzae

<400> 199

```
Cys Ser Gly Gly Gly Gly Ser Phe Asp Val Asp Asp Val Ser Asn Pro
1               5                  10                  15

Ser Ser Ser Lys Pro Arg Tyr Gln Asp Asp Thr Ser Ser Ser Arg Lys
            20                  25                  30

Lys Ser Asp Leu Glu Lys Leu Ser Ile Pro Ser Leu Gly Gly Gly Met
        35                  40                  45

Lys Leu Val Ala Gln Asn Leu Arg Gly Ser Glu Pro Ser Leu Leu Asn
    50                  55                  60

Glu Asp Gly Tyr Met Ile Phe Ser Ser Leu Ser Thr Ile Glu Glu Asp
65                  70                  75                  80

Val Lys Lys Val Lys Lys Glu Lys Asn Val Asp Thr Asn Pro Ile Gly
                85                  90                  95

Ser Ile Asp Glu Pro Ser Ala Ser Ala Thr Asn Pro Pro Gln Asn His
            100                 105                 110

His Gly Gln Lys Tyr Val Tyr Ser Gly Leu Tyr Tyr Ile Pro Ser Trp
        115                 120                 125

Asn Leu Ile Asp Ser Thr Lys Asn Lys Tyr Tyr Phe Gly Tyr Tyr Gly
    130                 135                 140

Tyr Ala Tyr Tyr Phe Gly Lys Glu Thr Ala Thr Thr Leu Pro Val Asn
145                 150                 155                 160

Gly Lys Val Thr Tyr Lys Gly Thr Trp Ser Phe Ile Thr Ala Thr Glu
                165                 170                 175

Lys Gly Lys Arg Tyr Glu Leu Phe Arg Arg Leu Gly Ser Pro Tyr Tyr
            180                 185                 190

Arg Arg Ser Ala Ile Ser Glu Asp Ile Asp Asp Ile Glu Asn His Pro
        195                 200                 205

Ser Asn Gly Asp Ala Gly Leu Ile Ser Glu Phe Ser Val Asp Phe Gly
    210                 215                 220

Glu Lys Lys Leu Thr Gly Glu Leu Tyr Tyr Asn Lys Arg Lys Thr Asn
225                 230                 235                 240
```

```
Val Asn Pro Ser Ala Asn Thr Lys His Thr Leu Tyr Asn Leu Glu Ala
                245                 250                 255

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

Asp Ser Lys Asp His Pro Phe Thr Ser Lys Gly Thr Leu Glu Gly Gly
        275                 280                 285

Phe Tyr Gly Pro Lys Gly Glu Glu Leu Gly Gly Lys Phe Leu Ala Gly
    290                 295                 300

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

Lys Ile Ile Gln Arg Asn Leu Ile Asp Gly Lys Leu Thr Thr Phe Ser
                325                 330                 335

Thr Lys Thr Thr Asn Gly Thr Thr Ile Thr Thr Thr Thr Asn Ala Ile
            340                 345                 350

Thr Asp Ala Thr Ala Asn Thr Lys Thr Asp Ala Thr Ala Asn Thr Lys
        355                 360                 365

Thr Asp Ala Lys Thr Asp Ala Lys Thr Asp Ala Glu Asn Phe Thr Thr
    370                 375                 380

Lys Asp Ile Ser Ser Phe Gly Glu Ala Asp Tyr Leu Leu Ile Asp Lys
385                 390                 395                 400

Tyr Pro Ile Pro Leu Leu Pro Glu Lys Asn Thr Asp Asp Phe Ile Ser
                405                 410                 415

Ser Arg His His Asp Val Gly Gly Lys Thr Tyr Lys Val Glu Ala Cys
            420                 425                 430

Cys Lys Asn Leu Ser Tyr Val Lys Phe Gly Met Tyr Tyr Glu Asp Lys
        435                 440                 445

Glu Lys Lys Asn Thr Asn Gln Thr Gly Gln Tyr His Gln Phe Leu Leu
    450                 455                 460

Gly Leu Arg Thr Pro Ser Ser Gln Ile Pro Val Thr Gly Asn Val Lys
465                 470                 475                 480

Tyr Leu Gly Ser Trp Phe Gly Tyr Ile Gly Asp Asp Lys Thr Ser Tyr
                485                 490                 495

Ser Thr Thr Gly Asn Lys Gln Gln Asp Lys Asn Ala Pro Ala Glu Phe
            500                 505                 510

Asp Val Asn Phe Asp Asn Lys Thr Leu Thr Gly Lys Leu Lys Arg Ala
        515                 520                 525

Asp Ser Gln Asn Thr Val Phe Asn Ile Glu Ala Thr Phe Lys Asn Gly
    530                 535                 540
```

```
Ser Asn Ala Phe Glu Gly Lys Ala Thr Ala Asn Val Val Ile Asp Pro
545                 550                 555                 560

Lys Asn Thr Gln Ala Thr Ser Lys Val Asn Phe Thr Thr Thr Val Asn
                565                 570                 575

Gly Ala Phe Tyr Gly Pro His Ala Thr Glu Leu Gly Gly Tyr Phe Thr
            580                 585                 590

Tyr Asn Gly Asn Asn Pro Thr Ala Thr Asn Ser Glu Ser Ser Ser Thr
        595                 600                 605

Val Pro Ser Pro Pro Asn Ser Pro Asn Ala Arg Ala Ala Val Val Phe
    610                 615                 620

Gly Ala Lys Arg Gln Val
625                 630
```

<210> 200

<211> 610

<212> PRT

<213> Haemophilus influenzae

<400> 200

```
Cys Ser Gly Gly Gly Gly Ser Phe Asp Val Asp Asp Val Ser Asn Pro
1               5                   10                  15

Ser Ser Ser Lys Pro Arg Tyr Gln Asp Asp Thr Leu Asn Gln Arg Lys
            20                  25                  30

Lys Ser Asn Leu Gln Lys Leu Ser Ile Pro Ser Leu Gly Gly Gly Met
        35                  40                  45

Lys Leu Val Ala Gln Asn Phe Ala Gly Ala Lys Glu Pro Ser Phe Leu
    50                  55                  60

Asn Glu Asn Asp Tyr Ile Ser Tyr Phe Ser Ser Leu Ser Thr Ile Lys
65                  70                  75                  80

Asp Asp Val Glu Asn Asn Asn Lys Asn Lys Asp Thr Pro Ile Gly Ser
                85                  90                  95

Ile Asp Glu Pro Arg Ala Pro Asn Ser Asn Glu Asn His Gln Asn His
            100                 105                 110

His Gly Gln Gln Tyr Val Tyr Ser Gly Leu Tyr Tyr Ile Pro Ser Trp
        115                 120                 125

Arg Leu Ile Asn Leu Pro Asn Lys Phe Tyr Ser Gly Tyr Tyr Gly Tyr
    130                 135                 140

Ala Tyr Tyr Phe Gly Lys Gln Thr Ala Thr Thr Leu Pro Val Asp Gly
145                 150                 155                 160

Val Ala Thr Tyr Lys Gly Thr Trp Ser Phe Ile Thr Ala Thr Glu Arg
```

```
                165                 170                 175

Gly Lys Asn Tyr Ser Leu Phe Asn Asn Arg Gly Gln Ala Tyr Ser Arg
            180                 185                 190

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

Leu Thr Ser Glu Phe Thr Val Asn Phe Gly Thr Lys Lys Leu Thr Gly
    210                 215                 220

Glu Leu Tyr Tyr Asn Glu Arg Glu Thr Asn Leu Asn Gln Ser Lys Asp
225                 230                 235                 240

Arg Lys His Lys Leu Tyr Asp Leu Glu Ala Asp Val Tyr Ser Asn Arg
                245                 250                 255

Phe Arg Gly Thr Val Lys Pro Thr Lys Lys Glu Ser Ser Glu Glu His
            260                 265                 270

Pro Phe Thr Ser Glu Gly Thr Leu Glu Gly Gly Phe Tyr Gly Pro Asn

        275                 280                 285

Gly Glu Glu Leu Gly Gly Lys Phe Leu Ala Gly Asp Asn Arg Val Phe
    290                 295                 300

Gly Val Phe Ser Ala Lys Glu Gln Gln Glu Thr Glu Glu Asn Lys Lys
305                 310                 315                 320

Leu Leu Lys Glu Thr Leu Ile Asp Gly Lys Leu Thr Thr Phe Ser Thr
                325                 330                 335

Lys Lys Thr Asp Thr Thr Thr Ser Thr Thr Thr Asn Thr Ala Ala Ser
            340                 345                 350

Thr Thr Thr Asp Glu Lys Thr Asn Ala Lys Asn Phe Thr Thr Glu Asp
        355                 360                 365

Ile Ser Ser Phe Gly Glu Ala Asp Tyr Leu Leu Ile Asp Asn Tyr Pro
    370                 375                 380

Val Pro Leu Leu Pro Glu Thr Glu Asn Ser Gly Asp Phe Ile Ser Ser
385                 390                 395                 400

Arg His His Asp Val Gly Gly Gly Lys Thr Tyr Lys Val Glu Ala Cys
                405                 410                 415

Cys Lys Asn Leu Ser Tyr Val Lys Phe Gly Ile Tyr Tyr Glu Asp Asn
            420                 425                 430

Glu Lys Asn Asn Lys Asn Glu Thr Glu Gln Tyr His Gln Phe Leu Leu
        435                 440                 445

Gly Leu Arg Thr Pro Ser Ser Gln Ile Pro Ala Thr Gly Asn Val Lys
    450                 455                 460
```

```
Tyr Arg Gly Ser Trp Phe Gly Tyr Ile Ser Asp Gly Lys Thr Ser Tyr
465                 470                 475                 480

Ser Thr Thr Gly Asp Lys Gln Gln Asp Lys Asn Ala Leu Ala Glu Phe
                485                 490                 495

Asp Val Asn Phe Asp Thr Lys Thr Leu Thr Gly Glu Leu Lys Arg Ala
            500                 505                 510

Gly Thr Gln Asn Thr Val Phe Thr Ile Asp Ala Thr Phe Lys Ser Gly
        515                 520                 525

Glu Asn Asn Phe Thr Gly Thr Ala Thr Ala Asn Asn Val Ala Ile Asp
    530                 535                 540

Ser Gln Asn Thr Gln Gly Thr Pro Lys Val Asn Phe Lys Thr Thr Val
545                 550                 555                 560

Asn Gly Ala Phe Tyr Gly Pro Asn Ala Ser Glu Leu Gly Gly Tyr Phe
                565                 570                 575

Thr Tyr Asn Gly Lys Asn Pro Thr Ala Thr Asn Ser Glu Ser Ser Ser
            580                 585                 590

Thr Val Pro Ser Pro Pro Asn Ser Pro Asn Ala Arg Ala Ala Val Val
        595                 600                 605

Phe Gly
    610
```

<210> 201

<211> 630

<212> PRT

<213> Haemophilus influenzae

<400> 201

```
Cys Ser Gly Gly Gly Gly Ser Phe Asp Val Asp Asp Val Ser Asn Pro
1               5                   10                  15

Ser Ser Ser Lys Pro Arg Tyr Gln Asp Asp Thr Ser Asn Gln Arg Thr
            20                  25                  30

Lys Ser Asn Leu Gln Asn Leu Ser Ile Pro Ser Leu Gly Gly Gly Met
        35                  40                  45

Lys Leu Val Ala Gln Asn Leu Leu Gly Lys Arg Glu Pro Ser Phe Leu
    50                  55                  60

Asn Glu Asp Gly Tyr Met Ile Phe Ser Ser Arg Ser Thr Ile Lys Asp
65                  70                  75                  80

Asp Val Glu Lys Val Lys Asn Lys Asn Gly Gly Gly Gly Leu Ile Gly
                85                  90                  95
```

```
Ser Ile Glu Glu Pro Asn Gly Thr Pro Gln Asn Ser Asn Ser Gln Lys
            100                 105                 110

Tyr Val Tyr Ser Gly Leu Tyr Tyr Ile Glu Asn Trp Lys Asp Phe Ser
        115                 120                 125

Gln Leu Gln Ala Pro Glu Lys Lys Ala Tyr Thr Gly His Tyr Gly Tyr
    130                 135                 140

Ala Tyr Tyr Phe Gly Asn Gln Thr Ala Thr Thr Leu Pro Val Asn Gly
145                 150                 155                 160

Glu Ala Thr Tyr Lys Gly Thr Trp Asn Phe Ile Thr Ala Thr Arg Tyr
                165                 170                 175

Asn Lys Asn Tyr Pro Leu Phe Gly Ser Gly Ser Gly Ala Tyr Ser Lys
            180                 185                 190

Arg Ser Ala Ile Ser Glu Asp Ile Asp Asn Leu Glu Asn Asn Ser Thr
        195                 200                 205

Asn Gly Asp Lys Gly Leu Thr Ser Glu Phe Thr Val Asn Phe Gly Thr
    210                 215                 220

Lys Lys Leu Thr Gly Gly Leu Tyr Tyr Asn Glu Arg Glu Thr His Arg
225                 230                 235                 240

Asn Gln Ser Gln Asp Arg Lys His Lys Leu Tyr Asp Leu Glu Ala Asp
                245                 250                 255

Val His Ser Asn Arg Phe Arg Gly Lys Ala Lys Pro Thr Glu Lys Asn
            260                 265                 270

Ser Thr Asp His Pro Phe Thr Ser Glu Gly Thr Leu Glu Gly Gly Phe
        275                 280                 285

Tyr Gly Pro Lys Gly Glu Glu Leu Gly Gly Lys Phe Leu Ala Asp Asp
    290                 295                 300

Asn Arg Val Phe Gly Val Phe Ser Ala Lys Glu Thr Glu Glu Thr Glu
305                 310                 315                 320

Lys Lys Asn Leu Ser Lys Glu Thr Leu Ile Asp Gly Lys Leu Ile Thr
                325                 330                 335

Phe Ser Thr Lys Lys Thr Asp Ala Thr Ala Asn Ala Thr Thr Asn Thr
            340                 345                 350

Thr Thr Asp Val Lys Asn Asn Ala Thr Thr Asp Thr Thr Ala Asn Ala
        355                 360                 365

Glu Asn Phe Thr Thr Lys Asp Ile Ser Ser Phe Gly Glu Ala Asp Tyr
    370                 375                 380

Leu Leu Ile Asp Asn Tyr Pro Val Pro Leu Leu Pro Glu Asn Thr Asn
385                 390                 395                 400

Asp Phe Ile Ser Ser Lys His His Glu Val Gly Gly Lys Arg Tyr Lys
```

```
                405                 410                 415

Val Glu Ala Cys Cys Lys Asn Leu Ser Tyr Val Lys Phe Gly Met Tyr
            420                 425                 430

Tyr Glu Asp Lys Glu Asn Asn Lys Asn Glu Thr Asp Lys Glu Lys Glu
        435                 440                 445

Lys Gln Thr Thr Thr Ser Ile Lys Thr Tyr Tyr Gln Phe Leu Leu Gly
    450                 455                 460

Leu Arg Thr Pro Ser Ser Glu Ile Pro Lys Met Gly Asn Val Thr Tyr
465                 470                 475                 480

Arg Gly Ser Trp Phe Gly Tyr Ile Gly Asp Asp Lys Thr Ser Tyr Ser
                485                 490                 495

Ala Thr Gly Asp Lys Arg Gln Asp Lys Asn Ala Pro Ala Glu Phe Asn
            500                 505                 510

Val Asp Phe Asn Asn Lys Lys Leu Thr Gly Thr Leu Lys Arg His Asp
        515                 520                 525

Asn Gln Asn Pro Val Phe Lys Ile Asn Ala Thr Phe Gln Asn Gly Arg
    530                 535                 540

Asn Asp Phe Glu Gly Thr Ala Thr Ala Glu Asn Phe Val Ile Asp Gly
545                 550                 555                 560

Lys Asp Ser Gln Gly Asn Thr Pro Ile Asn Ile Thr Thr Lys Val Asn
                565                 570                 575

Gly Ala Phe Tyr Gly Pro Asn Ala Thr Glu Leu Gly Gly Tyr Phe Thr
            580                 585                 590

Tyr Asn Gly Asn Pro Thr Ala Thr Asn Ser Glu Ser Ser Ser Thr Val
        595                 600                 605

Pro Ser Pro Pro Asn Ser Pro Asn Ala Arg Ala Ala Val Val Phe Gly
    610                 615                 620

Ala Lys Lys Gln Val Glu
625                 630
```

<210> 202

<211> 620

<212> PRT

<213> Haemophilus influenzae

<400> 202

```
Cys Ser Gly Gly Gly Gly Ser Phe Asp Val Asp Asp Val Ser Asn Pro
1               5                   10                  15

Ser Ser Ser Lys Pro Arg Tyr Gln Asp Asp Thr Ser Asn Gln Arg Lys
            20                  25                  30
```

```
Lys Ser Asp Leu Gln Lys Leu Ser Ile Pro Ser Leu Gly Gly Gly Met
        35                  40                  45

Lys Leu Val Ala Gln Asn Phe Ile Gly Ala Lys Glu Pro Ser Phe Leu
    50                  55                  60

Asn Glu Asn Gly Tyr Met Ile Phe Ser Ser Leu Ser Thr Ile Lys Asp
65                  70                  75                  80

Asp Val Glu Asn Val Lys Asn Asn Asn Gln Asn Gly Gly Ser Leu Ile
                85                  90                  95

Gly Ser Ile Glu Glu Pro Asn Gly Thr Ser Gln Asp Ser Asn Ser Gln
            100                 105                 110

Gln Tyr Val Tyr Ser Gly Leu Tyr Tyr Ile Asp Ser Trp Arg Asp His
        115                 120                 125

Lys Lys Gln Glu Asn Lys Ala Tyr Ala Gly Tyr Tyr Gly Tyr Ala Phe
    130                 135                 140

Tyr Tyr Gly Asn Lys Thr Ala Thr Asp Leu Pro Val Lys Gly Ile Ala
145                 150                 155                 160

Lys Tyr Lys Gly Thr Trp Asn Phe Ile Thr Ala Thr Glu Asn Gly Lys
                165                 170                 175

Arg Tyr Ser Leu Phe Ser Asn Asn Ser Gln Ala Tyr Ser Arg Arg Ser
            180                 185                 190

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

Glu Lys Gly Leu Val Ser Glu Phe Ser Val Asp Phe Asp Lys Lys Glu
    210                 215                 220

Leu Thr Gly Gly Leu Tyr Tyr Asn Glu Arg Glu Thr Asp Arg Asn Lys
225                 230                 235                 240

Ser Lys Asp Arg Lys His Lys Leu Tyr Asn Leu Lys Ala Lys Val Tyr
                245                 250                 255

Ser Asn Arg Phe Arg Gly Asn Val Ile Pro Glu Glu Pro Thr Ser Thr
            260                 265                 270

Asp His Pro Phe Thr Ser Asp Gly Thr Leu Glu Gly Gly Phe Tyr Gly
        275                 280                 285

Pro Asn Gly Glu Glu Leu Gly Gly Lys Phe Leu Ala Gly Asp Asn Arg
    290                 295                 300

Val Phe Gly Val Phe Ser Ala Lys Glu Asn Pro Glu Asn Lys Thr Leu
305                 310                 315                 320

Ser Arg Glu Thr Leu Ile Asp Gly Lys Leu Ile Thr Phe Ser Thr Lys
                325                 330                 335
```

```
Lys Thr Asp Ala Lys Thr Asn Ala Thr Thr Ser Thr Ala Ala Asn Thr
            340                 345                 350

Thr Thr Asp Thr Thr Ala Asn Thr Ile Thr Asp Glu Lys Asn Phe Lys
        355                 360                 365

Thr Glu Asp Ile Ser Ser Phe Gly Glu Ala Asp Tyr Leu Leu Ile Asp
    370                 375                 380

Lys Tyr Pro Ile Pro Leu Leu Pro Asp Lys Asn Thr Asn Asp Phe Ile
385                 390                 395                 400

Ser Ser Lys His His Thr Val Gly Asn Lys Arg Tyr Lys Val Glu Ala
                405                 410                 415

Cys Cys Ser Asn Leu Ser Tyr Val Lys Phe Gly Met Tyr Tyr Glu Ala
            420                 425                 430

Pro Pro Lys Glu Glu Glu Lys Glu Lys Glu Lys Asp Lys Glu Lys Lys
        435                 440                 445

Glu Lys Gln Thr Thr Thr Thr Ser Ile Asn Thr Tyr Tyr Gln Phe Leu
    450                 455                 460

Leu Gly His Arg Thr Pro Lys Asp Asp Ile Pro Lys Thr Gly Ser Ala

465                 470                 475                 480

Gln Tyr Arg Gly Asn Trp Phe Gly Tyr Ile Gly Asp Asp Lys Thr Ser
                485                 490                 495

Tyr Ser Ala Thr Gly Gly Lys Asn Ala Val Ala Glu Phe Asp Val Asn
            500                 505                 510

Phe Ala Asp Lys Thr Leu Lys Gly Val Leu Lys Arg His Asp Thr Gln
        515                 520                 525

Asn Pro Val Phe Asn Ile Glu Ala Asp Phe Lys Asn Gly Arg Asn Asp
    530                 535                 540

Phe Thr Gly Lys Ala Thr Ala Asn Val Val Ile Asp Pro Gln Asn Thr
545                 550                 555                 560

Gln Ala Thr Ser Lys Val Asn Phe Thr Ala Thr Val Asn Gly Ala Phe
                565                 570                 575

Tyr Gly Pro Asn Ala Thr Glu Leu Gly Gly Tyr Phe Thr Tyr Asn Gly
            580                 585                 590

Asn Pro Thr Asp Lys Ser Ser Ser Thr Val Pro Ser Pro Pro Asn Ser
        595                 600                 605

Pro Asn Ala Arg Ala Ala Val Val Phe Gly Ala Lys
    610                 615                 620
```

<210> 203

<211> 610

<212> PRT

<213> Haemophilus influenzae

<400> 203

```
Cys Ser Gly Gly Gly Gly Ser Phe Asp Val Asp Asp Val Ser Asn Pro
1               5                   10                  15

Ser Ser Ser Lys Pro Arg Tyr Gln Asp Asp Thr Ser Ser Ser Arg Thr
            20                  25                  30

Lys Ser Lys Leu Glu Asn Leu Ser Ile Pro Ser Leu Gly Gly Gly Met
        35                  40                  45

Lys Leu Val Ala Gln Asn Leu Arg Gly Asn Lys Glu Pro Ser Leu Leu
    50                  55                  60

Asn Glu Asp Gly Tyr Ile Pro Tyr Phe Ser Ser Leu Ser Thr Ile Lys

65                  70                  75                  80

Ala Asp Val Glu Lys Glu Asn Lys His Gly Thr Ser Pro Val Gly Ser
                85                  90                  95

Ile Asp Glu Pro Ser Thr Thr Asn Pro Pro Glu Lys His His Gly Gln
            100                 105                 110

Lys Tyr Val Tyr Ser Gly Leu Tyr Tyr Ile Gln Ser Trp Asn Asn Leu
        115                 120                 125

Ser Asn Gly Lys Phe Tyr Ser Gly Tyr Tyr Gly Tyr Ala Phe Tyr Tyr
    130                 135                 140

Gly Asn Lys Thr Ala Thr Asn Leu Pro Val Ser Gly Val Ala Lys Tyr
145                 150                 155                 160

Lys Gly Thr Trp Asn Phe Ile Thr Ala Thr Glu Asn Gly Lys Thr Tyr
                165                 170                 175

Ser Leu Leu Arg Asn Asn Gly Gly Gln Ala Tyr Ala Lys Arg Ser Ala
            180                 185                 190

Ile Pro Glu Asp Ile Asp Leu Asp Ser Lys Thr Gly Leu Ile Ser Glu
        195                 200                 205

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

Asn Lys Arg Lys Thr Asn Leu Ile Asn Glu Ser Gln Asp Arg Lys His
225                 230                 235                 240

Lys Leu Tyr Thr Leu Glu Ala Asp Val His Ser Asn Arg Phe Arg Gly
                245                 250                 255
```

```
Lys Ala Lys Pro Pro Glu Lys Asp Ser Ser Asp His Pro Phe Thr Ser
            260                 265                 270

Glu Gly Thr Leu Glu Gly Gly Phe Tyr Gly Pro Asp Gly Glu Glu Leu
        275                 280                 285

Gly Gly Lys Phe Leu Ala Gly Asp Lys Lys Val Phe Gly Val Phe Ser
    290                 295                 300

Ala Lys Glu Thr Glu Glu Thr Pro Glu Lys Lys Leu Ser Arg Glu Thr
305                 310                 315                 320

Leu Ile Asp Gly Lys Leu Ile Thr Phe Lys Arg Thr Asp Ala Thr Thr
                325                 330                 335

Asn Ala Thr Ala Ser Thr Thr Thr Asn Thr Ala Ala Asn Thr Ala Ala
            340                 345                 350

Asn Thr Lys Thr Asn Glu Lys Asn Phe Thr Thr Glu Asp Ile Ser Ser
        355                 360                 365

Phe Gly Glu Ala Asp Tyr Leu Leu Ile Asp Asn Tyr Pro Ile Pro Leu
    370                 375                 380

Phe Pro Glu Asn Thr Ser Asp Phe Ala Thr Ser Lys His His Asn Ile
385                 390                 395                 400

Gly Asn Lys Thr Tyr Lys Val Glu Ala Cys Cys Lys Asn Leu Ser Tyr
                405                 410                 415

Val Lys Phe Gly Ile Tyr Tyr Glu Asp Lys Pro Ile Lys Glu Glu Glu
            420                 425                 430

Lys Asp Lys Glu Lys Gln Thr Thr Ala Thr Thr Asn Thr Tyr Tyr Gln
        435                 440                 445

Phe Leu Leu Gly His Arg Thr Ala Asn Ala Glu Ile Pro Lys Lys Gly
    450                 455                 460

Ser Ala Lys Tyr His Gly Ser Trp Phe Gly Tyr Ile Thr Asp Gly Lys
465                 470                 475                 480

Thr Ser Tyr Ser Thr Thr Gly Ala Lys Gln Arg Asp Asn Ser Gly Val
                485                 490                 495

Ser Asp Phe Asp Val Asn Phe Asp Asn Lys Lys Leu Thr Gly Thr Leu
            500                 505                 510

Lys Arg His Asp Thr Gly Asn Thr Val Phe Ser Ile Glu Ala Asn Leu
        515                 520                 525

Lys Asn Gly Gly Asn Asp Phe Thr Gly Thr Ala Thr Ala Asn Asn Val
    530                 535                 540

Ala Ile Asp Ser Gln Asn Thr Gln Ala Asn Thr Ser Arg Val Asn Phe
545                 550                 555                 560
```

```
Thr Ala Thr Val Lys Gly Ala Phe Tyr Gly Pro Asn Ala Ser Glu Leu
                565                 570                 575

Gly Gly Tyr Phe Thr Tyr Asn Gly Lys Asn Pro Thr Asp Lys Asn Ser
            580                 585                 590

Ser Ala Val Ser Ser Ser Ser Asn Ser Glu Asn Ala Arg Ala Ala Val
        595                 600                 605

Val Leu
    610
```

<210> 204

<211> 640

<212> PRT

<213> Haemophilus influenzae

<400> 204

```
Cys Ser Gly Gly Gly Ser Phe Asp Val Asp Asn Val Ser Asn Thr Pro
1               5                   10                  15

Ser Ser Lys Pro Arg Tyr Gln Asp Asp Thr Ser Asn Gln Arg Lys Lys
            20                  25                  30

Ser Asn Leu Lys Lys Leu Phe Ile Pro Ser Leu Gly Gly Gly Met Lys
        35                  40                  45

Leu Val Ala Gln Asn Leu Arg Gly Asn Lys Glu Pro Ser Phe Leu Asn
    50                  55                  60

Glu Asp Asp Tyr Ile Ser Tyr Phe Ser Ser Leu Ser Thr Ile Glu Lys
65                  70                  75                  80

Asp Val Lys Asp Asn Asn Lys Asn Gly Ala Asp Leu Ile Gly Ser Ile
                85                  90                  95

Asp Glu Pro Ser Thr Thr Asn Pro Pro Glu Lys His His Gly Gln Lys
            100                 105                 110

Tyr Val Tyr Ser Gly Leu Tyr Tyr Thr Pro Ser Trp Ser Leu Asn Asp
        115                 120                 125

Ser Lys Asn Lys Phe Tyr Leu Gly Tyr Tyr Gly Tyr Ala Phe Tyr Tyr
    130                 135                 140

Gly Asn Lys Thr Ala Thr Asn Leu Pro Val Asn Gly Val Ala Lys Tyr
145                 150                 155                 160

Lys Gly Thr Trp Asp Phe Ile Thr Ala Thr Lys Asn Gly Lys Arg Tyr
                165                 170                 175

Pro Leu Leu Ser Asn Gly Ser His Ala Tyr Tyr Arg Arg Ser Ala Ile
            180                 185                 190

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

```
Leu Ile Ser Glu Phe Ser Ala Asp Phe Gly Thr Lys Lys Leu Thr Gly
    210                 215                 220

Gln Leu Ser Tyr Thr Lys Arg Lys Thr Asn Asn Gln Pro Tyr Glu Lys
225                 230                 235                 240

Lys Lys Leu Tyr Asp Ile Asp Ala Asp Ile Tyr Ser Asn Arg Phe Arg
                245                 250                 255

Gly Thr Val Lys Pro Thr Glu Lys Asp Ser Glu Glu His Pro Phe Thr
            260                 265                 270

Ser Glu Gly Thr Leu Glu Gly Gly Phe Tyr Gly Pro Asn Ala Glu Glu
        275                 280                 285

Leu Gly Gly Lys Phe Leu Ala Thr Asp Asn Arg Val Phe Gly Val Phe
    290                 295                 300

Ser Ala Lys Glu Thr Glu Glu Thr Lys Lys Glu Ala Leu Ser Lys Glu
305                 310                 315                 320

Thr Leu Ile Asp Gly Lys Leu Ile Thr Phe Ser Thr Lys Lys Thr Asp
                325                 330                 335

Ala Lys Thr Asn Ala Thr Thr Ser Thr Ala Ala Asn Thr Thr Thr Asp
            340                 345                 350

Thr Thr Ala Asn Thr Ile Thr Asp Glu Lys Asn Phe Lys Thr Glu Asp
        355                 360                 365

Ile Ser Ser Phe Gly Glu Ala Asp Tyr Leu Leu Ile Asp Lys Tyr Pro
    370                 375                 380

Ile Pro Leu Leu Pro Asp Lys Asn Thr Asn Asp Phe Ile Ser Ser Lys
385                 390                 395                 400

His His Thr Val Gly Asn Lys Arg Tyr Lys Val Glu Ala Cys Cys Ser
                405                 410                 415

Asn Leu Ser Tyr Val Lys Phe Gly Met Tyr Tyr Glu Asp Pro Leu Lys
            420                 425                 430

Glu Lys Glu Thr Glu Thr Glu Thr Glu Thr Glu Lys Asp Lys Glu Lys
        435                 440                 445

Glu Lys Glu Lys Asp Lys Asp Lys Glu Lys Gln Thr Ala Ala Thr Thr
    450                 455                 460

Asn Thr Tyr Tyr Gln Phe Leu Leu Gly His Arg Thr Pro Lys Asp Asp
465                 470                 475                 480

Ile Pro Lys Thr Gly Ser Ala Lys Tyr His Gly Ser Trp Phe Gly Tyr
                485                 490                 495

Ile Thr Asp Gly Lys Thr Ser Tyr Ser Pro Ser Gly Asp Lys Lys Arg
            500                 505                 510
```

500 505 510

Asp Lys Asn Ala Val Ala Glu Phe Asn Val Asp Phe Ala Glu Lys Lys
515 520 525

Leu Thr Gly Glu Leu Lys Arg His Asp Thr Gly Asn Pro Val Phe Ser
530 535 540

Ile Glu Ala Asn Phe Asn Asn Ser Ser Asn Ala Phe Thr Gly Thr Ala
545 550 555 560

Thr Ala Thr Asn Phe Val Ile Asp Gly Lys Asn Ser Gln Asn Lys Asn
565 570 575

Thr Pro Ile Asn Ile Thr Thr Lys Val Asn Gly Ala Phe Tyr Gly Pro
580 585 590

Lys Ala Ser Glu Leu Gly Gly Tyr Phe Thr Tyr Asn Gly Asn Ser Thr
595 600 605

Ala Thr Asn Ser Glu Ser Ser Ser Thr Val Ser Ser Ser Ser Asn Ser
610 615 620

Lys Asn Ala Arg Ala Ala Val Val Phe Gly Ala Arg Gln Gln Val Glu
625 630 635 640

<210> 205

<211> 91

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 205

Glu Thr Lys Arg Pro Ala Ala Lys Pro Lys Ala Gln Lys Lys Lys Arg
1 5 10 15

Lys Lys Lys Lys Thr Gly Val Lys Ser Val Lys Lys Gly Lys Lys Lys
20 25 30

Ile Lys Lys Lys Lys Gly Thr Lys Lys Ala Ala Val Lys Lys Lys Gly
35 40 45

Ser Lys Lys Lys Ala Val Lys Gly Lys Lys Lys Ala Lys Lys Pro Lys
50 55 60

Lys Lys Ser Pro Thr Lys Lys Gly Gly Ser Gly Ser Lys Gly Ile Leu
65 70 75 80

Pro Ala Pro Lys Ala Pro Lys Gly Arg Asn Ile
85 90

<210> 206

<211> 519

<212> PRT

<213> Mannheimia haemolytica

<400> 206

```
Thr Val Ser Ala Ser Glu Thr Glu Ala Leu Leu Gln Pro Gly Phe Gly
1               5                  10                  15

Phe Ser Ala Lys Ile Pro Arg Arg Asn Leu Leu Pro Gln Gly Lys Glu
            20                  25                  30

Asp Val Ala Pro Ile Gly Asp Ile Lys Glu Ile Thr Gly Asp Leu Pro
        35                  40                  45

Lys Ile Pro Tyr Glu Glu Glu Val Lys Ala Cys Gly Ser Ser Ala Asp
    50                  55                  60

Gly Phe Ser His Thr His Asp Arg Asn His Lys Leu Tyr Thr Arg Asp
65                  70                  75                  80

Phe Asn Phe Val Arg Ser Gly Tyr Val Val His Ser Gly Pro Lys Pro
                85                  90                  95

Glu Ile Lys Pro Lys Glu Ile Leu Arg Thr Gly Ala His Gly Tyr Val
            100                 105                 110

Tyr Tyr Leu Gly Ile Glu Pro Pro Lys Ala Ile Pro Thr Gln Lys Leu
        115                 120                 125

Thr Tyr Lys Gly Tyr Trp Asp Phe Thr Thr Tyr Ala Ala Lys Gly Arg
    130                 135                 140

Asp Ser Asn Ile Phe Leu Ile Pro Ala Gly Ile Asn Ser Gly Ala Ile
145                 150                 155                 160

Pro Glu Asn Ser His Asp Ile Asn Val Asp Asp Ser Glu Lys Pro Met
                165                 170                 175

Gly His Thr Gly Glu Phe Thr Ala Asp Phe Ala Asn Lys Thr Leu Thr
            180                 185                 190

Gly Thr Leu Val Arg Asn Gly Tyr Val Ser Arg Ser Lys Glu Gln Lys
        195                 200                 205

Ile Thr Thr Ile Tyr Asp Ile Asp Ala Lys Ile Lys Gly Asn Arg Phe
    210                 215                 220

Ser Gly Lys Ala Asn Pro Lys Lys Pro Met Ile Leu Ile Phe Gly Lys
225                 230                 235                 240

Ser Ser Thr Thr Leu Glu Gly Gly Phe Phe Gly Gly Glu Ala Gln Glu
                245                 250                 255

Leu Ala Gly Lys Phe Leu Ala Asp Asp Lys Ser Val Phe Val Val Phe
            260                 265                 270

Ala Gly Thr Arg Asp Ala Lys Lys Asp Asp Ser Glu Ser Ala Phe Asp
```

```
        275                 280                 285

Ala Phe Pro Ile Lys Leu Lys Asp Leu Asn Lys Ser Glu Met Asp Thr
    290                 295                 300

Phe Gly Asn Ala Thr His Leu Ile Ile Asn Asn Lys Gln Ile Pro Leu
305                 310                 315                 320

Ile Ala Glu Ala Thr Lys Ser Phe Ala Glu Met Lys Phe Asp Thr Tyr
                325                 330                 335

Arg Val Ser Val Cys Cys Asn Asn Leu Asp Tyr Val Lys Phe Gly Ile
            340                 345                 350

Tyr Ser Glu Gly Asn Asn Ser Asp Thr Ala Leu Gln Glu Tyr Leu Val
        355                 360                 365

Gly Glu Arg Thr Ala Leu Ala Asp Leu Pro Thr Gly Thr Val Lys Tyr
    370                 375                 380

Arg Gly Thr Trp Asp Gly Val Met Tyr Ser Lys Ser Gly Ser Ala Gly
385                 390                 395                 400

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

Val Asp Phe Val Asn Lys Lys Ile Asn Gly Lys Leu Ile Ala Asn Asp
            420                 425                 430

Gly Val Glu Glu Arg Pro Met Leu Thr Leu Glu Gly Asn Leu Lys Gly
        435                 440                 445

Asn Gly Phe Gly Gly Thr Ala Lys Thr Gly Asn Ser Gly Phe Asn Leu
    450                 455                 460

Asp Pro Lys Ser Thr Asn Gly Gly Thr Val Gly His Ile Asn Thr Gln
465                 470                 475                 480

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

Val Gln Asn Thr Glu Thr Asp Lys Asp Arg Val Ser Ile Thr Phe Gly
            500                 505                 510

Gly Lys Arg Gln Ile Glu Lys
        515
```

<210> 207

<211> 688

<212> PRT

<213> Neisseria gonorrhoeae

<400> 207

```
Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser Val Asp Thr Glu
1               5                   10                  15
```

```
Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Pro Ser Lys Lys Pro
            20                  25                  30

Glu Ala Arg Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Phe Lys
        35                  40                  45

Arg Arg Asn Trp His Pro Ser Ala Asn Pro Lys Glu Asp Glu Val Lys
    50                  55                  60

Leu Lys Asn Asp Asp Trp Glu Ala Thr Gly Leu Pro Thr Glu Pro Lys
65                  70                  75                  80

Lys Leu Pro Leu Lys Gln Gln Ser Val Ile Ser Glu Val Glu Thr Asn
                85                  90                  95

Gly Asn Ser Lys Met Tyr Thr Ser Pro Tyr Leu Ser Gln Asp Ala Asp
            100                 105                 110

Ser Ser His Ala Asn Gly Ala Asn Gln Pro Lys Asn Glu Val Thr Asp
        115                 120                 125

Tyr Lys Lys Phe Lys Tyr Val Tyr Ser Gly Trp Phe Tyr Lys His Ala
    130                 135                 140

Lys Ser Glu Val Lys Asn Glu Asn Gly Leu Val Ser Ala Lys Arg Gly
145                 150                 155                 160

Asp Asp Gly Tyr Ile Phe Tyr His Gly Asp Lys Pro Ser Arg Gln Leu
                165                 170                 175

Pro Ala Ser Glu Ala Val Thr Tyr Lys Gly Val Trp His Phe Val Thr
            180                 185                 190

Asp Thr Lys Gln Gly Gln Lys Phe Asn Asp Ile Leu Glu Thr Ser Lys
        195                 200                 205

Gly Gln Gly Asp Lys Tyr Ser Gly Phe Ser Gly Asp Glu Gly Glu Thr
    210                 215                 220

Thr Ser Asn Arg Thr Asp Ser Asn Leu Asn Asp Lys His Glu Gly Tyr
225                 230                 235                 240

Gly Phe Thr Ser Asn Phe Lys Val Asp Phe Asn Asn Lys Lys Leu Thr
                245                 250                 255

Gly Lys Leu Ile Arg Asn Asn Lys Val Ile Asn Thr Ala Ala Ser Asp
            260                 265                 270

Gly Tyr Thr Thr Glu Tyr Tyr Ser Leu Asp Ala Thr Leu Arg Gly Asn
        275                 280                 285

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

Thr Lys Leu His Pro Phe Val Phe Asp Ser Ser Ser Leu Ser Gly Gly
305                 310                 315                 320
```

```
Phe Phe Gly Pro Gln Gly Glu Glu Leu Gly Phe Arg Phe Leu Ser Asp
                325                 330                 335

Asp Gly Lys Val Ala Val Val Gly Ser Ala Lys Thr Lys Asp Ser Thr
            340                 345                 350

Ala Asn Gly Asn Ala Pro Ala Ala Ser Ser Gly Pro Gly Ala Ala Thr
        355                 360                 365

Met Pro Ser Glu Thr Arg Leu Thr Thr Val Leu Asp Ala Val Glu Leu
    370                 375                 380

Thr Pro Asp Gly Lys Glu Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala
385                 390                 395                 400

Thr Arg Leu Val Val Asp Gly Ile Met Ile Pro Leu Leu Pro Thr Glu
                405                 410                 415

Ser Gly Asn Gly Gln Ala Asp Lys Gly Lys Asn Gly Gly Thr Asp Phe
            420                 425                 430

Thr Tyr Glu Thr Thr Tyr Thr Pro Glu Ser Asp Lys Lys Asp Thr Lys
        435                 440                 445

Ala Gln Thr Gly Ala Gly Gly Met Gln Thr Ala Ser Gly Thr Ala Gly
    450                 455                 460

Val Asn Gly Gly Gln Val Gly Thr Lys Thr Tyr Lys Val Gln Val Cys
465                 470                 475                 480

Cys Ser Asn Leu Asn Tyr Leu Lys Tyr Gly Leu Leu Thr Arg Glu Asn
                485                 490                 495

Asn Asn Ser Val Met Gln Ala Val Lys Asn Ser Ser Gln Ala Asp Ala
            500                 505                 510

Lys Thr Lys Gln Ile Glu Gln Ser Met Phe Leu Gln Gly Glu Arg Thr
        515                 520                 525

Asp Glu Asn Lys Ile Pro Gln Glu Gln Gly Ile Val Tyr Leu Gly Phe
    530                 535                 540

Trp Tyr Gly Arg Ile Ala Asn Gly Thr Ser Trp Ser Gly Lys Ala Ser
545                 550                 555                 560

Asn Ala Thr Asp Gly Asn Arg Ala Lys Phe Thr Val Asn Phe Asp Arg
                565                 570                 575

Lys Glu Ile Thr Gly Thr Leu Thr Ala Glu Asn Arg Ser Glu Ala Thr
            580                 585                 590

Phe Thr Ile Asp Ala Met Ile Glu Gly Asn Gly Phe Lys Gly Thr Ala
        595                 600                 605
```

```
Lys Thr Gly Asn Asp Gly Phe Ala Pro Asp Gln Asn Asn Ser Thr Val
    610                 615                 620

Thr His Lys Val His Ile Ala Asn Ala Glu Val Gln Gly Gly Phe Tyr
625                 630                 635                 640

Gly Pro Asn Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly Asn
                645                 650                 655

Glu Gln Thr Lys Asn Ala Thr Val Glu Ser Gly Asn Gly Asn Ser Ala
            660                 665                 670

Ser Ser Ala Thr Val Val Phe Gly Ala Lys Arg Gln Lys Leu Val Lys
        675                 680                 685
```

<210> 208

<211> 683

<212> PRT

<213> Neisseria gonorrhoeae

<400> 208

```
Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser Val Asp Thr Glu
1               5                   10                  15

Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Pro Ser Lys Lys Pro
            20                  25                  30

Glu Ala Arg Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Phe Lys
        35                  40                  45

Arg Arg Asn Trp Tyr Pro Pro Ser Asn Pro Lys Glu Asn Glu Ile Arg
    50                  55                  60

Leu Ser Glu Gly Asp Trp Glu Gln Thr Gly Asn Gly Asn Ile Lys Asn
65                  70                  75                  80

Pro Ser Lys Gln Lys Asn Ile Ile Asp Ala Leu Ser Gly Asn Gly Glu
                85                  90                  95

Ala Pro Leu Gln Asp Ser Ser Gln Gln Gly Glu Gly Ile Ser Lys Val
            100                 105                 110

Thr Asp Tyr His Asp Phe Lys Tyr Val Trp Ser Gly Phe Phe Tyr Lys
        115                 120                 125

Gln Ile Gly Asn Thr Ile Lys Lys Asp Asp Ser Ser Ser Lys Ile Ile
    130                 135                 140

Glu Ala Arg Asn Gly Pro Asp Gly Tyr Ile Phe Tyr Lys Gly Thr Asp
145                 150                 155                 160

Pro Ser Arg Lys Leu Pro Val Ser Gly Ser Val Glu Tyr Lys Gly Thr
                165                 170                 175

Trp Asp Phe Leu Thr Asp Val Gln Ala Asn Gln Lys Phe Thr Asp Leu
            180                 185                 190
```

```
Gly Ser Ala Phe Thr Lys Ser Gly Asp Arg Tyr Ser Ala Phe Ser Gly
        195                 200                 205

Glu Leu Asp Tyr Ile Val Arg Lys Glu Glu Asp Lys Lys Asp Gly His
    210                 215                 220

Val Gly Leu Gly Leu Thr Thr Glu Ile Thr Val Asn Phe Glu Lys Lys
225                 230                 235                 240

Thr Leu Ser Gly Lys Leu Ile Lys Asn Asn Met Val Ile Asn Asn Gly
                245                 250                 255

Asp Glu Pro Thr Thr Gln Tyr Tyr Ser Leu Glu Ala Gln Val Thr Gly
            260                 265                 270

Asn Arg Phe Asn Gly Lys Ala Met Val Thr Asp Lys Pro Glu Asn Ser
        275                 280                 285

Lys Ser Lys Gln His Pro Phe Val Ser Asp Ser Ser Ser Leu Ser Gly
    290                 295                 300

Gly Phe Phe Gly Pro Gln Gly Glu Glu Leu Gly Phe Arg Phe Leu Ser
305                 310                 315                 320

Asn Asp Asn Lys Val Ala Val Val Gly Ser Ala Lys Thr Lys Asp Glu
                325                 330                 335

Thr Ala Ser Ser Gly Gly Thr Ser Gly Gly Ala Ser Val Ser Ala Ser
            340                 345                 350

Asn Gly Ala Thr Gly Thr Ser Ser Gly Asn Ser Asn Leu Thr Thr Val
        355                 360                 365

Leu Asp Ala Val Glu Leu Thr Pro Asp Gly Lys Glu Ile Lys Asp Leu
    370                 375                 380

Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met Ile
385                 390                 395                 400

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

Asn Gly Gly Thr Asp Phe Thr Tyr Thr Thr Thr Tyr Met Pro Glu Ser
            420                 425                 430

Asp Lys Lys Asp Thr Lys Ala Gln Thr Gly Ala Gly Gly Met Gln Thr
        435                 440                 445

Ala Ser Asp Ala Ala Gly Val Asn Gly Gly Gln Ala Gly Thr Lys Thr
    450                 455                 460

Tyr Lys Val Glu Ala Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr Gly
465                 470                 475                 480

Leu Leu Thr Arg Glu Asn Ser Asn Ser Val Met Gln Thr Val Arg Asn
                485                 490                 495
```

```
Ser Ser Gln Ala Ala Ala Arg Thr Ala Gln Gly Ala Gln Ser Met Phe
            500                 505                 510

Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Lys Glu Gln Lys
        515                 520                 525

Val Val Tyr Leu Gly Thr Trp Tyr Gly His Ile Ala Ala Asn Gly Thr
    530                 535                 540

Ser Trp Thr Gly Asn Ala Ser Asp Gln Gln Ser Gly Asn Arg Ala Lys
545                 550                 555                 560

Phe Asp Val Asn Phe Lys Asp Lys Lys Ile Thr Gly Thr Leu Thr Ala
                565                 570                 575

Ala Asn Arg Gln Glu Ala Thr Phe Thr Ile Asp Ala Met Ile Asp Asp
            580                 585                 590

Asn Gly Phe Lys Gly Thr Ala Lys Thr Gly Asn Asp Gly Phe Ala Pro
        595                 600                 605

Asp Gln Asn Ser Ser Thr Gly Thr Tyr Lys Val His Ile Ala Asn Ala
    610                 615                 620

Glu Val Gln Gly Gly Phe Tyr Gly Pro Asn Ala Glu Glu Leu Gly Gly
625                 630                 635                 640

Trp Phe Ala Tyr Pro Gly Asn Gly Gln Thr Lys Asn Ala Gln Glu Asn
                645                 650                 655

Ala Gln Ala Ser Ser Gly Asn Gly Asn Ser Ala Val Ser Ala Thr Val
            660                 665                 670

Val Phe Gly Ala Lys Arg Gln Gln Leu Val Lys
        675                 680
```

<210> 209

<211> 679

<212> PRT

<213> Neisseria gonorrhoeae

<400> 209

```
Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser Val Asp Thr Glu
1               5                   10                  15

Ala Pro Arg Ala Ala Pro Lys Tyr Gln Asp Val Pro Ser Lys Lys Pro
            20                  25                  30

Glu Ala Arg Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Phe Lys
        35                  40                  45

Arg Arg Asn Trp Tyr Ser Gln Ala Asn Leu Lys Glu Asp Lys Ile Pro
    50                  55                  60

Leu Ser Glu Gly Asp Trp Glu Gln Thr Asp Asn Gly Asn Ile Lys Asn
```

```
65                  70                  75                  80

Pro Ser Lys Gln Lys Asn Ile Ile Asn Ala Leu Ser Gly Asn Glu Glu
                85                  90                  95

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

Lys Asp His His Asn Phe Gln Tyr Val Trp Ser Gly Phe Phe Tyr Lys
        115                 120                 125

Gln Ile Ser Ser Thr Ile Lys Arg Asp Asp Ser Ser Asn Lys Ile Ile
    130                 135                 140

Glu Val Arg Asn Gly Pro Asp Gly Tyr Ile Phe Tyr Lys Gly Lys Asp
145                 150                 155                 160

Pro Ser Arg Lys Leu Pro Ala Ser Asn Glu Val Thr Tyr Lys Gly Thr
                165                 170                 175

Trp Asp Phe Leu Thr Asp Val Lys Ala Asn Gln Lys Phe Thr Asp Leu
            180                 185                 190

Ala Asn Thr Phe Ala Arg Pro Gly Asp Arg Tyr Ser Ala Phe Ser Gly
        195                 200                 205

Glu Leu Asp Tyr Ile Val Lys Lys Gln Glu Asp Lys Lys Glu Lys His
    210                 215                 220

Lys Gly Leu Gly Leu Thr Thr Glu Ile Thr Val Asp Phe Gly Lys Lys
225                 230                 235                 240

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

Ser Asp Asp Gln Asn Lys Tyr Thr Thr Glu Tyr Tyr Thr Leu Asp Ala
            260                 265                 270

Thr Leu Arg Gly Asn Arg Phe Ser Gly Lys Ala Met Ala Thr Asp Lys
        275                 280                 285

Ser Ser Asp Gly Gln Ala Lys Gln His Pro Phe Val Ser Asn Ser Ser
    290                 295                 300

Ser Leu Ser Gly Gly Phe Phe Gly Pro Gln Gly Lys Glu Leu Gly Phe
305                 310                 315                 320

Arg Phe Leu Ser Asp Asp Asn Lys Val Ala Val Val Gly Ser Ala Lys
                325                 330                 335

Thr Lys Asp Glu Ala Thr Asn Gly Asn Thr Ala Ala Ala Ser Ser Gly
            340                 345                 350

Pro Gly Ala Ala Thr Met Pro Ser Glu Thr Arg Leu Thr Thr Val Leu
        355                 360                 365
```

```
Asp Ala Val Glu Leu Thr Pro Asp Gly Lys Glu Ile Lys Asp Leu Asp
    370                 375                 380

Asn Phe Ser Asp Ala Thr Arg Leu Val Val Asp Gly Ile Met Ile Pro
385                 390                 395                 400

Leu Leu Pro Lys Asp Ser Glu Ser Gly Val Ser Gln Pro Asp Lys Gly

                405                 410                 415

Glu Asn Gly Gly Thr Asp Phe Thr Tyr Thr Thr Thr Tyr Met Pro Glu
            420                 425                 430

Ser Asp Lys Lys Asp Thr Lys Ala Gln Thr Gly Ala Gly Gly Met Gln
        435                 440                 445

Thr Ala Ser Gly Ala Ala Gly Val Asn Ser Gly Gln Ala Gly Thr Lys
    450                 455                 460

Thr Tyr Lys Val Glu Ala Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr
465                 470                 475                 480

Gly Met Leu Thr Arg Lys Asn Ser Glu Ser Ala Met Gln Ala Gly Gly
                485                 490                 495

Ser Ser Asn Gln Ala Asp Ala Lys Thr Glu Gln Ala Glu Gln Ser Met
            500                 505                 510

Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Gln Ile Pro Lys Asp Glu
        515                 520                 525

Asn Val Val Tyr Leu Gly Ser Trp Tyr Gly Arg Ile Ala Asn Gly Thr
    530                 535                 540

Ser Trp Ser Gly Asn Ala Ser Asn Thr Thr Ser Gly Asn Lys Ala Glu
545                 550                 555                 560

Phe Thr Val Asn Phe Asp Lys Lys Glu Ile Thr Gly Met Leu Thr Ala
                565                 570                 575

Ala Asn Arg Pro Glu Ala Thr Phe Thr Ile Asp Ala Met Ile Asp Gly
            580                 585                 590

Asn Gly Phe Lys Gly Thr Ala Lys Thr Gly Asn Asp Gly Phe Ala Pro
        595                 600                 605

Asp Gln Asn Asn Ser Thr Val Thr His Lys Val His Ile Ala Glu Ala
    610                 615                 620

Lys Val Arg Gly Gly Phe Tyr Gly Pro Asn Ala Glu Glu Leu Gly Gly
625                 630                 635                 640

Trp Phe Ala Tyr Pro Gly Asn Gly Gln Ala Lys Asn Ala Gln Thr Ser
                645                 650                 655

Ser Gly Asp Gly Asn Ser Ala Gly Ser Ala Thr Val Val Phe Gly Ala
            660                 665                 670
```

660 665 670

Lys Arg Gln Glu Leu Val Gln
675

<210> 210

<211> 679

<212> PRT

<213> Neisseria gonorrhoeae

<400> 210

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

Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Pro Ser Lys Lys Pro
20 25 30

Glu Ala Arg Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Phe Lys
35 40 45

Arg Arg Asn Trp Tyr Pro Pro Ser Asn Pro Lys Glu Asn Glu Ile Arg
50 55 60

Leu Ser Glu Gly Asp Trp Glu Gln Thr Asp Asn Gly Asn Ile Lys Asn
65 70 75 80

Pro Ser Lys Gln Lys Asn Ile Ile Asn Ala Leu Ser Gly Asn Gly Gly
85 90 95

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

Thr Asp His His Asp Phe Lys Tyr Val Trp Ser Gly Phe Phe Tyr Lys
115 120 125

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

Arg Asn Gly Pro Asp Gly Tyr Ile Phe Tyr Lys Gly Lys Asp Pro Ser
145 150 155 160

Arg Glu Leu Pro Val Leu Gly Ser Val Glu Tyr Lys Gly Thr Trp Asp
165 170 175

Phe Leu Thr Asp Val Arg Val Asn Gln Lys Phe Thr Asp Leu Gly Ser
180 185 190

Ala Tyr Thr Arg Ser Gly Asp Arg Tyr Ser Ala Phe Ser Gly Glu Leu
195 200 205

Asp Tyr Ile Val Lys Lys Glu Asp Asp Lys Lys Glu Lys His Lys Gly
210 215 220

Leu Gly Leu Thr Thr Glu Ile Thr Val Asp Phe Glu Lys Lys Thr Leu
225 230 235 240

```
Asn Gly Lys Leu Ile Lys Asn Asn His Val Ile Gly Asn Val Ala Thr
                245                 250                 255

Glu Asn Lys Tyr Thr Thr Glu Tyr Tyr Thr Leu Asp Ala Thr Leu Arg
            260                 265                 270

Gly Asn Arg Phe Ser Gly Thr Ala Thr Ala Thr Asp Lys Ser Ser Asp
        275                 280                 285

Gly Gln Ala Lys Gln His Pro Phe Val Ser Asp Ser Ser Ser Leu Ser
    290                 295                 300

Gly Gly Phe Phe Gly Pro Lys Gly Glu Glu Leu Gly Phe Arg Phe Leu
305                 310                 315                 320

Ser Asp Asp Gln Lys Val Ala Val Val Gly Ser Ala Lys Thr Arg Asp
                325                 330                 335

Lys Ala Glu Asn Gly Gly Gly Asn Gly Ala Ser Gly Gly Ala Ser Val
            340                 345                 350

Ser Ala Ser Asn Gly Ala Ala Gly Met Pro Ser Glu Asn Gly Lys Leu
        355                 360                 365

Thr Thr Val Leu Asp Ala Val Glu Leu Glu Ser Asp Gly Lys Lys Val
    370                 375                 380

Lys Asn Leu Asp Asn Phe Ser Asp Ala Thr Arg Leu Val Val Asp Gly
385                 390                 395                 400

Ile Met Ile Pro Leu Leu Pro Thr Glu Ser Gly Asn Gly Gln Ala Asp
                405                 410                 415

Lys Gly Lys Asn Gly Gly Thr Asp Phe Thr Tyr Thr Thr Thr Tyr Thr
            420                 425                 430

Pro Glu Ser Asp Lys Glu Asp Thr Gln Thr Gly Met Ala Ala Asn Gly
        435                 440                 445

Val Gln Thr Val Ser Asn Ala Ala Gly Gly Thr Ser Gly Lys Thr Lys
    450                 455                 460

Thr His Tyr Glu Val Gln Ala Cys Cys Ser Asn Leu Asn Tyr Leu Lys
465                 470                 475                 480

Tyr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn Thr Gly Gly Gly Gly
                485                 490                 495

Asn Gly Ser Gln Ala Val Gln Thr Ala Gln Gly Ala Gln Ser Met Phe
            500                 505                 510

Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Lys Asp Gly Asn
        515                 520                 525

Val Val Tyr Leu Gly Thr Trp Tyr Gly His Ile Ala Ile Asn Gly Thr
    530                 535                 540
```

```
Ser Trp Thr Arg Glu Ala Ser Asn Gln Glu Asn Gly Asn Arg Ala Lys
545                 550                 555                 560

Phe Asp Val Asn Phe Lys Asp Lys Lys Ile Thr Gly Thr Leu Thr Ala
                565                 570                 575

Ala Asn Arg Gln Glu Ala Thr Phe Thr Ile Asp Ala Met Ile Glu Gly
            580                 585                 590

Asn Gly Phe Lys Gly Thr Ala Lys Thr Gly Asp Gly Gly Phe Ala Pro
        595                 600                 605

Asp Gln Asn Asn Ser Thr Gly Thr His Lys Val His Ile Ala Glu Ala
    610                 615                 620

Lys Val Gln Gly Gly Phe Tyr Gly Pro Asn Ala Glu Glu Leu Gly Gly
625                 630                 635                 640

Trp Phe Ala Tyr Pro Gly Asn Gly Gln Ala Glu Asn Ala Gln Thr Ser
                645                 650                 655

Ser Gly Asn Gly Asn Ser Ala Gly Ser Ala Thr Val Val Phe Gly Ala
            660                 665                 670

Lys Arg Gln Glu Leu Val Lys
        675
```

<210> 211

<211> 673

<212> PRT

<213> Neisseria gonorrhoeae

<400> 211

```
Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser Val Asp Thr Glu
1               5                   10                  15

Ala Pro Arg Pro Ala Pro Lys Tyr Lys Asp Val Pro Ser Lys Lys Pro
            20                  25                  30

Glu Ala Arg Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Phe Lys
        35                  40                  45

Arg Arg Asn Trp Tyr Pro Pro Ser Asn Pro Lys Glu Asn Glu Ile Arg
    50                  55                  60

Leu Ser Glu Gly Asn Trp Glu Gln Thr Asp Asp Gly Glu Ile Lys Thr
65                  70                  75                  80

Pro Ser Lys Gln Lys Asn Ile Ile Asn Ala Leu Ser Gly Asn Glu Gly
                85                  90                  95

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

```
Thr Asp His His Asp Phe Lys Tyr Val Trp Ser Gly Phe Phe Tyr Lys
        115                 120                 125

Arg Ile Gly Ile Thr Thr Lys Lys Asp Asp Leu Ser Asn Lys Ile Ile
    130                 135                 140

Glu Ala Arg Asn Gly Pro Asp Gly Tyr Ile Phe Tyr Lys Gly Thr Asp
145                 150                 155                 160

Pro Ser Arg Lys Leu Pro Val Ser Gly Ser Val Glu Tyr Lys Gly Thr
                165                 170                 175

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

Gly Asn Thr Ser Thr Lys Ser Gly Asp Arg Tyr Ser Ala Phe Ser Gly
        195                 200                 205

Glu Leu Asp Tyr Ile Val Lys Lys Glu Ser Asp Lys Lys Asp Gly His
    210                 215                 220

Val Gly Leu Gly Leu Thr Thr Glu Ile Thr Val Asp Phe Gly Lys Lys
225                 230                 235                 240

Thr Leu Ser Gly Lys Leu Ile Lys Asn Asn Met Val Ile Asn Asn Gly
                245                 250                 255

Asp Glu Pro Thr Thr Gln Tyr Tyr Ser Leu Glu Ala Gln Val Thr Gly
            260                 265                 270

Asn Arg Phe Asn Gly Lys Ala Ile Ala Thr Asp Lys Pro Lys Val Asn
        275                 280                 285

Glu Thr Lys Glu His Pro Phe Val Ser Asp Ser Ser Ser Leu Ser Gly
    290                 295                 300

Gly Phe Phe Gly Pro Gln Gly Glu Glu Leu Gly Phe Arg Phe Leu Ser
305                 310                 315                 320

His Asp Asn Lys Val Ala Val Val Gly Ser Ala Lys Thr Lys Asp Lys
                325                 330                 335

Asn Ala Asn Gly Asn Thr Ala Ala Ala Gly Thr Ala Gly Ala Ala Gly
            340                 345                 350

Met Ser Ser Glu Asp Thr Lys Leu Thr Thr Val Leu Asp Ala Val Glu
        355                 360                 365

Leu Thr Pro Asp Gly Lys Lys Val Lys Asn Leu Asp Asn Phe Ser Asp
    370                 375                 380

Ala Thr Gln Leu Val Val Asp Gly Ile Met Ile Pro Leu Leu Pro Thr
385                 390                 395                 400

Glu Ser Gly Asn Gly Gln Ala Asp Lys Gly Glu Asn Gly Lys Thr Ala
                405                 410                 415
```

```
Phe Ile Tyr Glu Thr Thr Tyr Thr Pro Glu Ser Asp Lys Lys Asp Thr
            420                 425                 430

Gln Thr Gly Met Ala Thr Asn Gly Val Gln Thr Val Ser Asn Thr Ala
        435                 440                 445

Gly Gly Thr Ser Gly Lys Thr Lys Thr His Tyr Lys Val Gln Ala Cys
    450                 455                 460

Cys Ser Asn Leu Asn Tyr Leu Lys Tyr Gly Leu Leu Thr Arg Glu Asn
465                 470                 475                 480

Ser Asn Ser Val Met Gln Thr Val Arg Asn Ser Ser Gln Ala Ala Ala

                485                 490                 495

Arg Thr Glu Gln Gly Ala Gln Ser Met Phe Leu Gln Gly Glu Arg Thr
            500                 505                 510

Asp Glu Lys Glu Ile Pro Lys Glu Gln Lys Val Val Tyr Leu Gly Thr
        515                 520                 525

Trp Tyr Gly His Ile Ala Ala Asn Gly Thr Ser Trp Thr Gly Lys Ala
    530                 535                 540

Ser Asp Gln Gln Ser Gly Asn Arg Ala Lys Phe Asp Val Asn Phe Lys
545                 550                 555                 560

Asp Lys Lys Ile Thr Gly Thr Leu Thr Ala Ala Asn Arg Gln Ala Glu
                565                 570                 575

Thr Phe Thr Ile Ser Gly Met Ile Asp Gly Asn Gly Phe Glu Gly Thr
            580                 585                 590

Ala Lys Thr Gly Asn Gly Gly Phe Ala Leu Asp Ala Asn Asn Thr Ala
        595                 600                 605

Ala Thr His Lys Ala His Ile Ala Glu Ala Lys Val Arg Gly Gly Phe
    610                 615                 620

Tyr Gly Pro Asn Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly
625                 630                 635                 640

Asn Gly Gln Ala Lys Asn Ala Gln Ala Ser Ser Gly Asn Glu Asn Ser
                645                 650                 655

Ala Gly Ser Ala Thr Val Val Phe Gly Ala Lys Arg Gln Gln Leu Val
            660                 665                 670

Gln
```

<210> 212

<211> 682

<212> PRT

<213> Neisseria gonorrhoeae

<400> 212

```
Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser Val Asp Thr Glu
1               5                  10                  15

Ala Pro Arg Ala Ala Pro Lys Tyr Gln Asp Val Pro Ser Lys Lys Pro

            20                  25                  30

Glu Ala Arg Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Phe Lys
        35                  40                  45

Arg Arg Asn Trp Tyr Pro Pro Ala Asn Pro Lys Glu Glu Lys Ile Pro
    50                  55                  60

Leu Ser Glu Asn Asp Trp Glu Gln Thr Asp Asn Gly Asn Ile Lys Asn
65                  70                  75                  80

Pro Ser Lys Gln Lys Asn Ile Ile Asn Ala Leu Ser Gly Asn Gly Gly
                85                  90                  95

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

Thr Asp His His Asp Phe Lys Tyr Val Trp Ser Gly Phe Phe Tyr Lys
        115                 120                 125

Gln Ile Gly Asn Thr Ile Lys Arg Asp Asp Ser Ser Ser Lys Val Ile
    130                 135                 140

Glu Ala Arg Asn Gly Pro Asp Gly Tyr Ile Phe Tyr Lys Gly Thr Asp
145                 150                 155                 160

Pro Ser Arg Lys Leu Pro Val Ser Gly Ser Val Glu Tyr Lys Gly Thr
                165                 170                 175

Trp Asp Phe Leu Thr Asp Val Gln Ala Asn Gln Lys Phe Thr Asp Leu
            180                 185                 190

Gly Ser Ala Phe Thr Lys Ser Gly Asp Arg Tyr Ser Ala Phe Ser Gly
        195                 200                 205

Glu Leu Asp Tyr Ile Val Arg Lys Glu Glu Asp Lys Lys Asp Lys His
    210                 215                 220

Val Gly Leu Gly Leu Thr Thr Glu Ile Thr Val Asp Phe Glu Lys Lys
225                 230                 235                 240

Thr Leu Asn Gly Lys Leu Ile Lys Asn Asn Met Val Ile Asn Asn Lys
                245                 250                 255

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

Asn Arg Phe Ser Gly Lys Ala Met Ala Thr Asp Lys Ser Lys Asn Gly
```

```
        275                 280                 285

Glu Thr Gly Asp Gln Thr Lys Gln His Pro Phe Val Ser Asp Ser Ser
    290                 295                 300

Ser Leu Ser Gly Gly Phe Phe Gly Pro Lys Gly Glu Glu Leu Gly Phe
305                 310                 315                 320

Arg Phe Leu Ser Asp Asp Gly Lys Val Ala Val Val Gly Ser Ala Lys
                325                 330                 335

Thr Lys Asp Lys Ala Glu Asn Gly Gly Gly Asn Gly Asp Ser Gly Gly
            340                 345                 350

Ala Ser Val Ser Ala Ser Gly Gly Thr Thr Gly Thr Pro Ser Glu Asn
        355                 360                 365

Gly Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Pro Asn Gly
    370                 375                 380

Lys Glu Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
385                 390                 395                 400

Val Asp Gly Ile Met Ile Pro Leu Leu Pro Thr Glu Ser Gly Asn Gly
                405                 410                 415

Gln Ala Asp Lys Gly Glu Asn Gly Lys Thr Ala Phe Ile Tyr Glu Thr
            420                 425                 430

Thr Tyr Thr Pro Glu Ser Asp Glu Lys Asp Thr Gln Thr Gly Met Ala
        435                 440                 445

Ala Asn Gly Val Gln Thr Val Ser Asn Ala Ala Gly Gly Thr Ser Gly
    450                 455                 460

Lys Thr Lys Thr His Tyr Glu Val Gln Ala Cys Cys Ser Asn Leu Asn
465                 470                 475                 480

Tyr Leu Lys Tyr Gly Leu Leu Thr Arg Lys Thr Ala Asp Asn Thr Gly
                485                 490                 495

Gly Gly Gly Lys Gly Ser Gln Ala Ala Ala Gln Thr Ala Gln Gly Ala
            500                 505                 510

Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Gln Ile Pro
        515                 520                 525

Lys Asp Glu Asn Val Val Tyr Leu Gly Ser Trp Tyr Gly Tyr Ile Ala
    530                 535                 540

Asn Gly Thr Ser Trp Ser Gly Asn Ala Ser Asn Thr Thr Ser Gly Asn
545                 550                 555                 560

Lys Ala Glu Phe Thr Val Asn Phe Asp Lys Lys Lys Ile Thr Gly Met
                565                 570                 575

Leu Thr Ala Ala Asn Arg Gln Glu Ala Thr Phe Thr Ile Asp Ala Met
```

```
            580                 585                 590

Ile Glu Ser Asn Gly Phe Lys Gly Met Ala Lys Thr Gly Asn Gly Gly
        595                 600                 605

Phe Ala Pro Asp Gln Asn Ser Ser Thr Gly Thr His Lys Val His Ile
    610                 615                 620

Thr Ser Ala Ala Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu
625                 630                 635                 640

Leu Gly Gly Trp Phe Ala Tyr Pro Gly Asn Gly Gln Thr Lys Asn Ala
                645                 650                 655

Gln Ala Ser Ser Gly Asn Gly Asn Ser Ala Gly Ser Ala Thr Val Val
            660                 665                 670

Phe Gly Ala Lys Arg Gln Gln Leu Val Lys
        675                 680
```

<210> 213

<211> 341

<212> PRT

<213> Neisseria gonorrhoeae

<400> 213

```
Thr Lys Asp Ser Thr Ala Asn Gly Asn Ala Pro Ala Ala Ser Ser Gly
1               5                   10                  15

Pro Gly Ala Ala Thr Met Pro Ser Glu Thr Arg Leu Thr Thr Val Leu
            20                  25                  30

Asp Ala Val Glu Leu Thr Pro Asp Gly Lys Glu Ile Lys Asn Leu Asp
        35                  40                  45

Asn Phe Ser Asn Ala Thr Arg Leu Val Val Asp Gly Ile Met Ile Pro
    50                  55                  60

Leu Leu Pro Thr Glu Ser Gly Asn Gly Gln Ala Asp Lys Gly Lys Asn
65                  70                  75                  80

Gly Gly Thr Asp Phe Thr Tyr Glu Thr Thr Tyr Thr Pro Glu Ser Asp
                85                  90                  95

Lys Lys Asp Thr Lys Ala Gln Thr Gly Ala Gly Gly Met Gln Thr Ala
            100                 105                 110

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

Lys Val Gln Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr Gly Leu
    130                 135                 140

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

```
Ser Gln Ala Asp Ala Lys Thr Lys Gln Ile Glu Gln Ser Met Phe Leu
                165                 170                 175

Gln Gly Glu Arg Thr Asp Glu Asn Lys Ile Pro Gln Glu Gln Gly Ile
            180                 185                 190

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

Ser Gly Lys Ala Ser Asn Ala Thr Asp Gly Asn Arg Ala Lys Phe Thr
    210                 215                 220

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

Arg Ser Glu Ala Thr Phe Thr Ile Asp Ala Met Ile Glu Gly Asn Gly
                245                 250                 255

Phe Lys Gly Thr Ala Lys Thr Gly Asn Asp Gly Phe Ala Pro Asp Gln
            260                 265                 270

Asn Asn Ser Thr Val Thr His Lys Val His Ile Ala Asn Ala Glu Val
        275                 280                 285

Gln Gly Gly Phe Tyr Gly Pro Asn Ala Glu Glu Leu Gly Gly Trp Phe
    290                 295                 300

Ala Tyr Pro Gly Asn Glu Gln Thr Lys Asn Ala Thr Val Glu Ser Gly
305                 310                 315                 320

Asn Gly Asn Ser Ala Ser Ser Ala Thr Val Val Phe Gly Ala Lys Arg
                325                 330                 335

Gln Lys Leu Val Lys
            340
```

<210> 214

<211> 301

<212> PRT

<213> Neisseria gonorrhoeae

<400> 214

```
Asp Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp Gly Ile
1               5                   10                  15

Met Ile Pro Leu Leu Ser Thr Glu Ser Gly Asn Gly Gln Ala Asp Lys
            20                  25                  30

Gly Lys Asn Gly Gly Thr Asp Phe Thr Tyr Thr Thr Thr Tyr Met Pro
        35                  40                  45

Glu Ser Asp Lys Lys Asp Thr Lys Ala Gln Thr Gly Ala Gly Gly Met
    50                  55                  60

Gln Thr Ala Ser Asp Ala Ala Gly Val Asn Gly Gly Gln Ala Gly Thr
65                  70                  75                  80
```

```
Lys Thr Tyr Lys Val Glu Ala Cys Cys Ser Asn Leu Asn Tyr Leu Lys
                85                  90                  95

Tyr Gly Leu Leu Thr Arg Glu Asn Ser Asn Ser Val Met Gln Thr Val
            100                 105                 110

Arg Asn Ser Ser Gln Ala Ala Ala Arg Thr Ala Gln Gly Ala Gln Ser
        115                 120                 125

Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Lys Glu
    130                 135                 140

Gln Lys Val Val Tyr Leu Gly Thr Trp Tyr Gly His Ile Ala Ala Asn
145                 150                 155                 160

Gly Thr Ser Trp Thr Gly Asn Ala Ser Asp Gln Gln Ser Gly Asn Arg
                165                 170                 175

Ala Lys Phe Asp Val Asn Phe Lys Asp Lys Lys Ile Thr Gly Thr Leu
            180                 185                 190

Thr Ala Ala Asn Arg Gln Glu Ala Thr Phe Thr Ile Asp Ala Met Ile
        195                 200                 205

Asp Asp Asn Gly Phe Lys Gly Thr Ala Lys Thr Gly Asn Asp Gly Phe
    210                 215                 220

Ala Pro Asp Gln Asn Ser Ser Thr Gly Thr Tyr Lys Val His Ile Ala
225                 230                 235                 240

Asn Ala Glu Val Gln Gly Gly Phe Tyr Gly Pro Asn Ala Glu Glu Leu
                245                 250                 255

Gly Gly Trp Phe Ala Tyr Pro Gly Asn Gly Gln Thr Lys Asn Ala Gln
            260                 265                 270

Glu Asn Ala Gln Ala Ser Ser Gly Asn Gly Asn Ser Ala Val Ser Ala
        275                 280                 285

Thr Val Val Phe Gly Ala Lys Arg Gln Gln Leu Val Lys
    290                 295                 300
```

<210> 215

<211> 343

<212> PRT

<213> Neisseria gonorrhoeae

<400> 215

```
Thr Lys Asp Glu Ala Thr Asn Gly Asn Thr Ala Ala Ala Ser Ser Gly
1               5                   10                  15

Pro Gly Ala Ala Thr Met Pro Ser Glu Thr Arg Leu Thr Thr Val Leu
            20                  25                  30
```

```
Asp Ala Val Glu Leu Thr Pro Asp Gly Lys Glu Ile Lys Asp Leu Asp
        35                  40                  45

Asn Phe Ser Asp Ala Thr Arg Leu Val Val Asp Gly Ile Met Ile Pro
    50                  55                  60

Leu Leu Pro Lys Asp Ser Glu Ser Gly Val Ser Gln Pro Asp Lys Gly
65                  70                  75                  80

Glu Asn Gly Gly Thr Asp Phe Thr Tyr Thr Thr Thr Tyr Met Pro Glu
                85                  90                  95

Ser Asp Lys Lys Asp Thr Lys Ala Gln Thr Gly Ala Gly Gly Met Gln
            100                 105                 110

Thr Ala Ser Gly Ala Ala Gly Val Asn Ser Gly Gln Ala Gly Thr Lys
        115                 120                 125

Thr Tyr Lys Val Glu Ala Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr
    130                 135                 140

Gly Met Leu Thr Arg Lys Asn Ser Glu Ser Ala Met Gln Ala Gly Gly
145                 150                 155                 160

Ser Ser Asn Gln Ala Asp Ala Lys Thr Glu Gln Ala Glu Gln Ser Met
                165                 170                 175

Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Gln Ile Pro Lys Asp Glu
            180                 185                 190

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

Ser Trp Ser Gly Asn Ala Ser Asn Thr Thr Ser Gly Asn Lys Ala Glu
    210                 215                 220

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

Ala Asn Arg Pro Glu Ala Thr Phe Thr Ile Asp Ala Met Ile Asp Gly
                245                 250                 255

Asn Gly Phe Lys Gly Thr Ala Lys Thr Gly Asn Asp Gly Phe Ala Pro
            260                 265                 270

Asp Gln Asn Asn Ser Thr Val Thr His Lys Val His Ile Ala Glu Ala
        275                 280                 285

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

Trp Phe Ala Tyr Pro Gly Asn Gly Gln Ala Lys Asn Ala Gln Thr Ser
305                 310                 315                 320

Ser Gly Asp Gly Asn Ser Ala Gly Ser Ala Thr Val Val Phe Gly Ala
                325                 330                 335
```

```
Lys Arg Gln Glu Leu Val Gln
            340
```

<210> 216

<211> 346

<212> PRT

<213> Neisseria gonorrhoeae

<400> 216

```
Thr Arg Asp Lys Ala Glu Asn Gly Gly Gly Asn Gly Ala Ser Gly Gly
1               5                  10                  15

Ala Ser Val Ser Ala Ser Asn Gly Ala Ala Gly Met Pro Ser Glu Asn
            20                  25                  30

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

Lys Lys Val Lys Asn Leu Asp Asn Phe Ser Asp Ala Thr Arg Leu Val
    50                  55                  60

Val Asp Gly Ile Met Ile Pro Leu Leu Pro Thr Glu Ser Gly Asn Gly
65                  70                  75                  80

Gln Ala Asp Lys Gly Lys Asn Gly Gly Thr Asp Phe Thr Tyr Thr Thr
                85                  90                  95

Thr Tyr Thr Pro Glu Ser Asp Lys Glu Asp Thr Gln Thr Gly Met Ala
            100                 105                 110

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

Lys Thr Lys Thr His Tyr Glu Val Gln Ala Cys Cys Ser Asn Leu Asn
    130                 135                 140

Tyr Leu Lys Tyr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn Thr Gly
145                 150                 155                 160

Gly Gly Gly Asn Gly Ser Gln Ala Val Gln Thr Ala Gln Gly Ala Gln
                165                 170                 175

Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Lys
            180                 185                 190

Asp Gly Asn Val Val Tyr Leu Gly Thr Trp Tyr Gly His Ile Ala Ile
        195                 200                 205

Asn Gly Thr Ser Trp Thr Arg Glu Ala Ser Asn Gln Glu Asn Gly Asn
    210                 215                 220

Arg Ala Lys Phe Asp Val Asn Phe Lys Asp Lys Lys Ile Thr Gly Thr
```

```
225                 230                 235                 240

Leu Thr Ala Ala Asn Arg Gln Glu Ala Thr Phe Thr Ile Asp Ala Met
                245                 250                 255

Ile Glu Gly Asn Gly Phe Lys Gly Thr Ala Lys Thr Gly Asp Gly Gly
            260                 265                 270

Phe Ala Pro Asp Gln Asn Asn Ser Thr Gly Thr His Lys Val His Ile
        275                 280                 285

Ala Glu Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Asn Ala Glu Glu
    290                 295                 300

Leu Gly Gly Trp Phe Ala Tyr Pro Gly Asn Gly Gln Ala Glu Asn Ala
305                 310                 315                 320

Gln Thr Ser Ser Gly Asn Gly Asn Ser Ala Gly Ser Ala Thr Val Val
                325                 330                 335

Phe Gly Ala Lys Arg Gln Glu Leu Val Lys
            340                 345
```

<210> 217

<211> 341

<212> PRT

<213> Neisseria gonorrhoeae

<400> 217

```
Thr Lys Asp Lys Asn Ala Asn Gly Asn Thr Ala Ala Ala Gly Thr Ala
1               5                   10                  15

Gly Ala Ala Gly Met Ser Ser Glu Asp Thr Lys Leu Thr Thr Val Leu
            20                  25                  30

Asp Ala Val Glu Leu Thr Pro Asp Gly Lys Lys Val Lys Asn Leu Asp
        35                  40                  45

Asn Phe Ser Asp Ala Thr Gln Leu Val Val Asp Gly Ile Met Ile Pro
    50                  55                  60

Leu Leu Pro Thr Glu Ser Gly Asn Gly Gln Ala Asp Lys Gly Glu Asn
65                  70                  75                  80

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

Lys Lys Asp Thr Gln Thr Gly Met Ala Thr Asn Gly Val Gln Thr Val

            100                 105                 110

Ser Asn Thr Ala Gly Gly Thr Ser Gly Lys Thr Lys Thr His Tyr Lys
        115                 120                 125

Val Gln Ala Cys Cys Ser Asn Leu Asp Tyr Leu Lys Tyr Glu Leu Leu
```

```
Val Gln Ala Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr Gly Leu Leu
    130                 135                 140

Thr Arg Glu Asn Ser Asn Ser Val Met Gln Thr Val Arg Asn Ser Ser
145                 150                 155                 160

Gln Ala Ala Ala Arg Thr Glu Gln Gly Ala Gln Ser Met Phe Leu Gln
                165                 170                 175

Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Lys Glu Gln Lys Val Val
            180                 185                 190

Tyr Leu Gly Thr Trp Tyr Gly His Ile Ala Ala Asn Gly Thr Ser Trp
        195                 200                 205

Thr Gly Lys Ala Ser Asp Gln Gln Ser Gly Asn Arg Ala Lys Phe Asp
    210                 215                 220

Val Asn Phe Lys Asp Lys Lys Ile Thr Gly Thr Leu Thr Ala Ala Asn
225                 230                 235                 240

Arg Gln Ala Glu Thr Phe Thr Ile Ser Gly Met Ile Asp Gly Asn Gly
                245                 250                 255

Phe Glu Gly Thr Ala Lys Thr Gly Asn Gly Gly Phe Ala Leu Asp Ala
            260                 265                 270

Asn Asn Thr Ala Ala Thr His Lys Ala His Ile Ala Glu Ala Lys Val
        275                 280                 285

Arg Gly Gly Phe Tyr Gly Pro Asn Ala Glu Glu Leu Gly Gly Trp Phe
    290                 295                 300

Ala Tyr Pro Gly Asn Gly Gln Ala Lys Asn Ala Gln Ala Ser Ser Gly
305                 310                 315                 320

Asn Glu Asn Ser Ala Gly Ser Ala Thr Val Val Phe Gly Ala Lys Arg
                325                 330                 335

Gln Gln Leu Val Gln
            340
```

<210> 218

<211> 346

<212> PRT

<213> Neisseria gonorrhoeae

<400> 218

```
Thr Lys Asp Lys Ala Glu Asn Gly Gly Gly Asn Gly Asp Ser Gly Gly
1               5                   10                  15

Ala Ser Val Ser Ala Ser Gly Gly Thr Thr Gly Thr Pro Ser Glu Asn
            20                  25                  30

Gly Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Pro Asn Gly
        35                  40                  45
```

```
Lys Glu Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
    50                  55                  60

Val Asp Gly Ile Met Ile Pro Leu Leu Pro Thr Glu Ser Gly Asn Gly
65                  70                  75                  80

Gln Ala Asp Lys Gly Glu Asn Gly Lys Thr Ala Phe Ile Tyr Glu Thr
                85                  90                  95

Thr Tyr Thr Pro Glu Ser Asp Glu Lys Asp Thr Gln Thr Gly Met Ala
            100                 105                 110

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

Lys Thr Lys Thr His Tyr Glu Val Gln Ala Cys Cys Ser Asn Leu Asn
    130                 135                 140

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

Gly Gly Gly Lys Gly Ser Gln Ala Ala Ala Gln Thr Ala Gln Gly Ala
                165                 170                 175

Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Gln Ile Pro
            180                 185                 190

Lys Asp Glu Asn Val Val Tyr Leu Gly Ser Trp Tyr Gly Tyr Ile Ala
        195                 200                 205

Asn Gly Thr Ser Trp Ser Gly Asn Ala Ser Asn Thr Thr Ser Gly Asn
    210                 215                 220

Lys Ala Glu Phe Thr Val Asn Phe Asp Lys Lys Lys Ile Thr Gly Met
225                 230                 235                 240

Leu Thr Ala Ala Asn Arg Gln Glu Ala Thr Phe Thr Ile Asp Ala Met
                245                 250                 255

Ile Glu Ser Asn Gly Phe Lys Gly Met Ala Lys Thr Gly Asn Gly Gly
            260                 265                 270

Phe Ala Pro Asp Gln Asn Ser Ser Thr Gly Thr His Lys Val His Ile
        275                 280                 285

Thr Ser Ala Ala Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu
    290                 295                 300

Leu Gly Gly Trp Phe Ala Tyr Pro Gly Asn Gly Gln Thr Lys Asn Ala
305                 310                 315                 320

Gln Ala Ser Ser Gly Asn Gly Asn Ser Ala Gly Ser Ala Thr Val Val
                325                 330                 335

Phe Gly Ala Lys Arg Gln Gln Leu Val Lys
```

340 345

<210> 219

<211> 706

<212> PRT

<213> Moraxella catarrhalis

<400> 219

```
Met Lys His Ile Pro Leu Thr Thr Leu Cys Val Ala Ile Ser Ala Val
1               5                   10                  15

Leu Leu Thr Ala Cys Gly Gly Ser Gly Gly Ser Asn Pro Pro Ala Pro
            20                  25                  30

Thr Pro Ile Pro Asn Ala Ser Gly Ser Gly Asn Thr Gly Asn Thr Gly
        35                  40                  45

Asn Ala Gly Gly Thr Asp Asn Thr Ala Asn Ala Gly Asn Thr Gly Gly
    50                  55                  60

Thr Asn Ser Gly Thr Gly Ser Ala Asn Thr Pro Glu Pro Lys Tyr Lys
65                  70                  75                  80

Asp Val Pro Thr Asp Glu Asn Lys Lys Asp Glu Val Ser Gly Ile Gln
                85                  90                  95

Glu Pro Ala Met Gly Tyr Gly Met Ala Leu Ser Lys Met Asn Leu His
            100                 105                 110

Lys Gln Gln Asp Thr Pro Leu Asp Glu Lys Asp Ile Ile Thr Leu Asp
        115                 120                 125

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

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

Glu Ala Asp Lys Asn Ala Ile Gly Asp Arg Ile Lys Lys Asp Asn Lys
                165                 170                 175

Asp Lys Ser Leu Ser Lys Ala Glu Leu Ala Lys Gln Ile Lys Glu Asp
            180                 185                 190

Val Arg Lys Ser His Glu Phe Gln Gln Val Leu Ser Ser Leu Lys Asn
        195                 200                 205

Lys Ile Phe His Ser Asn Asp Gly Thr Thr Lys Ala Thr Thr Arg Asp
    210                 215                 220

Leu Gln Tyr Val Asp Tyr Gly Tyr Tyr Leu Val Asn Asp Gly Asn Tyr
225                 230                 235                 240

Leu Thr Val Lys Thr Asp Glu Leu Trp Asn Leu Gly Pro Val Gly Gly
                245                 250                 255
```

```
Val Phe Tyr Asn Gly Thr Thr Thr Ala Lys Glu Leu Pro Thr Gln Asp
            260                 265                 270

Ala Val Lys Tyr Lys Gly His Trp Asp Phe Met Thr Asp Val Ala Lys
        275                 280                 285

Gln Arg Asn Arg Phe Ser Glu Val Lys Glu Asn Leu Gln Ala Gly Arg
    290                 295                 300

Tyr Tyr Gly Ala Ser Ser Lys Asp Glu Tyr Asn Arg Leu Leu Thr Asp
305                 310                 315                 320

Glu Lys Asn Lys Pro Glu Arg Tyr Asn Gly Glu Tyr Gly His Ser Ser
                325                 330                 335

Glu Phe Thr Val Asn Phe Lys Asp Lys Lys Leu Thr Gly Glu Leu Phe
            340                 345                 350

Ser Asn Leu Gln Asp Ser Arg Lys Gly Asn Val Thr Lys Thr Lys Arg
        355                 360                 365

Tyr Asp Ile Asp Ala Asn Ile Tyr Gly Asn Arg Phe Arg Gly Ser Ala
    370                 375                 380

Thr Ala Ser Asp Lys Ala Glu Ala Ser Lys Thr Lys His Pro Phe Thr
385                 390                 395                 400

Ser Asp Ala Lys Asn Ser Leu Glu Gly Gly Phe Tyr Gly Pro Asn Ala
                405                 410                 415

Glu Glu Leu Ala Gly Lys Phe Leu Thr Asn Asp Asn Lys Leu Phe Gly
            420                 425                 430

Val Phe Gly Ala Lys Arg Glu Ser Lys Ala Gly Glu Lys Thr Glu Ala
        435                 440                 445

Ile Leu Asp Ala Tyr Ala Leu Gly Thr Phe Asn Lys Asn Asn Ala Thr
    450                 455                 460

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

Lys Lys Leu Val Leu Gly Ser Thr Val Ile Asp Leu Val Pro Thr Gly
                485                 490                 495

Val Thr Lys Asp Val Asn Glu Phe Thr Lys Asn Lys Pro Asp Ser Ala
            500                 505                 510

Thr Asn Lys Ala Gly Glu Thr Leu Met Val Asn Asp Lys Val Ser Val
        515                 520                 525

Lys Thr Tyr Gly Tyr Gly Arg Asn Phe Glu Tyr Leu Lys Phe Gly Glu
    530                 535                 540

Leu Ser Val Gly Thr Ser Asn Ser Val Phe Leu Gln Gly Glu Arg Thr
545                 550                 555                 560
```

```
Ala Thr Thr Gly Glu Lys Ala Val Pro Thr Lys Gly Thr Ala Lys Tyr
                565                 570                 575

Leu Gly Asn Trp Val Gly Tyr Ile Thr Gly Lys Asp Ser Ser Lys Ser
            580                 585                 590

Phe Asn Glu Ala Gln Asp Val Ala Asp Phe Asp Ile Asp Phe Glu Lys
        595                 600                 605

Lys Ser Val Lys Gly Lys Leu Thr Thr Lys Asp Arg Gln Asp Pro Val
    610                 615                 620

Phe Asn Ile Thr Gly Asp Ile Ala Gly Asn Gly Trp Thr Gly Lys Ala
625                 630                 635                 640

Ser Thr Thr Lys Ala Asp Ala Gly Gly Tyr Lys Ile Asp Ser Ser Ser
                645                 650                 655

Thr Gly Lys Ser Ile Val Ile Lys Asp Ala Glu Val Thr Gly Gly Phe
            660                 665                 670

Tyr Gly Pro Asn Ala Asn Glu Met Gly Gly Ser Phe Thr His Asn Thr
        675                 680                 685

Asp Asp Ser Lys Ala Ser Val Val Phe Gly Thr Lys Arg Gln Glu Glu
    690                 695                 700

Val Lys
705
```

<210> 220

<211> 714

<212> PRT

<213> Moraxella catarrhalis

<400> 220

```
Met Lys His Ile Pro Leu Thr Thr Leu Cys Val Ala Ile Ser Ala Val
1               5                   10                  15

Leu Leu Thr Ala Cys Gly Gly Ser Gly Gly Ser Asn Pro Pro Ala Pro
            20                  25                  30

Thr Pro Ile Pro Asn Ala Ser Gly Ser Gly Asn Thr Gly Asn Thr Gly
        35                  40                  45

Asn Ala Gly Gly Thr Asp Asn Thr Ala Asn Ala Gly Asn Thr Gly Gly
    50                  55                  60

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

Asp Val Pro Thr Asp Lys Asn Glu Lys Glu Gln Val Ser Pro Ile Gln
                85                  90                  95

Glu Pro Ala Met Gly Tyr Gly Met Ala Leu Ser Lys Ile Asn Leu His
            100                 105                 110
```

```
Asn Arg Gln Asp Thr Pro Leu Asp Glu Lys Asn Ile Ile Thr Leu Asp
        115                 120                 125

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

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

Glu Ala Asp Lys Asn Ala Ile Gly Asp Arg Ile Lys Arg Glu Asn Glu
                165                 170                 175

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

Asn Val Arg Lys Ser Pro Asp Phe Gln Lys Val Leu Ser Ser Ile Lys
        195                 200                 205

Ala Lys Thr Phe His Ser Asn Asp Gly Thr Thr Lys Ala Thr Thr Arg
    210                 215                 220

Asp Leu Gln Tyr Val Asp Tyr Gly Tyr Tyr Leu Val Asn Asp Ala Asp
225                 230                 235                 240

Tyr Leu Thr Val Lys Thr Asp Ser Pro Lys Leu Trp Asn Leu Gly Pro
                245                 250                 255

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

Thr Gln Asp Ala Val Lys Tyr Lys Gly His Trp Asp Phe Met Thr Asp
        275                 280                 285

Val Ala Asn Lys Arg Asn Arg Phe Ser Glu Val Lys Glu Thr Pro Gln
    290                 295                 300

Ala Gly Trp Tyr Tyr Gly Ala Ser Ser Lys Asp Glu Tyr Asn Arg Leu
305                 310                 315                 320

Leu Thr Arg Lys Asp Ser Ala Pro Asp Asn Tyr Ser Gly Glu Tyr Gly
                325                 330                 335

His Ser Ser Glu Phe Thr Val Asn Phe Lys Glu Lys Lys Leu Thr Gly
            340                 345                 350

Glu Leu Ser Ser Asn Leu Gln Asp Arg His Lys Gly Asp Val Thr Lys

        355                 360                 365

Thr Lys Arg Tyr Asp Ile Lys Ala Asp Ile His Gly Asn Arg Phe Arg
    370                 375                 380

Gly Ser Ala Ile Ala Ser Asp Lys Asp Asp Ala Ser Lys Ala Lys His
385                 390                 395                 400
```

```
Pro Phe Thr Ser Asp Ala Lys Asp Arg Leu Glu Gly Gly Phe Tyr Gly
                405                 410                 415

Pro Lys Gly Glu Glu Leu Ala Gly Lys Phe Leu Thr Asp Asp Lys Lys
            420                 425                 430

Leu Phe Gly Val Phe Gly Ala Lys Arg Glu Ser Lys Ala Glu Glu Lys
        435                 440                 445

Thr Glu Ala Ile Leu Asp Ala Tyr Ala Leu Gly Thr Phe Asn Asn Thr
    450                 455                 460

Asn Lys Ala Thr Thr Phe Thr Pro Phe Thr Lys Lys Gln Leu Asp Asn
465                 470                 475                 480

Phe Gly Asn Ala Lys Lys Leu Val Leu Gly Ser Thr Val Ile Asp Leu
                485                 490                 495

Val Ser Thr Asp Ala Thr Lys Asn Glu Phe Thr Lys Glu Phe Thr Lys
            500                 505                 510

Asp Lys Pro Thr Ser Ala Thr Asn Lys Ala Gly Glu Thr Leu Met Val
        515                 520                 525

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

Lys Phe Gly Glu Leu Ser Val Gly Gly Ser His Ser Val Phe Leu Gln
545                 550                 555                 560

Gly Glu Arg Thr Ala Thr Thr Gly Asp Lys Ala Val Pro Thr Thr Gly
                565                 570                 575

Thr Ala Lys Tyr Leu Gly Asn Trp Val Gly Tyr Ile Thr Gly Lys Asp
            580                 585                 590

Thr Gly Thr Gly Thr Gly Lys Ser Phe Thr Asp Ala Gln Asp Val Ala
        595                 600                 605

Asp Phe Asp Ile Asp Phe Gly Asn Lys Ser Val Ser Gly Lys Leu Ile
    610                 615                 620

Thr Lys Gly Arg Gln Asp Pro Val Phe Asn Ile Thr Gly Gln Ile Ala
625                 630                 635                 640

Gly Asn Gly Trp Thr Gly Lys Ala Ser Thr Ala Lys Ala Asp Ala Gly
                645                 650                 655

Gly Tyr Lys Ile Asp Ser Ser Ser Thr Gly Lys Ser Ile Val Ile Glu
            660                 665                 670

Asn Ala Glu Val Thr Gly Gly Phe Tyr Gly Pro Asn Ala Asn Glu Met
        675                 680                 685

Gly Gly Ser Phe Thr His Asn Ala Asp Asp Lys Val Ser Val Val Phe
    690                 695                 700
```

```
Gly Thr Lys Lys Gln Glu Val Lys Gln Lys
705                 710
```

<210> 221

<211> 709

<212> PRT

<213> Moraxella catarrhalis

<400> 221

```
Met Lys His Ile Pro Leu Thr Thr Leu Cys Val Ala Ile Ser Ala Val
1               5                   10                  15

Leu Leu Thr Ala Cys Gly Gly Ser Ser Gly Gly Phe Asn Pro Pro Ala
            20                  25                  30

Ser Thr Pro Ile Pro Asn Ala Gly Asn Ser Gly Asn Ala Gly Asn Ala
        35                  40                  45

Gly Asn Ala Gly Gly Thr Gly Gly Ala Asn Ser Gly Ala Gly Asn Ala
    50                  55                  60

Gly Gly Thr Gly Gly Ala Asn Ser Gly Ala Gly Ser Ala Ser Thr Pro
65                  70                  75                  80

Glu Pro Lys Tyr Lys Asp Val Pro Thr Asp Glu Asn Lys Lys Ala Glu
                85                  90                  95

Val Ser Gly Ile Gln Glu Pro Ala Met Gly Tyr Gly Val Glu Leu Lys
            100                 105                 110

Leu Arg Asn Trp Ile Pro Gln Glu Gln Glu Glu His Ala Lys Ile Asn
        115                 120                 125

Thr Asn Asp Val Val Lys Leu Glu Gly Asp Leu Lys His Asn Pro Phe
    130                 135                 140

Asp Asn Ser Ile Trp Gln Asn Ile Lys Asn Ser Lys Glu Val Gln Thr
145                 150                 155                 160

Val Tyr Asn Gln Glu Lys Gln Asn Ile Glu Asp Gln Ile Lys Arg Glu
                165                 170                 175

Asn Lys Gln Arg Pro Asp Lys Lys Leu Asp Asp Val Ala Leu Gln Ala
            180                 185                 190

Tyr Ile Glu Lys Val Leu Asp Asp Arg Leu Thr Glu Leu Ala Lys Pro
        195                 200                 205

Ile Tyr Glu Lys Asn Ile Asn Tyr Ser His Asp Lys Gln Asn Lys Ala
    210                 215                 220

Arg Thr Arg Asp Leu Lys Tyr Val Arg Ser Gly Tyr Ile Tyr Arg Ser
225                 230                 235                 240

Gly Tyr Ser Asn Ile Ile Pro Lys Lys Ile Ala Lys Thr Gly Phe Asp
```

```
               245                 250                 255

Gly Ala Leu Phe Tyr Gln Gly Thr Gln Thr Ala Lys Gln Leu Pro Val
            260                 265                 270

Ser Gln Val Lys Tyr Lys Gly Thr Trp Asp Phe Met Thr Asp Ala Lys
        275                 280                 285

Lys Gly Gln Ser Phe Ser Ser Phe Gly Thr Ser Gln Arg Leu Ala Gly
    290                 295                 300

Asp Arg Tyr Ser Ala Met Ser Tyr His Glu Tyr Pro Ser Leu Leu Thr
305                 310                 315                 320

Asp Glu Lys Asn Lys Pro Asp Asn Tyr Asn Gly Glu Tyr Gly His Ser
                325                 330                 335

Ser Glu Phe Thr Val Asp Phe Ser Lys Lys Ser Leu Lys Gly Glu Leu
            340                 345                 350

Ser Ser Asn Ile Gln Asp Gly His Lys Gly Ser Val Asn Lys Thr Lys
        355                 360                 365

Arg Tyr Asp Ile Asp Ala Asn Ile Tyr Gly Asn Arg Phe Arg Gly Ser
    370                 375                 380

Ala Thr Ala Ser Asp Thr Thr Glu Ala Ser Lys Ser Lys His Pro Phe
385                 390                 395                 400

Thr Ser Asp Ala Lys Asn Ser Leu Glu Gly Gly Phe Tyr Gly Pro Asn
                405                 410                 415

Ala Glu Glu Leu Ala Gly Lys Phe Leu Thr Asn Asp Asn Lys Leu Phe
            420                 425                 430

Gly Val Phe Gly Ala Lys Arg Glu Ser Glu Ala Lys Glu Lys Thr Glu
        435                 440                 445

Ala Ile Leu Asp Ala Tyr Ala Leu Gly Thr Phe Asn Lys Pro Gly Thr
    450                 455                 460

Thr Asn Pro Ala Phe Thr Ala Asn Ser Lys Lys Glu Leu Asp Asn Phe
465                 470                 475                 480

Gly Asn Ala Lys Lys Leu Val Leu Gly Ser Thr Val Ile Asp Leu Val
                485                 490                 495

Pro Thr Gly Ala Thr Lys Asp Val Asn Glu Phe Lys Glu Lys Pro Lys
            500                 505                 510

Ser Ala Thr Asn Lys Ala Gly Glu Thr Leu Met Val Asn Asp Glu Val
        515                 520                 525

Ile Val Lys Thr Tyr Gly Tyr Gly Arg Asn Phe Glu Tyr Leu Lys Phe
    530                 535                 540

Gly Glu Leu Ser Ile Gly Gly Ser His Ser Val Phe Leu Gln Gly Glu
545                 550                 555                 560
```

545 550 555 560

Arg Thr Ala Glu Lys Ala Val Pro Thr Glu Gly Thr Ala Lys Tyr Leu
565 570 575

Gly Asn Trp Val Gly Tyr Ile Thr Gly Lys Asp Thr Gly Thr Ser Thr
580 585 590

Gly Lys Ser Phe Asn Glu Ala Gln Asp Ile Ala Asp Phe Asp Ile Asp
595 600 605

Phe Glu Arg Lys Ser Val Lys Gly Lys Leu Thr Thr Gln Gly Arg Gln
610 615 620

Asp Pro Val Phe Asn Ile Thr Gly Gln Ile Ala Gly Asn Gly Trp Thr
625 630 635 640

Gly Thr Ala Ser Thr Ala Lys Ala Asn Val Gly Gly Tyr Lys Ile Asp
645 650 655

Ser Ser Ser Thr Gly Lys Ser Ile Val Ile Glu Asn Ala Lys Val Thr
660 665 670

Gly Gly Phe Tyr Gly Pro Asn Ala Asn Glu Met Gly Gly Ser Phe Thr
675 680 685

His Asp Thr Asp Asp Ser Lys Ala Ser Val Val Phe Gly Thr Lys Arg
690 695 700

Gln Glu Glu Val Lys
705

<210> 222

<211> 709

<212> PRT

<213> Moraxella catarrhalis

<400> 222

Met Lys His Ile Pro Leu Thr Thr Leu Cys Val Ala Ile Ser Ala Val
1 5 10 15

Leu Leu Thr Ala Cys Gly Gly Ser Gly Gly Ser Asn Pro Pro Ala Pro
20 25 30

Thr Pro Ile Pro Asn Ala Ser Gly Ser Gly Asn Thr Gly Asn Thr Gly
35 40 45

Asn Ala Gly Gly Thr Asp Asn Thr Ala Asn Ala Gly Asn Thr Gly Gly
50 55 60

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

Asp Val Pro Thr Asp Lys Asn Glu Lys Glu Gln Val Ser Pro Ile Gln
85 90 95

```
Glu Pro Ala Met Gly Tyr Gly Met Ala Leu Ser Lys Ile Asn Leu His
            100                 105                 110

Asn Arg Gln Asp Thr Pro Leu Asp Glu Lys Asn Ile Ile Thr Leu Asp
        115                 120                 125

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

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

Lys Ala Asp Lys Asn Ala Ile Arg Arg Arg Ile Glu Ser Glu Asn Lys
                165                 170                 175

Ala Lys Pro Leu Ser Glu Ala Glu Leu Ala Glu Lys Ile Lys Glu Ala
            180                 185                 190

Val Arg Lys Ser Tyr Glu Phe Gln Gln Val Met Thr Ser Leu Glu Asn
        195                 200                 205

Lys Ile Phe His Ser Asn Asp Gly Thr Thr Lys Ala Thr Thr Arg Asp
    210                 215                 220

Leu Gln Tyr Val Asp Tyr Gly Tyr Tyr Leu Ala Asn Asp Ala Asn Tyr
225                 230                 235                 240

Leu Thr Val Lys Thr Asp Lys Pro Lys Leu Trp Asn Ser Gly Pro Val
                245                 250                 255

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

Gln Asp Ala Val Lys Tyr Lys Gly His Trp Asp Phe Met Thr Asp Val
        275                 280                 285

Ala Asn Lys Gly Asn Arg Phe Ser Glu Val Lys Gly Thr Arg Gln Ala
    290                 295                 300

Gly Trp Trp Tyr Gly Ala Ser Ser Lys Asp Glu Tyr Asn Arg Leu Leu
305                 310                 315                 320

Thr Asp Glu Lys Asn Lys Pro Asp Gly Tyr Asn Gly Glu Tyr Gly His
                325                 330                 335

Ser Ser Glu Phe Thr Val Asn Phe Lys Glu Lys Lys Leu Thr Gly Gly
            340                 345                 350

Leu Phe Ser Asn Leu Gln Asp Ser His Lys Gln Lys Val Thr Lys Thr
        355                 360                 365

Lys Arg Tyr Asp Ile Asp Ala Asn Ile His Gly Asn Arg Phe Arg Gly

    370                 375                 380

Ser Ala Ile Ala Ser Asp Lys Glu Lys Asp Ser Glu Thr Lys His Pro
```

385 390 395 400

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

Lys Gly Glu Glu Leu Ala Gly Lys Phe Leu Thr Asp Asp Asn Lys Leu
420 425 430

Phe Gly Val Phe Gly Ala Lys Gln Glu Ser Lys Ala Asp Lys Thr Glu
435 440 445

Ala Ile Leu Asp Ala Tyr Ala Leu Gly Ala Phe Asn Lys Asn Asp Ala
450 455 460

Asn Thr Phe Thr Pro Phe Thr Lys Lys Gln Leu Asp Asn Phe Gly Asn
465 470 475 480

Ala Lys Lys Leu Val Leu Gly Ser Thr Val Ile Asp Leu Val Pro Thr
485 490 495

Gly Ala Ala Lys Asp Val Asn Glu Phe Thr Lys Glu Lys Pro Lys Ser
500 505 510

Ala Thr Asn Glu Ala Gly Glu Thr Leu Met Val Asn Asp Glu Val Ile
515 520 525

Val Lys Thr Tyr Gly Tyr Gly Lys Asn Phe Glu Tyr Leu Lys Phe Gly
530 535 540

Glu Leu Ser Val Gly Asp Ser His Ser Val Phe Leu Gln Gly Glu Arg
545 550 555 560

Thr Ala Thr Thr Gly Glu Lys Ala Val Pro Thr Lys Gly Thr Ala Lys
565 570 575

Tyr Leu Gly Asn Trp Val Gly Tyr Ile Thr Gly Lys Asp Ser Ser Lys
580 585 590

Ser Phe Asn Glu Ala Gln Asp Val Ala Asp Phe Asp Ile Asp Phe Glu
595 600 605

Lys Lys Ser Val Lys Gly Lys Leu Thr Thr Lys Asp Arg Thr Asp Pro
610 615 620

Val Phe Asn Ile Thr Gly Gln Ile Ala Gly Asn Gly Trp Thr Gly Lys
625 630 635 640

Ala Ser Thr Ala Lys Ala Asp Ala Gly Gly Tyr Lys Ile Asp Ser Ser
645 650 655

Ser Thr Gly Lys Ser Ile Val Ile Glu Asn Ala Asn Val Thr Gly Gly
660 665 670

Phe Tyr Gly Pro Asn Ala Asn Glu Met Gly Gly Ser Phe Thr His Asn
675 680 685

```
Ala Asp Asp Ser Lys Ala Ser Val Val Phe Gly Thr Lys Arg Gln Gln
    690                 695                 700

Glu Val Lys Gln Lys
705
```

<210> 223

<211> 711

<212> PRT

<213> Moraxella catarrhalis

<400> 223

```
Met Lys His Ile Pro Leu Thr Thr Leu Cys Val Ala Ile Ser Ala Val
1               5                   10                  15

Leu Leu Thr Ala Cys Gly Gly Ser Gly Gly Ser Asn Pro Pro Ala Pro
            20                  25                  30

Thr Pro Ile Pro Asn Ala Ser Gly Ser Gly Asn Thr Gly Asn Thr Gly
        35                  40                  45

Asn Ala Gly Gly Thr Asp Asn Thr Ala Asn Ala Gly Asn Thr Gly Gly
    50                  55                  60

Thr Ser Ser Gly Thr Gly Ser Ala Ser Thr Ser Glu Pro Lys Tyr Gln
65                  70                  75                  80

Asp Val Pro Thr Thr Pro Asn Thr Lys Glu Gln Val Ser Ser Ile Gln
                85                  90                  95

Glu Pro Ala Met Gly Tyr Ala Met Glu Leu Lys Leu Arg Asn Ala His
            100                 105                 110

Pro His Asn Pro Asn Lys Glu Thr Glu Lys Arg Ile Ala Leu Asp Gln
        115                 120                 125

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

Lys Asn Leu Ile Glu Tyr Leu Lys Lys Ser Pro Glu Val Val Ser Lys
145                 150                 155                 160

Phe Asn Glu Gln Lys Gly Gly Ile Glu Asn Asn Thr Arg Leu Thr His
                165                 170                 175

Lys Asp Leu Ser Ser Glu Gln Lys Glu Ala Lys Val Lys Glu Ala Leu
            180                 185                 190

Asp Asn Ala Leu Thr Gln Phe Ala Gln Glu Lys Tyr Lys Glu Leu Ile
        195                 200                 205

Glu Asn Ala His Asp Lys Lys Ser Asp Ala Arg Asn Arg Asp Leu Lys
    210                 215                 220

Tyr Val Lys Ser Gly Phe Asn Tyr Leu Ser Gly Tyr Thr Ala Thr Asp
225                 230                 235                 240
```

```
His Asp Lys Lys Thr Asn Tyr Arg Gly Tyr Tyr Gly Ala Leu Tyr Tyr
               245                 250                 255

Lys Gly Ser Glu Thr Ala Lys Glu Leu Pro Gln Thr Ser Ala Lys Tyr
            260                 265                 270

Lys Gly Tyr Trp Asp Phe Met Thr Asp Ala Thr Leu Asp Asn Lys Tyr
        275                 280                 285

Thr Asp Leu Pro Gly Ile Ala Arg Gln Thr Gln Trp Arg Ser Leu Val
    290                 295                 300

Ser Thr Asp Glu Tyr Ala Thr Leu Leu Thr Asp Lys Asn Asn Lys Pro
305                 310                 315                 320

Ser Asp Tyr Asn Gly Ala Tyr Gly His Ser Ser Glu Phe Asp Val Asn
               325                 330                 335

Phe Ala Asp Lys Lys Val Thr Gly Lys Leu Ile Ser Asn Gln Leu Ser
            340                 345                 350

Gly Lys Thr Val Thr Ala Lys Glu Arg Tyr Lys Ile Glu Ala Asp Ile
        355                 360                 365

His Gly Asn Arg Phe Arg Gly Ser Ala Ile Ala Ser Glu Lys Thr Asp
    370                 375                 380

Glu Ser Lys Ser Lys His Pro Phe Thr Ser Asp Ala Lys Asp Arg Leu
385                 390                 395                 400

Glu Gly Gly Phe Tyr Gly Pro Lys Gly Glu Glu Leu Ala Gly Lys Phe
               405                 410                 415

Leu Thr Asp Asp Asn Lys Leu Phe Gly Val Phe Gly Ala Lys Arg Glu
            420                 425                 430

Ser Lys Val Glu Lys Thr Glu Ala Ile Leu Asp Ala Tyr Ala Leu Gly
        435                 440                 445

Thr Phe Asn Lys Ser Gly Thr Thr Asn Pro Ala Phe Asn Ala Asn Ser
    450                 455                 460

Lys Lys Glu Leu Asp Asn Phe Gly Asn Ile Asn Lys Leu Val Leu Gly
465                 470                 475                 480

Ser Thr Val Ile Asp Leu Thr Gln Gly Asn Asp Phe Val Lys Thr Ile
               485                 490                 495

Asp Lys Glu Lys Pro Ala Thr Thr Ser Asn Gln Ala Gly Glu Pro Leu
            500                 505                 510

Thr Val Asn Asp Arg Val Gln Val Gln Val Cys Cys Ser Asn Leu Glu
        515                 520                 525

His Leu Lys Phe Gly Ser Leu Ser Ile Gly Gly Ser Asn Ser Val Phe
    530                 535                 540
```

```
Leu Gln Gly Glu Arg Thr Ala Thr Thr Gly Asp Lys Ala Ile Pro Val
545                 550                 555                 560

Ala Gly Asn Ala Lys Tyr Arg Gly Thr Trp Ala Gly Tyr Val Thr Gly
                565                 570                 575

Ser Gly Asn Thr Ser Lys Gly Tyr Glu Ala Gln Lys Phe Ala Asp Asn
            580                 585                 590

Ala Asn Arg Ala Glu Phe Asp Val Asp Phe Ala Lys Lys Ser Leu Thr
        595                 600                 605

Gly Lys Leu Ile Pro Asn Thr Ser Ser Asp Gly Lys Ser Ala Phe Asp
    610                 615                 620

Ile Thr Ala Thr Ile Asp Gly Asn Gly Phe Ser Gly Lys Ala Asn Thr
625                 630                 635                 640

Pro Asp Ile Lys Thr Gly Gly Leu Lys Ile Asp Ser Lys Asn Thr Glu
                645                 650                 655

Ser Gly Arg Val Ile Val Lys Asp Ala Val Val Thr Gly Gly Phe Tyr
            660                 665                 670

Gly Pro Gln Ala Asn Glu Leu Gly Gly Ser Phe Thr Tyr Lys Ser Asn
        675                 680                 685

Asp Ala Glu Asn Lys Asp Ser Ser Ala Pro Val Val Phe Gly Ala Arg
    690                 695                 700

Lys Gln Gln Glu Val Lys Gln
705                 710
```

<210> 224

<211> 583

<212> PRT

<213> Mannheimia haemolytica

<400> 224

```
Met Phe Lys Leu Lys Ser Ser Phe Val Leu Leu Asn Ala Ala Leu Leu
1               5                   10                  15

Ala Ala Cys Ser Ser Asn Gly Gly Ser Phe Asp Val Gln Ser Ala Lys
            20                  25                  30

Val Glu Ser Gln Thr Gln Thr Thr Pro Lys Lys Pro Ser Leu Gln Asp
        35                  40                  45

Asp Asn Ser Asn Ala Arg Arg Thr Val Ser Ala Ser Glu Thr Glu Ala
    50                  55                  60

Leu Leu Gln Pro Gly Phe Gly Phe Ser Ala Lys Ile Pro Arg Arg Asn
65                  70                  75                  80

Leu Phe Pro Gln Gly Lys Glu Asp Val Ala Pro Ile Gly Asp Ile Lys
                85                  90                  95
```

```
                85                  90                  95

Glu Ile Thr Gly Asp Leu Thr Lys Ile Pro Tyr Glu Glu Glu Val Lys
            100                 105                 110

Ala Tyr Gly Ser Ser Ala Asp Gly Phe Ser His Thr His Asp Arg Asn
        115                 120                 125

His Lys Leu Tyr Thr Arg Asp Phe Asn Phe Val Arg Ser Gly Tyr Val
    130                 135                 140

Leu His Ser Gly Ala Lys Pro Glu Ile Lys Pro Lys Glu Ile Leu Arg
145                 150                 155                 160

Thr Gly Ala His Gly Tyr Val Tyr Tyr Leu Gly Ile Glu Pro Ala Lys
                165                 170                 175

Ala Ile Pro Thr Gln Lys Ala Thr Tyr Lys Gly Tyr Trp Asp Phe Thr
            180                 185                 190

Thr Asp Ala Arg Lys Gly Arg Asp Ser Lys Tyr Phe Ser Asn Ser Ala
        195                 200                 205

Gly Ile Asn Ile Gly Ala Thr Pro Glu Asn Ser Tyr Asp Ile Asn Val
    210                 215                 220

Asp Asp Ser Glu Lys Pro Met Gly His Thr Gly Glu Phe Thr Ala Asp
225                 230                 235                 240

Phe Ala Asn Lys Thr Leu Thr Gly Thr Leu Val Arg Asn Gly Tyr Val
                245                 250                 255

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

Lys Ile Lys Gly Asn Arg Phe Ser Gly Lys Ala Asn Ala Lys Asn Thr
        275                 280                 285

Asp Asp Pro Tyr Phe Gly Lys Ser Ser Thr Thr Leu Glu Gly Gly Phe
    290                 295                 300

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

Lys Ser Val Phe Val Val Phe Ala Gly Lys Arg Asp Ala Lys Lys Asp
                325                 330                 335

Asp Ser Glu Ser Ala Phe Asp Ala Phe Lys Ile Lys Leu Lys Asp Leu
            340                 345                 350

Asn Lys Ser Glu Met Asp Thr Phe Gly Asn Ala Thr His Leu Ile Ile
        355                 360                 365

Asn Asn Lys Gln Ile Pro Leu Ile Ala Glu Gly Lys Lys Ser Phe Ala
    370                 375                 380

Glu Met Lys Phe Asp Asp Leu Val Thr Arg Thr Ile Asp Glu Lys Thr
```

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

385 390 395 400

Tyr Arg Val Ser Val Cys Cys Asn Asn Leu Asp Tyr Val Lys Phe Gly
405 410 415

Thr Tyr Ser Glu Gly Asn Asn Ser Asp Thr Ala His Gln Tyr Leu Val
420 425 430

Gly Glu Arg Thr Ala Val Ala Asp Leu Pro Thr Gly Thr Val Lys Tyr
435 440 445

Arg Gly Thr Trp Asp Gly Val Met Tyr Ser Lys Ser Gly Ser Ala Gly
450 455 460

Ala Glu Ser Pro Ser Asn Ser Glu Ser Gly Thr Arg Ser Leu Phe Asp
465 470 475 480

Val Asp Phe Val Asn Lys Lys Ile Asn Gly Lys Leu Ile Ala Asn Asp
485 490 495

Gly Val Glu Glu Arg Pro Met Leu Thr Leu Glu Gly Asn Leu Lys Gly
500 505 510

Asn Gly Phe Ala Gly Thr Ala Lys Thr Gly Asn Ser Gly Phe Asn Leu
515 520 525

Asp Pro Lys Ser Thr Asn Gly Gly Thr Val Val His Ile Asn Thr Gln
530 535 540

Phe Glu Gly Gly Phe Tyr Gly Pro Lys Ala Thr Glu Leu Gly Gly Ile
545 550 555 560

Val His Ser Ala Glu Thr Asp Lys Asp Arg Val Ser Ile Thr Phe Gly
565 570 575

Gly Lys Arg Gln Ile Glu Lys
580

<210> 225

<211> 559

<212> PRT

<213> Mannheimia haemolytica

<400> 225

Val Gln Ser Ala Lys Val Glu Ser Gln Thr Gln Thr Thr Pro Lys Lys
1 5 10 15

Pro Ser Leu Gln Asp Asp Asn Ser Asn Ala Arg Arg Thr Val Ser Ala
20 25 30

Ser Glu Thr Glu Ala Leu Leu Gln Pro Gly Phe Gly Phe Ser Ala Lys
35 40 45

```
Ile Pro Arg Arg Asn Leu Asn Pro Lys Gly Lys Glu Asp Val Ala Pro
    50                  55                  60

Ile Gly Asp Ile Thr Glu Ile Thr Gly Asp Leu Thr Lys Ile Pro His
65                  70                  75                  80

Glu Glu Glu Val Lys Lys Tyr Gly Ser Ser Asp Asp Gly Phe Ser His
                85                  90                  95

Thr His Asp Gly Asn His Lys Leu His Thr Arg Asp Phe Asn Phe Val
            100                 105                 110

Arg Ser Gly Tyr Val Leu His Ser Gly Ala Lys Pro Glu Ile Ile Arg
        115                 120                 125

Ser Asp Asn Ile Leu Arg Ile Gly Ala His Gly Tyr Val Tyr Tyr Leu
    130                 135                 140

Gly Ile Glu Pro Ala Lys Ala Ile Pro Thr Gln Lys Ala Thr Tyr Lys
145                 150                 155                 160

Gly Tyr Trp Asp Phe Thr Thr Asp Ala Arg Lys Gly Arg Asp Asn Lys
                165                 170                 175

Tyr Phe Ser Asn Ser Ala Gly Ile Asn Ile Gly Ala Ile Pro Glu Asn
            180                 185                 190

Ser His Asp Ile Asn Val Asp Asp Ser Thr Lys Pro Met Gly His Thr
        195                 200                 205

Gly Glu Phe Thr Ala Asp Phe Ala Asn Lys Thr Leu Thr Gly Thr Leu
    210                 215                 220

Val Arg Asn Gly Tyr Val Ser Arg Ile Lys Glu Gln Lys Ile Thr Pro
225                 230                 235                 240

Ile Tyr Asp Ile Asp Ala Lys Ile Lys Gly Asn Arg Phe Ser Gly Lys
                245                 250                 255

Ala Asn Ala Lys Asn Ala Asn Asp Pro Tyr Phe Gly Lys Ser Ser Thr
            260                 265                 270

Thr Leu Glu Gly Gly Phe Phe Gly Gly Glu Ala Gln Glu Leu Ala Gly
        275                 280                 285

Lys Phe Leu Ala Asp Asp Lys Ser Val Phe Val Val Phe Ala Gly Lys
    290                 295                 300

Arg Asp Ala Lys Glu Asn Asp Ser Glu Arg Thr Phe Asp Ala Phe Lys
305                 310                 315                 320

Ile Lys Leu Lys Asp Leu Asn Lys Ser Glu Met Asp Thr Phe Gly Asn
                325                 330                 335

Ala Thr His Leu Ile Ile Asn Asn Lys Gln Ile Pro Leu Ile Ala Glu
            340                 345                 350
```

```
Gly Lys Lys Ser Phe Ala Glu Met Lys Phe Asp Asp Leu Val Thr Arg
        355                 360                 365

Thr Ile Asp Gly Lys Thr Tyr Arg Val Ser Val Cys Cys Asn Asn Leu
    370                 375                 380

Asp Tyr Val Lys Phe Gly Ile Tyr Ser Glu Gly Asn Asn Asn Asn Ser
385                 390                 395                 400

Asp Thr Ala His Gln Tyr Leu Val Gly Glu Arg Thr Ala Val Ala Asp
                405                 410                 415

Leu Pro Thr Gly Thr Val Lys Tyr Arg Gly Thr Trp Asp Gly Val Met
            420                 425                 430

Tyr Ser Lys Ser Gly Ser Ala Gly Ala Glu Ser Pro Ser Asn Ser Glu
        435                 440                 445

Ser Gly Thr Arg Ser Leu Phe Asp Val Asp Phe Val Asn Lys Lys Ile
    450                 455                 460

Asn Gly Lys Leu Ile Ala Asn Asp Gly Val Glu Glu Arg Pro Met Leu
465                 470                 475                 480

Thr Leu Glu Gly Glu Leu Lys Gly Asn Gly Phe Ala Gly Thr Ala Lys
                485                 490                 495

Thr Gly Asp Ser Gly Phe Asn Leu Asp Pro Lys Ser Thr Asn Gly Gly
            500                 505                 510

Thr Val Val His Met Asn Ala Gln Phe Glu Gly Gly Phe Tyr Gly Pro
        515                 520                 525

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

Asp Lys Val Ser Ile Thr Phe Gly Gly Lys Arg Gln Ile Glu Lys
545                 550                 555
```

<210> 226

<211> 559

<212> PRT

<213> Mannheimia haemolytica

<400> 226

```
Val Gln Ser Ser Lys Ala Glu Ser His Thr Pro Asn Val Pro Gln Lys
1               5                   10                  15

Pro Ser Leu Gln Asp Asp Asn Ser Asn Ala Arg Arg Thr Val Asn Ser
            20                  25                  30

Thr Glu Ala Glu Ala Leu Leu Lys Pro Gly Phe Gly Phe Ser Ala Lys
        35                  40                  45

Ile Pro Arg Arg Asn Leu Gln Pro Phe Ala Lys Gly Gly Glu Glu Val
```

```
    50                  55                  60

Ala Pro Ile Gly Asp Ile Thr Glu Ile Thr Gly Asp Ile Thr Lys Ile
65                  70                  75                  80

Pro Tyr Glu Glu Glu Val Lys Ala Tyr Gly Arg Ser Asp Asp Gly Phe
                85                  90                  95

Ser His Thr His Asp Gly Lys His Lys Leu His Thr Arg Asp Phe Asn
            100                 105                 110

Phe Val Arg Ser Gly Tyr Val Leu His Ser Gly Ala Lys Pro Glu Arg
        115                 120                 125

Glu Ala Lys Asp Ile Phe Arg Ile Gly Ala His Gly Tyr Val Tyr Tyr
    130                 135                 140

Leu Gly Thr Glu Pro Ala Lys Ala Met Pro Ala Gln Lys Ala Thr Tyr
145                 150                 155                 160

Asn Gly Tyr Trp Asp Phe Thr Thr Asp Ala Arg Lys Gly Lys Asp Asn
                165                 170                 175

Lys Tyr Phe Asn Asp Ser Ala Ala Gly Ile Asn Ile Gly Ala Thr Pro
            180                 185                 190

Glu Asn Arg His Asp Val Asn Val Asp Asp Ala Thr Lys Pro Met Gly
        195                 200                 205

His Thr Gly Glu Phe Thr Ala Asp Phe Thr Asn Lys Thr Leu Thr Gly
    210                 215                 220

Thr Leu Val Ser Asn Gly Tyr Val Ser Arg Thr Thr Glu Gln Glu Ile
225                 230                 235                 240

Lys Pro Met Tyr Tyr Ile Asp Ala Lys Ile Lys Gly Asn Arg Phe Ala
                245                 250                 255

Gly Lys Ala Asn Ala Lys Asn Pro Asp Asp Pro Tyr Phe Gly Lys Ser
            260                 265                 270

Ser Thr Thr Leu Glu Gly Gly Phe Phe Gly Gly Gln Ala Gln Glu Leu
        275                 280                 285

Ala Gly Lys Phe Leu Ala Asp Asp Lys Ser Ile Phe Val Val Phe Ala
    290                 295                 300

Gly Lys Arg Asp Ala Lys Glu Asn Asp Ser Glu Ser Thr Phe Asp Ala
305                 310                 315                 320

Leu Lys Ile Asn Leu Lys Asp Leu Ser Lys Thr Glu Met Asp Thr Phe
                325                 330                 335

Gly Asn Ala Thr His Leu Ile Ile Asn Asn Gln Gln Ile Pro Leu Ile
            340                 345                 350
```

```
Ala Glu Gly Lys Asn Ser Phe Ser Glu Met Lys Phe Asp Asp Val Val
        355                 360                 365

Thr Arg Thr Ile Asn Gly Lys Thr Tyr Arg Ile Ser Val Cys Cys Asn
    370                 375                 380

Asn Leu Asp Tyr Val Lys Phe Gly Thr Tyr Asn Val Glu Asn Asp Asn
385                 390                 395                 400

Asp Ser Ala His Gln Tyr Leu Val Gly Glu Arg Thr Ala Val Met Asp
                405                 410                 415

Leu Pro Ser Gly Met Val Gln Tyr Arg Gly Thr Trp Asn Gly Ile Ile
            420                 425                 430

His Ser Lys Ser Gly Pro Val Gly Ala Glu Ser Pro Ser Asn Ser Glu
        435                 440                 445

Ser Gly Thr Arg Ser Leu Phe Asp Val Asp Phe Ala Asn Lys Lys Ile
    450                 455                 460

Asn Gly Lys Leu Ile Ala Asn Asp Gly Val Glu Glu Arg Pro Met Leu
465                 470                 475                 480

Thr Leu Glu Gly Glu Val Lys Ala Asn Gly Phe Ala Gly Thr Ala Lys
                485                 490                 495

Thr Ser Asp Ser Gly Phe Asn Leu Asp Pro Lys Ser Thr Asn Gly Gly
            500                 505                 510

Thr Val Val His Ile Asn Thr Gln Phe Glu Gly Gly Phe Tyr Gly Pro
        515                 520                 525

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

Asp Lys Val Ser Ile Met Phe Gly Gly Lys Arg Gln Ile Glu Lys
545                 550                 555
```

<210> 227

<211> 588

<212> PRT

<213> Mannheimia haemolytica

<400> 227

```
Met Phe Lys Ile Lys Asn Ser Val Ile Leu Leu Asn Ala Val Leu Leu
1               5                   10                  15

Ser Ala Cys Thr Ser Asn Gly Gly Ser Phe Asp Thr Asn Ser Val Lys
            20                  25                  30

Ala Ser Ser Ser Tyr Ser Ser Ser Ser Lys Asp Ser Thr Ala Gln Pro
        35                  40                  45

Lys Ser Glu Arg Arg Thr Ile Ser Ser Thr Glu Ser Leu Ala Gln Pro
    50                  55                  60
```

```
Ser Leu Gly Phe Gln Thr Lys Ile Pro Arg Arg Asn Phe Phe Gly Gly
65                  70                  75                  80

Thr Gly Glu Glu Asn Gly Ala Ile Gly Glu Ile Thr Pro Ile Val Gly
                85                  90                  95

Glu Pro Gly Lys Pro Leu Ser Leu Glu Glu Glu Met Lys Lys Leu Glu
            100                 105                 110

Glu Glu Val Lys Lys Phe Gly Tyr Asp Glu Asp Asp Ile Ile His Thr
        115                 120                 125

His Asp Gly Lys Lys Leu His Arg Lys Arg Glu Met Lys Phe Val Arg
    130                 135                 140

Ser Gly Tyr Phe Ile His Leu Gly Ala Ala Ala Glu Thr Lys Arg Glu
145                 150                 155                 160

Glu Pro Arg Leu Leu Lys Thr Gly Pro Thr Gly Tyr Val Tyr Tyr Leu
                165                 170                 175

Gly Thr Gln Pro Ser Lys Ala Phe Pro Thr Gln Val Ala Thr Tyr Glu
            180                 185                 190

Gly Thr Trp Asp Phe Thr Thr Asn Ala Ser Thr Lys Asn Lys Ser Lys
        195                 200                 205

Tyr Phe Glu Gly Gly Ala Ala Gly Thr Asn Val Gly Ala Thr Pro Glu
    210                 215                 220

Asn Asn Gln Ala Asn Thr Glu Val Glu Gly Asn Pro Ile Gly His Ser
225                 230                 235                 240

Ser Lys Phe Glu Val Asn Phe Ser Asp Lys Thr Leu Lys Gly Thr Leu
                245                 250                 255

Thr Lys Asn Gly Tyr Val Asn Leu Arg Lys Lys Asp Lys Gln Glu Ile
            260                 265                 270

Thr Asp His Tyr Lys Ile Glu Ala Asn Ile His Gly Asn Arg Phe Asn
        275                 280                 285

Gly Lys Ala Glu Ala Leu Lys Thr Asp Asp Pro Tyr Phe Gly Lys Asp
    290                 295                 300

Ser Asn Thr Val Glu Gly Gly Phe Tyr Gly Asp Lys Ala Gln Glu Leu
305                 310                 315                 320

Ala Gly Lys Phe Leu Ala Asp Asp Lys Ser Ile Phe Val Val Phe Ala
                325                 330                 335

Gly Lys Arg Asp Glu Lys Gly Glu Asp Lys Val Glu Lys Lys Phe Asp
            340                 345                 350

Ser Val Gln Val Ser Leu Lys Asp Leu Ala Lys Ser Asp Met Asp Thr
```

```
        355                 360                 365

Phe Gly Leu Ala Thr His Leu Val Ile Asp Gly Val Gln Ile Ala Leu
    370                 375                 380

Leu Pro Glu Gly Lys Thr Arg Phe Ala Asp Met Asp Phe Tyr Gln Val
385                 390                 395                 400

Leu Thr Lys Asn Ile Asn Gly Lys Asp Tyr Lys Ile Thr Val Cys Cys
                405                 410                 415

Asn Asn Leu Asp Tyr Val Lys Phe Gly Thr Phe Glu Gln Lys Gly Lys
            420                 425                 430

Asp Gly His Gln Tyr Leu Val Gly Glu Arg Thr Ala Val Ala Asp Leu
        435                 440                 445

Pro Lys Glu Ala Arg Ile Tyr Arg Tyr Thr Gly Thr Trp Asn Gly Ser
    450                 455                 460

Ile Arg Ser Lys Asp Glu Arg Val Gly Gly Asp Ser Pro Ser Asp Lys
465                 470                 475                 480

Ala His Gly Thr Arg Ser Ile Phe Asn Val Asn Phe Ala Asp Lys Lys
                485                 490                 495

Ile Glu Gly Lys Leu Ile Ala Asn Asp Gly Leu Glu Thr Asn Pro Met
            500                 505                 510

Leu Thr Leu Asp Gly Lys Ile Glu Gly Asn Gly Phe Ser Gly Thr Ala
        515                 520                 525

Lys Thr Gly Glu Lys Gly Phe Asn Ile Asp Asn Lys Ser Thr Ala Gly
    530                 535                 540

Gly Thr Asp Val His Leu Asn Ala Lys Phe Glu Gly Gly Phe Tyr Gly
545                 550                 555                 560

Pro Gln Ala Ala Glu Leu Gly Gly Ile Val His Ser Ala Glu Thr Asn
                565                 570                 575

Lys Asp Lys Val Ser Ile Thr Phe Gly Gly Lys Arg
            580                 585
```

<210> 228

<211> 555

<212> PRT

<213> Bibersteinia trehalosi

<400> 228

```
Val Gln Ser Val Lys Val Glu Ser Asn Lys Pro Asp Ser Pro Lys Pro
1               5                   10                  15

Ser Leu Gln Asp Asp Asn Ser Ser Ala Arg Arg Thr Ile Asn Asn Thr
```

```
            20                  25                  30

Glu Ala Thr Ala Leu Leu Gln Pro Gly Phe Gly Phe Ser Ala Lys Ile
        35                  40                  45

Pro Arg Arg Asn Gln Leu Pro Gln Ala Asn Glu Asn Ala Ala Pro Ile
    50                  55                  60

Gly Glu Ile Thr Pro Ile Ala Gly Asp Leu Thr Lys Ile Pro Tyr Glu
65                  70                  75                  80

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

His Asp Gly His Asn Gly His Asn Thr Arg Asp Phe Lys Phe Val Arg
            100                 105                 110

Ser Gly Tyr Val Leu His Ser Gly Ala Lys Pro Glu Ile Lys His Lys
        115                 120                 125

Glu Val Leu Arg Thr Gly Ala His Gly Tyr Val Tyr Tyr Leu Gly Thr
    130                 135                 140

His Pro Ala Lys Ala Met Pro Ala Gln Lys Ala Ile Tyr Lys Gly Tyr
145                 150                 155                 160

Trp Asp Phe Thr Thr Asp Ala Arg Lys Asp Arg Asp Ser Gln Tyr Phe
                165                 170                 175

Ser Asn Ser Ala Gly Val Asn Ile Gly Ala Thr Pro Glu Asn Ser Arg
            180                 185                 190

Asp Val Asn Leu Asp Asp Ala Glu Lys Pro Met Gly His Thr Gly Glu
        195                 200                 205

Phe Thr Ala Asp Phe Ser Asn Lys Thr Leu Thr Gly Thr Leu Val Arg
    210                 215                 220

Asn Gly Tyr Val Lys Pro Arg Thr Asn Glu Gln Lys Ile Thr Pro Leu
225                 230                 235                 240

Tyr Asp Ile Asn Ala Thr Ile Gln Gly Asn Arg Phe Ser Gly Lys Ala
                245                 250                 255

Asn Ala Arg Asn Thr Glu Asp Pro Tyr Phe Gly Lys Asp Ser Ser Thr
            260                 265                 270

Leu Glu Gly Gly Phe Phe Gly Asp Asn Thr Gln Glu Leu Ala Gly Lys
        275                 280                 285

Phe Leu Ala Asp Asp Lys Ser Ile Phe Val Val Phe Ala Gly Lys Arg
    290                 295                 300

Asp Ala Gln Glu Asn Asp Ser Glu Arg Ala Phe Asp Ala Leu Lys Val
305                 310                 315                 320
```

```
Ser Leu Lys Asp Leu Ser Lys Ser Glu Met Asp Thr Phe Gly Asn Ala
                325                 330                 335

Thr His Leu Leu Ile Asn Asn Thr Gln Ile Pro Leu Ile Ala Glu Gly
            340                 345                 350

Lys Lys Ser Phe Ala Glu Met Lys Phe Asp Asp Leu Val Met Pro Thr
        355                 360                 365

Val Gly Gly Lys Thr Tyr Arg Ile Ser Val Cys Cys Asn Asn Leu Asp
    370                 375                 380

Tyr Val Lys Phe Gly Thr Tyr Ser Glu Glu Asn Asp Lys Asp Ser Ser
385                 390                 395                 400

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

Gly Lys Ala Gln Tyr Arg Gly Thr Trp Asn Gly Ile Met Arg Ser Glu
            420                 425                 430

Ala Gly Ser Ala Gly Ala Glu Ser Pro Ser Asn Ser Glu Ser Gly Thr
        435                 440                 445

Arg Ser Leu Phe Asp Val Asp Phe Ala Asn Lys Lys Ile Asn Gly Lys
    450                 455                 460

Leu Ile Ala Asn Asp Gly Val Glu Glu Arg Pro Met Leu Thr Leu Glu
465                 470                 475                 480

Gly Glu Ile Lys Ala Asn Gly Phe Ala Gly Thr Ala Lys Thr Ser Asp
                485                 490                 495

Ser Gly Phe Asn Leu Asp Pro Lys Ser Thr Trp Gly Gly Thr Val Ile
            500                 505                 510

His Val Asp Ser Gln Phe Glu Gly Ala Phe Tyr Gly Lys Asn Ala Leu
        515                 520                 525

Glu Leu Gly Gly Ile Val His Asp Ser Asn Ser Lys Asp Lys Val Ser
    530                 535                 540

Ile Thr Phe Ala Gly Lys Arg Gln Ile Ala Lys
545                 550                 555
```

<210> 229

<211> 342

<212> PRT

<213> Moraxella catarrhalis

<400> 229

```
Glu Pro Ala Met Gly Tyr Gly Met Ala Leu Ser Lys Ile Asn Leu His
1               5                   10                  15

Asn Arg Gln Asp Thr Pro Leu Asp Glu Lys Asn Ile Ile Thr Leu Asp
            20                  25                  30
```

```
Gly Lys Lys Gln Val Ala Glu Gly Lys Lys Ser Pro Leu Pro Phe Ser
        35                  40                  45

Leu Asp Val Glu Asn Lys Leu Leu Asp Gly Tyr Ile Ala Lys Met Asn
    50                  55                  60

Val Ala Asp Lys Asn Ala Ile Gly Asp Arg Ile Lys Lys Gly Asn Lys
65                  70                  75                  80

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

Lys Ser His Glu Phe Gln Gln Val Leu Ser Ser Leu Glu Asn Lys Ile
            100                 105                 110

Phe His Ser Asn Asp Gly Thr Thr Lys Ala Thr Thr Arg Asp Leu Lys
        115                 120                 125

Tyr Val Asp Tyr Gly Tyr Tyr Leu Ala Asn Asp Gly Asn Tyr Leu Thr
    130                 135                 140

Val Lys Thr Asp Lys Leu Trp Asn Leu Gly Pro Val Gly Gly Val Phe
145                 150                 155                 160

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

Lys Tyr Lys Gly His Trp Asp Phe Met Thr Asp Val Ala Asn Arg Arg
            180                 185                 190

Asn Arg Phe Ser Glu Val Lys Glu Asn Ser Gln Ala Gly Trp Tyr Tyr
        195                 200                 205

Gly Ala Ser Ser Lys Asp Glu Tyr Asn Arg Leu Leu Thr Lys Glu Asp
    210                 215                 220

Ser Ala Pro Asp Gly His Ser Gly Glu Tyr Gly His Ser Ser Glu Phe
225                 230                 235                 240

Thr Val Asn Phe Lys Glu Lys Lys Leu Thr Gly Lys Leu Phe Ser Asn
                245                 250                 255

Leu Gln Asp Arg His Lys Gly Asn Val Thr Lys Thr Glu Arg Tyr Asp
            260                 265                 270

Ile Asp Ala Asn Ile His Gly Asn Arg Phe Arg Gly Ser Ala Thr Ala
        275                 280                 285

Ser Asn Lys Asn Asp Thr Ser Lys His Pro Phe Thr Ser Asp Ala Asn
    290                 295                 300

Asn Arg Leu Glu Gly Gly Phe Tyr Gly Pro Lys Gly Glu Glu Leu Ala
305                 310                 315                 320

Gly Lys Phe Leu Thr Asn Asp Asn Lys Leu Phe Gly Val Phe Gly Ala
```

```
                325                 330                 335

Lys Arg Glu Ser Lys Ala
            340
```

<210> 230

<211> 264

<212> PRT

<213> Moraxella catarrhalis

<400> 230

```
Glu Glu Lys Thr Glu Ala Ile Leu Asp Ala Tyr Ala Leu Gly Thr Phe
1               5                  10                  15

Asn Thr Ser Asn Ala Thr Thr Phe Thr Pro Phe Thr Glu Lys Gln Leu
            20                  25                  30

Asp Asn Phe Gly Asn Ala Lys Lys Leu Val Leu Gly Ser Thr Val Ile
        35                  40                  45

Asp Leu Val Pro Thr Asp Ala Thr Lys Asn Glu Phe Thr Lys Asp Lys
    50                  55                  60

Pro Glu Ser Ala Thr Asn Glu Ala Gly Glu Thr Leu Met Val Asn Asp
65                  70                  75                  80

Glu Val Ser Val Lys Thr Tyr Gly Lys Asn Phe Glu Tyr Leu Lys Phe
                85                  90                  95

Gly Glu Leu Ser Ile Gly Gly Ser His Ser Val Phe Leu Gln Gly Glu
            100                 105                 110

Arg Thr Ala Thr Thr Gly Glu Lys Ala Val Pro Thr Thr Gly Thr Ala
        115                 120                 125

Lys Tyr Leu Gly Asn Trp Val Gly Tyr Ile Thr Gly Lys Asp Thr Gly
    130                 135                 140

Thr Gly Thr Gly Lys Ser Phe Thr Asp Ala Gln Asp Val Ala Asp Phe
145                 150                 155                 160

Asp Ile Asp Phe Gly Asn Lys Ser Val Ser Gly Lys Leu Ile Thr Lys
                165                 170                 175

Gly Arg Gln Asp Pro Val Phe Ser Ile Thr Gly Gln Ile Ala Gly Asn
            180                 185                 190

Gly Trp Thr Gly Thr Ala Ser Thr Thr Lys Ala Asp Ala Gly Gly Tyr
        195                 200                 205

Lys Ile Asp Ser Ser Ser Thr Gly Lys Ser Ile Ala Ile Lys Asp Ala
    210                 215                 220

Asn Val Thr Gly Gly Phe Tyr Gly Pro Asn Ala Asn Glu Met Gly Gly
225                 230                 235                 240
```

```
Ser Phe Thr His Asn Ala Asp Asp Ser Lys Ala Ser Val Val Phe Gly
                245                 250                 255

Thr Lys Arg Gln Gln Glu Val Lys
            260
```

<210> 231

<211> 284

<212> PRT

<213> Mannheimia haemolytica

<400> 231

```
Thr Val Ser Ala Ser Glu Thr Glu Ala Leu Leu Gln Pro Gly Phe Gly
1               5                   10                  15

Phe Ser Ala Lys Ile Pro Arg Arg Asn Leu Leu Pro Gln Gly Lys Glu
            20                  25                  30

Asp Val Ala Pro Ile Gly Asp Ile Lys Glu Ile Thr Gly Asp Leu Pro
        35                  40                  45

Lys Ile Pro Tyr Glu Glu Glu Val Lys Ala Cys Gly Ser Ser Ala Asp
    50                  55                  60

Gly Phe Ser His Thr His Asp Arg Asn His Lys Leu Tyr Thr Arg Asp
65                  70                  75                  80

Phe Asn Phe Val Arg Ser Gly Tyr Val Val His Ser Gly Pro Lys Pro
                85                  90                  95

Glu Ile Lys Pro Lys Glu Ile Leu Arg Thr Gly Ala His Gly Tyr Val
            100                 105                 110

Tyr Tyr Leu Gly Ile Glu Pro Pro Lys Ala Ile Pro Thr Gln Lys Leu
        115                 120                 125

Thr Tyr Lys Gly Tyr Trp Asp Phe Thr Thr Tyr Ala Ala Lys Gly Arg
    130                 135                 140

Asp Ser Asn Ile Phe Leu Ile Pro Ala Gly Ile Asn Ser Gly Ala Ile
145                 150                 155                 160

Pro Glu Asn Ser His Asp Ile Asn Val Asp Asp Ser Glu Lys Pro Met
                165                 170                 175

Gly His Thr Gly Glu Phe Thr Ala Asp Phe Ala Asn Lys Thr Leu Thr
            180                 185                 190

Gly Thr Leu Val Arg Asn Gly Tyr Val Ser Arg Ser Lys Glu Gln Lys
        195                 200                 205

Ile Thr Thr Ile Tyr Asp Ile Asp Ala Lys Ile Lys Gly Asn Arg Phe
    210                 215                 220
```

```
Ser Gly Lys Ala Asn Pro Lys Lys Pro Met Ile Leu Ile Phe Gly Lys
225                 230                 235                 240

Ser Ser Thr Thr Leu Glu Gly Gly Phe Phe Gly Gly Glu Ala Gln Glu
                245                 250                 255

Leu Ala Gly Lys Phe Leu Ala Asp Asp Lys Ser Val Phe Val Val Phe
            260                 265                 270

Ala Gly Thr Arg Asp Ala Lys Lys Asp Asp Ser Glu
        275                 280
```

<210> 232

<211> 235

<212> PRT

<213> Mannheimia haemolytica

<400> 232

```
Ser Ala Phe Asp Ala Phe Pro Ile Lys Leu Lys Asp Leu Asn Lys Ser
1               5                   10                  15

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

Gln Ile Pro Leu Ile Ala Glu Ala Thr Lys Ser Phe Ala Glu Met Lys
        35                  40                  45

Phe Asp Thr Tyr Arg Val Ser Val Cys Cys Asn Asn Leu Asp Tyr Val
    50                  55                  60

Lys Phe Gly Ile Tyr Ser Glu Gly Asn Asn Ser Asp Thr Ala Leu Gln
65                  70                  75                  80

Glu Tyr Leu Val Gly Glu Arg Thr Ala Leu Ala Asp Leu Pro Thr Gly
                85                  90                  95

Thr Val Lys Tyr Arg Gly Thr Trp Asp Gly Val Met Tyr Ser Lys Ser
            100                 105                 110

Gly Ser Ala Gly Val Glu Ser Pro Ser Asn Ser Glu Ser Gly Thr Arg
        115                 120                 125

Ser Leu Phe Asp Val Asp Phe Val Asn Lys Lys Ile Asn Gly Lys Leu
    130                 135                 140

Ile Ala Asn Asp Gly Val Glu Glu Arg Pro Met Leu Thr Leu Glu Gly
145                 150                 155                 160

Asn Leu Lys Gly Asn Gly Phe Gly Gly Thr Ala Lys Thr Gly Asn Ser
                165                 170                 175

Gly Phe Asn Leu Asp Pro Lys Ser Thr Asn Gly Gly Thr Val Gly His
            180                 185                 190

Ile Asn Thr Gln Phe Glu Gly Gly Phe Tyr Gly Pro Lys Ala Thr Glu
        195                 200                 205
```

```
        ---                 ---                 ---

Leu Gly Gly Ile Val Gln Asn Thr Glu Thr Asp Lys Asp Arg Val Ser
    210                 215                 220

Ile Thr Phe Gly Gly Lys Arg Gln Ile Glu Lys
225                 230                 235
```

<210> 233

<211> 283

<212> PRT

<213> Mannheimia haemolytica

<400> 233

```
Thr Val Ser Ala Ser Glu Thr Glu Ala Leu Leu Gln Pro Gly Phe Gly
1               5                   10                  15

Phe Ser Ala Lys Ile Pro Arg Arg Asn Leu Asn Pro Lys Gly Lys Glu
            20                  25                  30

Asp Val Ala Pro Ile Gly Asp Ile Thr Glu Ile Thr Gly Asp Leu Thr
        35                  40                  45

Lys Ile Pro His Glu Glu Glu Val Lys Lys Tyr Gly Ser Ser Asp Asp
    50                  55                  60

Gly Phe Ser His Thr His Asp Gly Asn His Lys Leu His Thr Arg Asp
65                  70                  75                  80

Phe Asn Phe Val Arg Ser Gly Tyr Val Leu His Ser Gly Ala Lys Pro
                85                  90                  95

Glu Ile Ile Arg Ser Asp Asn Ile Leu Arg Ile Gly Ala His Gly Tyr
            100                 105                 110

Val Tyr Tyr Leu Gly Ile Glu Pro Ala Lys Ala Ile Pro Thr Gln Lys
        115                 120                 125

Ala Thr Tyr Lys Gly Tyr Trp Asp Phe Thr Asn Asp Ala Arg Lys Gly
    130                 135                 140

Arg Asp Ser Lys Tyr Phe Ser Asn Ser Ala Gly Ile Asn Ile Gly Ala
145                 150                 155                 160

Ile Pro Glu Asn Ser His Asp Ile Asn Val Asp Asp Ser Thr Lys Pro
                165                 170                 175

Met Gly His Thr Gly Glu Phe Thr Ala Asp Phe Ala Asn Lys Thr Leu
            180                 185                 190

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

Lys Ile Thr Pro Ile Tyr Asp Ile Asp Ala Lys Ile Lys Gly Asn Arg
    210                 215                 220
```

```
Phe Ser Gly Lys Ala Asn Ala Lys Asn Ala Asn Asp Pro Tyr Phe Gly
225                 230                 235                 240

Lys Ser Ser Thr Thr Leu Glu Gly Gly Phe Phe Gly Gly Glu Ala Gln
                245                 250                 255

Glu Leu Pro Val Ile Leu Ala Asp Asp Lys Ser Val Phe Val Val Phe
            260                 265                 270

Ala Gly Lys Arg Asp Ala Lys Glu Asn Asp Gly
        275                 280
```

<210> 234

<211> 247

<212> PRT

<213> Mannheimia haemolytica

<400> 234

```
Glu Arg Thr Phe Asp Ala Phe Lys Ile Lys Leu Lys Asp Leu Asn Lys
1               5                   10                  15

Ser Glu Met Asp Thr Phe Gly Asn Ala Thr His Leu Ile Ile Asn Asn
            20                  25                  30

Lys Gln Ile Pro Leu Ile Ala Glu Gly Lys Lys Ser Phe Ala Glu Met
        35                  40                  45

Lys Phe Asp Asp Leu Val Thr Arg Thr Ile Asp Gly Lys Thr Tyr Arg
    50                  55                  60

Val Ser Val Cys Cys Asn Asn Leu Asp Tyr Val Lys Phe Gly Ile Tyr
65                  70                  75                  80

Ser Glu Gly Asn Asn Asn Asn Ser Asp Thr Ala His Gln Tyr Leu Val
                85                  90                  95

Gly Glu Arg Thr Ala Val Ala Asp Leu Pro Thr Gly Thr Val Lys Tyr
            100                 105                 110

Arg Gly Thr Trp Asp Gly Val Met Tyr Ser Lys Ser Gly Ser Ala Gly
        115                 120                 125

Ala Glu Ser Pro Ser Asn Ser Glu Ser Gly Thr Arg Ser Leu Phe Asp
    130                 135                 140

Val Asp Phe Val Asn Lys Lys Ile Asn Gly Lys Leu Ile Ala Asn Asp
145                 150                 155                 160

Gly Val Glu Glu Arg Pro Met Leu Thr Leu Glu Gly Glu Leu Lys Gly
                165                 170                 175

Asn Gly Phe Ala Gly Thr Ala Lys Thr Gly Asp Ser Gly Phe Asn Leu
            180                 185                 190

Asp Pro Lys Ser Thr Asn Gly Gly Thr Val Val His Met Asn Ala Gln
```

```
        195                 200                 205

Phe Glu Gly Gly Phe Tyr Gly Pro Lys Ala Thr Glu Leu Gly Gly Ile
    210                 215                 220

Val His Ser Ala Glu Thr Asp Lys Asp Lys Val Ser Ile Thr Phe Gly
225                 230                 235                 240

Gly Lys Arg Gln Ile Glu Lys
                245
```

<210> 235

<211> 330

<212> PRT

<213> Neisseria meningitidis

<400> 235

```
Thr Lys Asp Lys Pro Ala Asn Gly Asn Thr Ala Glu Ala Ser Gly Gly
1               5                   10                  15

Ala Gly Ala Ala Thr Met Pro Ser Glu Thr Arg Leu Thr Thr Val Leu
            20                  25                  30

Asp Ala Val Glu Leu Lys Ser Asp Gly Lys Lys Val Glu Asn Leu Asp
        35                  40                  45

Asn Phe Ser Asp Ala Thr Arg Leu Val Val Asp Gly Ile Met Ile Pro
    50                  55                  60

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

Lys Asn Gly Gly Thr Asp Phe Thr Tyr Thr Thr Thr Tyr Thr Pro Glu
                85                  90                  95

Ser Asp Lys Lys Asp Thr Gln Ala Gln Thr Gly Ala Gly Gly Met Gln
            100                 105                 110

Thr Ala Ser Gly Ala Ala Gly Val Asn Gly Gly Gln Ala Gly Thr Lys
        115                 120                 125

Thr Tyr Lys Val Lys Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr
    130                 135                 140

Gly Leu Leu Thr Arg Glu Asn Ser Asn Ser Val Met Gln Thr Val Arg
145                 150                 155                 160

Asn Ser Ser Gln Ala Ala Ala Ala Gln Thr Ala Gln Gly Ala Gln Ser
                165                 170                 175

Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Lys Asp
            180                 185                 190

Glu Asn Val Val Tyr Leu Gly Thr Trp Tyr Gly His Ile Ala Thr Asn
        195                 200                 205
```

```
Gly Thr Ser Trp Thr Arg Glu Ala Ser Asn Gln Glu Asn Gly Asn Arg
    210                 215                 220

Ala Lys Phe Asp Val Asn Phe Lys Tyr Lys Lys Ile Thr Gly Thr Leu
225                 230                 235                 240

Thr Ala Glu Asn Arg Ser Glu Ala Thr Phe Thr Ile Asp Gly Met Ile
                245                 250                 255

Gln Gly Asn Gly Phe Lys Gly Thr Ala Lys Thr Gly Asn Asp Gly Phe
            260                 265                 270

Ala Pro Asp Gln Asn Asn Ser Thr Val Thr His Lys Val His Ile Ala
        275                 280                 285

Asn Ala Glu Val Gln Gly Gly Phe Tyr Gly Pro Asn Ala Glu Glu Leu
    290                 295                 300

Gly Gly Trp Phe Ala Tyr Pro Gly Asn Gly Gln Ala Lys Asn Ala Thr

305                 310                 315                 320

Ala Val Ser Gly Asn Gly Asn Ser Ala Gly
                325                 330
```

<210> 236

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 236

```
Thr Gln Asp Lys Pro Glu Asn Gly Ala Ala Ala Ser Gly Gly Thr Asp
1               5                   10                  15

Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys
            20                  25                  30

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

Val Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
    50                  55                  60

Gly Ile Met Ile Pro Leu Leu Pro Lys Asp Ser Glu Ser Gly Asn Thr
65                  70                  75                  80

Gln Ala Asp Lys Gly Lys Asn Gly Gly Thr Glu Phe Thr Arg Lys Phe
                85                  90                  95

Glu His Thr Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln
            100                 105                 110

Thr Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly
        115                 120                 125
```

```
Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
    130                 135                 140

Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln
145                 150                 155                 160

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

Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro
            180                 185                 190

Thr Asp Gln Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly Tyr Ile Ala

        195                 200                 205

Asn Asp Lys Ser Thr Ser Trp Ser Gly Asn Ala Ser Asp Arg Glu Gly
    210                 215                 220

Gly Asn Arg Ala Asp Phe Thr Val Asn Phe Gly Glu Lys Lys Ile Thr
225                 230                 235                 240

Gly Thr Leu Thr Ala Glu Asn Arg Gln Ala Ala Thr Phe Thr Ile Glu
                245                 250                 255

Gly Asp Ile Glu Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr Asp Asn
            260                 265                 270

Leu Gly Phe Asp Leu Asp Gln Ser Asp Asn Thr Arg Thr Pro Lys Ala
        275                 280                 285

Tyr Ile Thr Asp Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Arg Ala
    290                 295                 300

Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Lys
305                 310                 315                 320

Asn Ala Pro Val Ala Ser Gly Asn Gly Asn Ser Ala Ser Ser Ala Thr
                325                 330                 335

Val Val Phe Gly
            340
```

<210> 237

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 237

```
Thr Gln Asp Lys Ala Ala Asn Gly Asn Thr Ala Ala Ala Ser Gly Gly
1               5                   10                  15

Thr Asp Ala Ala Ala Ser Gly Gly Ala Ala Gly Thr Ser Ser Glu Asn
            20                  25                  30
```

```
Ser Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp
        35                  40                  45

Lys Lys Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
    50                  55                  60

Val Asp Gly Ile Met Ile Pro Leu Leu Pro Lys Asp Ser Glu Ile Gly

65                  70                  75                  80

Ser Asn Gln Ala Asp Lys Gly Lys Asn Gly Gly Thr Asp Phe Thr Arg
                85                  90                  95

Lys Phe Asp His Thr Pro Lys Ser Asp Glu Lys Asp Thr Gln Ala Gln
            100                 105                 110

Thr Gly Ala Gly Gly Ala Gln Thr Ala Ser Gly Thr Glu Gly Val Asn
        115                 120                 125

Gly Gly Gln Ala Gly Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser
    130                 135                 140

Asn Leu Asn Tyr Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys
145                 150                 155                 160

Ser Ala Met Gln Ala Gly Gly Asn Ser Ser Gln Ala Asp Ala Lys Thr
                165                 170                 175

Glu Gln Val Glu Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu
            180                 185                 190

Lys Glu Ile Pro Lys Glu Gln Gln Asp Ile Val Tyr Arg Gly Ser Trp
        195                 200                 205

Tyr Gly His Ile Ala Ser Ser Thr Ser Trp Ser Gly Asn Ala Ser Asp
    210                 215                 220

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

Lys Ile Asn Gly Thr Leu Thr Ala Glu Asn Arg Gln Gln Ala Thr Phe
                245                 250                 255

Thr Ile Glu Gly Asp Ile Lys Asp Asn Gly Phe Glu Gly Thr Ala Lys
            260                 265                 270

Thr Ala Glu Leu Gly Phe Asp Leu Asp Gln Ser Asp Asn Thr Arg Thr
        275                 280                 285

Pro Lys Ala Tyr Ile Thr Asn Ala Lys Val Gln Gly Gly Phe Tyr Gly
    290                 295                 300

Pro Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys
305                 310                 315                 320
```

```
Gln Ala Gln Pro Pro Ala Ser Gly Ser Gly Thr Ser Ala Ala Asn Ser
                325                 330                 335

Ala Thr Val Val
            340
```

<210> 238

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 238

```
Thr Lys Asp Lys Asp Ala Asn Gly Asn Thr Glu Ala Ala Ser Gly Gly
1               5                   10                  15

Thr Gly Ser Ala Ala Ser Gly Gly Val Ala Asp Met Pro Ser Glu Asn
            20                  25                  30

Gly Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp
        35                  40                  45

Lys Lys Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
    50                  55                  60

Val Asp Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly
65                  70                  75                  80

Asn Asn Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg
                85                  90                  95

Lys Phe Asp His Thr Pro Asn Ser Asp Glu Lys Asp Thr Gln Ala Gly
            100                 105                 110

Thr Ala Glu Asn Gly Asn Pro Ala Ala Ser Asn Thr Ala Gly Asp Ala
        115                 120                 125

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

Asn Tyr Leu Lys Tyr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn Thr
145                 150                 155                 160

Gly Glu Gly Gly Asn Gly Ser Pro Thr Ala Ala Gln Thr Asp Ala Gln
                165                 170                 175

Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Ser
            180                 185                 190

Glu Gln Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Asn
        195                 200                 205

Asp Thr Ser Trp Ser Gly Asn Ala Ser Asp Arg Glu Gly Gly Asn Arg
    210                 215                 220

Ala Asp Phe Thr Val Asn Phe Gly Thr Lys Lys Ile Asn Gly Thr Leu
225                 230                 235                 240
```

```
225                 230                 235                 240

Thr Ala Glu Asn Arg Gln Gln Ala Thr Phe Thr Ile Glu Gly Asp Ile
                245                 250                 255

Lys Asp Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala Asp Leu Gly Phe
            260                 265                 270

Asp Leu Asp Gln Ser Asn Thr Thr Gly Thr Pro Lys Ala Tyr Ile Thr
        275                 280                 285

Asn Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Asp Glu Leu
    290                 295                 300

Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Glu Asn Ala Thr
305                 310                 315                 320

Val Ala Ser Gly Asn Gly Asn Ser Ala Ser Ser Ala Thr Val Val Phe
                325                 330                 335

Gly Ala Lys Arg
            340
```

<210> 239

<211> 350

<212> PRT

<213> Neisseria meningitidis

<400> 239

```
Thr Lys Asp Lys Asp Ala Asn Gly Asn Thr Glu Ala Ala Ser Gly Gly
1               5                   10                  15

Thr Gly Ala Ala Ala Ser Gly Gly Ala Ala Ala Met Pro Ser Glu Asn
            20                  25                  30

Gly Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Arg Gly Gly
        35                  40                  45

Lys Ala Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
    50                  55                  60

Val Asp Gly Ile Met Ile Pro Leu Leu Pro Lys Asp Ser Glu Ser Gly
65                  70                  75                  80

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

Gly Thr Asp Phe Thr Tyr Lys Thr Thr Tyr Thr Pro Lys Ser Asp Glu
            100                 105                 110

Lys Asp Thr Gln Ala Gly Thr Pro Thr Asn Gly Ala Gln Thr Ala Ser
        115                 120                 125

Asn Thr Ala Gly Asp Thr Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu
    130                 135                 140
```

```
Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr Gly Met Leu Thr Arg
145                 150                 155                 160

Lys Asn Ser Lys Ser Ala Met Gln Ala Gly Glu Ser Ser Ser Gln Ala
                165                 170                 175

Asp Ala Lys Thr Glu Gln Val Glu Gln Ser Met Phe Leu Gln Gly Glu
            180                 185                 190

Arg Thr Asp Glu Lys Glu Ile Pro Lys Glu Gln Asn Val Val Tyr Arg
        195                 200                 205

Gly Ser Trp Tyr Gly His Ile Ala Asn Asp Thr Ser Trp Ser Gly Asn
    210                 215                 220

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

Ala Asp Lys Lys Ile Thr Gly Lys Leu Thr Ala Glu Asn Arg Gln Ala
                245                 250                 255

Gln Thr Phe Thr Ile Glu Gly Met Ile Gln Gly Asn Gly Phe Glu Gly
            260                 265                 270

Thr Ala Lys Thr Ala Glu Ser Gly Phe Asp Leu Asp Gln Lys Asn Thr
        275                 280                 285

Thr Arg Thr Pro Lys Ala Tyr Ile Thr Asp Ala Lys Val Lys Gly Gly
    290                 295                 300

Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro
305                 310                 315                 320

Gly Asp Lys Gln Thr Lys Asn Ala Thr Ala Thr Ser Ser Asp Gly Lys
                325                 330                 335

Ser Ala Ser Ser Ala Thr Val Val Phe Gly Ala Lys Arg Gln
            340                 345                 350
```

<210> 240

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 240

```
Thr Lys Asp Asn Thr Ala Asn Gly Asn Thr Ala Ala Ala Ser Gly Gly
1               5                   10                  15

Ala Gly Ala Ala Ala Ser Gly Gly Ala Ala Ala Met Pro Ser Glu Asn
            20                  25                  30

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

Thr Ala Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
    50                  55                  60
```

```
Val Asp Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly
65                  70                  75                  80

Asn Thr Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
                85                  90                  95

Ala His Thr Pro Lys Ser Asp Glu Lys Asp Thr Gln Ala Gly Thr Ala
            100                 105                 110

Ala Asn Gly Asp Gln Ala Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly
        115                 120                 125

Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
    130                 135                 140

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

Gly Gly Asn Gly Ser Pro Thr Ala Ala Gln Thr Gly Ala Gln Ser Met
                165                 170                 175

Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Lys Glu Gln
            180                 185                 190

Gln Asn Ile Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Asn Gly
        195                 200                 205

Thr Ser Trp Ser Gly Asn Ala Ser Asn Ala Thr Ser Gly Asn Lys Ala
    210                 215                 220

Asp Phe Thr Val Asn Phe Gly Glu Lys Lys Ile Asn Gly Thr Leu Thr
225                 230                 235                 240

Ala Glu Asn Arg Gln Ala Ala Thr Phe Thr Ile Glu Gly Met Ile Gln
                245                 250                 255

Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala Asp Leu Gly Phe Asp
            260                 265                 270

Leu Asp Gln Ser Asn Thr Thr Gly Thr Pro Lys Ala Tyr Ile Thr Asn
        275                 280                 285

Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly
    290                 295                 300

Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Glu Asn Ala Thr Val
305                 310                 315                 320

Ala Ser Gly Asn Gly Asn Ser Ala Ser Ser Ala Thr Val Val Phe Gly
                325                 330                 335

Ala Lys Arg Gln
            340
```

<210> 241

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 241

```
Thr Lys Asp Asn Thr Ala Asn Gly Asn Thr Ala Ala Ala Ser Gly Gly
1               5                  10                  15

Ala Gly Ala Ala Ala Ser Gly Gly Ala Ala Ala Met Pro Ser Glu Asn
            20                  25                  30

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

Thr Ala Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
    50                  55                  60

Val Asp Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly
65                  70                  75                  80

Asn Thr Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
                85                  90                  95

Ala His Thr Pro Lys Ser Asp Glu Lys Asp Thr Gln Ala Gly Thr Ala
            100                 105                 110

Ala Asn Gly Asp Gln Ala Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly
        115                 120                 125

Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
    130                 135                 140

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

Gly Gly Asn Gly Ser Pro Thr Ala Ala Gln Thr Gly Ala Gln Ser Met
                165                 170                 175

Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Lys Glu Gln
            180                 185                 190

Gln Asn Ile Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Asn Gly
        195                 200                 205

Thr Ser Thr Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly Asn
    210                 215                 220

Arg Ala Asp Phe Thr Val Asn Phe Gly Glu Lys Lys Ile Asn Gly Thr
225                 230                 235                 240

Leu Thr Ala Glu Asn Arg Gln Gln Ala Thr Phe Thr Ile Glu Gly Met
                245                 250                 255

Ile Gln Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala Asp Ser Gly
            260                 265                 270
```

```
Phe Asp Leu Asp Gln Ser Asn Thr Thr Gly Thr Pro Lys Ala Tyr Ile
        275                 280                 285

Thr Asn Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu
    290                 295                 300

Leu Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln Ala Gln Pro Pro
305                 310                 315                 320

Ala Ser Gly Ser Gly Ala Ser Ala Ala Asn Ser Ala Thr Val Val Phe
                325                 330                 335

Gly Ala Lys Arg
            340
```

<210> 242

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 242

```
Thr Gln Asp Lys Pro Gly Asn Gly Ala Ala Ala Ser Asp Gly Ala Gly
1               5                   10                  15

Ala Ala Ala Ser Asn Gly Ala Ala Ala Met Pro Ser Glu Asn Gly Lys
            20                  25                  30

Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr His Gly Gly Thr Ala
        35                  40                  45

Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
    50                  55                  60

Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly Asn Asn
65                  70                  75                  80

Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
                85                  90                  95

Asp His Thr Pro Lys Ser Asp Glu Lys Asp Thr Gln Ala Gly Thr Ala
            100                 105                 110

Ala Asn Gly Asn Pro Ala Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly
        115                 120                 125

Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
    130                 135                 140

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

Ser Gly Asn Gly Ser Pro Thr Ala Ala Ala Gln Thr Asp Ala Gln Ser
                165                 170                 175

Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Ser Glu
            180                 185                 190
```

```
Gln Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Asn Ser
        195                 200                 205

Thr Ser Trp Ser Gly Asn Ala Ser Asn Ala Thr Ser Gly Asn Lys Ala
    210                 215                 220

Asp Phe Thr Val Asn Phe Gly Glu Lys Lys Ile Thr Gly Thr Leu Thr
225                 230                 235                 240

Ala Glu Asn Arg Gln Ala Ala Thr Phe Thr Ile Glu Gly Thr Ile Gln
                245                 250                 255

Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala Asp Ser Gly Phe Asp
            260                 265                 270

Leu Asp Gln Ser Asn Thr Thr Gly Thr Pro Lys Ala Tyr Ile Thr Asn
        275                 280                 285

Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Met Gly
    290                 295                 300

Gly Trp Phe Ala Tyr Pro Gly Asp Ser Gln Thr Gln Pro Ser Ala Ser
305                 310                 315                 320

Gly Ser Gly Ala Ser Ala Ala Asn Ser Ala Thr Val Val Phe Gly Ala
                325                 330                 335

Lys Arg Gln Gln
            340
```

<210> 243

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 243

```
Thr Gln Asp Lys Pro Gly Asn Gly Ala Ala Ala Ser Asp Gly Ala Gly
1               5                   10                  15

Ala Ala Ala Ser Asn Gly Ala Ala Ala Met Pro Ser Glu Asn Gly Lys
            20                  25                  30

Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr His Gly Gly Thr Ala
        35                  40                  45

Ile Lys Lys Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
    50                  55                  60

Gly Ile Met Ile Pro Leu Leu Pro Lys Asp Ser Glu Ser Gly Asn Asn
65                  70                  75                  80

Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
                85                  90                  95
```

```
Ala His Thr Pro Lys Ser Asp Glu Lys Asp Thr Gln Ala Gly Thr Ala
            100                 105                 110

Ala Asn Gly Asp Gln Ala Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly
        115                 120                 125

Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
    130                 135                 140

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

Gly Gly Asn Ser Ser Pro Thr Ala Ala Gln Thr Ala Gln Gly Ala Gln
                165                 170                 175

Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Asn Lys Ile Pro Thr
            180                 185                 190

Asp Gln Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Asn
        195                 200                 205

Gly Thr Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly Asn Arg
    210                 215                 220

Ala Glu Phe Thr Val Asn Phe Asp Lys Lys Lys Ile Asn Gly Thr Leu
225                 230                 235                 240

Thr Ala Asp Asn Arg Gln Ala Ala Thr Phe Thr Ile Glu Gly Asp Ile
                245                 250                 255

Glu Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala Asp Ser Gly Phe
            260                 265                 270

Asp Leu Asp Gln Ser Asn Asn Thr Arg Thr Pro Lys Ala Tyr Ile Thr
        275                 280                 285

Asn Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu
    290                 295                 300

Gly Gly Trp Phe Ala Tyr Ser Asp Asp Lys Gln Thr Lys Asn Ala Thr

305                 310                 315                 320

Asp Ala Ser Gly Asn Gly Asn Ser Ala Ser Ser Ala Thr Val Val Phe
                325                 330                 335

Gly Ala Lys Arg
            340
```

<210> 244

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 244

```
Thr Gln Asp Lys Pro Gly Asn Gly Ala Ala Ala Ser Asp Gly Ala Gly
```

```
1               5                   10                  15

Ala Ala Ala Ser Asn Gly Ala Ala Ala Met Pro Ser Glu Asn Gly Lys
            20                  25                  30

Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr His Gly Gly Thr Ala
        35                  40                  45

Ile Lys Lys Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
    50                  55                  60

Gly Ile Met Ile Pro Leu Leu Pro Lys Asp Ser Glu Ser Gly Asn Asn
65                  70                  75                  80

Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
                85                  90                  95

Ala His Thr Pro Lys Ser Asp Glu Lys Asp Thr Gln Ala Gly Thr Ala
            100                 105                 110

Ala Asn Gly Asp Gln Ala Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly
        115                 120                 125

Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
    130                 135                 140

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

Gly Gly Asn Gly Ser Pro Thr Ala Ala Gln Thr Gly Ala Gln Ser Met
                165                 170                 175

Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Asn Asp Gln

            180                 185                 190

Asn Ile Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Asn Gly Thr
        195                 200                 205

Ser Trp Ser Gly Asn Ala Ser Asn Ala Thr Ser Gly Asn Arg Ala Asp
    210                 215                 220

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

Glu Asn Arg Gln Ala Ala Thr Phe Thr Ile Glu Gly Met Ile Gln Gly
                245                 250                 255

Asn Gly Phe Glu Gly Thr Ala Lys Thr Gly Asp Gly Gly Phe Ala Leu
            260                 265                 270

Asp Pro Lys Asn Thr Glu Ala Ser His Lys Ala Ser Ile Asn Ala Thr
        275                 280                 285

Val Thr Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Met Gly Gly Trp
```

```
Val Thr Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Met Gly Gly Trp
    290                 295                 300

Phe Ala Tyr Pro Gly Asp Ser Gln Thr Gln Pro Ser Ala Ser Gly Ser
305                 310                 315                 320

Gly Ala Ser Ala Ala Asn Ser Ala Thr Val Val Phe Gly Ala Lys Arg
                325                 330                 335

Gln Gln Leu Val
            340
```

<210> 245

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 245

```
Thr Gln Asp Lys Pro Gly Asn Gly Ala Ala Ala Ser Asp Gly Ala Gly
1               5                   10                  15

Ala Ala Ala Ser Asn Gly Ala Ala Ala Met Pro Ser Glu Asn Gly Lys
            20                  25                  30

Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr His Gly Gly Thr Ala
        35                  40                  45

Ile Lys Lys Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp

    50                  55                  60

Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly Asn Asn
65                  70                  75                  80

Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
                85                  90                  95

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

Ala Asn Gly Asp Gln Ala Ala Ser Asn Thr Ala Gly Asp Ala Asn Gly
        115                 120                 125

Lys Thr Lys Thr Tyr Ala Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
    130                 135                 140

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

Gly Gly Asn Gly Ser Pro Thr Ala Ala Ala Gln Thr Asp Ala Gln Ser
                165                 170                 175

Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Asn Asp
            180                 185                 190

Gln Asp Ile Val Tyr Arg Glu Ser Tyr Tyr Glu His Ile Ala Asp Glu
```

```
Gln Asn Ile Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Asn Gly
        195                 200                 205

Thr Ser Trp Ser Gly Asn Ala Ser Asn Ala Thr Ser Gly Asn Lys Ala
    210                 215                 220

Asp Phe Thr Val Asn Phe Gly Glu Lys Lys Ile Asn Gly Thr Leu Thr
225                 230                 235                 240

Ala Glu Asn Arg Gln Ala Ala Thr Phe Thr Ile Glu Gly Thr Ile Gln
                245                 250                 255

Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala Asp Ser Gly Phe Asp
            260                 265                 270

Leu Asp Gln Ser Asn Thr Thr Gly Thr Pro Lys Ala Tyr Ile Thr Asp
        275                 280                 285

Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly
    290                 295                 300

Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln Ala Gln Pro Ser Val Ser
305                 310                 315                 320

Gly Ser Gly Ala Ser Ala Ala Asn Ser Ala Thr Val Val Phe Gly Ala
                325                 330                 335

Lys Arg Gln Gln
            340
```

<210> 246

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 246

```
Thr Lys Asp Asn Thr Ala Asn Gly Asn Thr Ala Ala Ala Ser Gly Gly
1               5                   10                  15

Thr Gly Ala Ala Ala Ser Gly Gly Ala Ala Ala Met Pro Ser Glu Asn
            20                  25                  30

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

Lys Glu Val Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
    50                  55                  60

Val Asp Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly
65                  70                  75                  80

His Asn Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg
                85                  90                  95

Lys Phe Asp Tyr Thr Pro Asn Ser Asp Glu Lys Asp Thr Gln Ala Gly
            100                 105                 110
```

```
Thr Ala Glu Asn Gly Asn Pro Ala Ala Ser Asn Thr Ala Gly Asp Ala
        115                 120                 125

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

Asn Tyr Leu Lys Tyr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn Thr
145                 150                 155                 160

Val Gly Ser Gly Asn Gly Ser Pro Thr Ala Ala Ala Gln Thr Ala Gln
                165                 170                 175

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

Ile Pro Ser Glu Gln Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His
        195                 200                 205

Ile Ala Asn Gly Thr Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly
    210                 215                 220

Gly Asn Arg Ala Glu Phe Thr Val Asn Phe Ala Asp Lys Lys Leu Asp
225                 230                 235                 240

Gly Thr Leu Thr Ala Gly Glu Arg Thr Ser Pro Thr Phe Thr Ile Thr
                245                 250                 255

Ala Thr Ile Gln Gly Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala Asp
            260                 265                 270

Ser Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr Arg Thr Pro Lys Ala
        275                 280                 285

Tyr Ile Thr Asn Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala
    290                 295                 300

Glu Glu Leu Gly Gly Trp Phe Val Tyr Pro Gly Asp Ser Gln Ala Gln
305                 310                 315                 320

Pro Ser Ala Ser Gly Ser Gly Thr Ser Ala Ala Asn Ser Ala Thr Val
                325                 330                 335

Val Phe Gly Ala
            340
```

<210> 247

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 247

```
Thr Gln Asp Lys Asp Ala Asn Gly Asn Thr Glu Ala Ala Ser Gly Gly
1               5                   10                  15
```

```
Thr Gly Ala Ala Ala Ser Gly Gly Ala Ala Ala Met Pro Ser Glu Asn
            20                  25                  30

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

Lys Glu Val Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
    50                  55                  60

Val Asp Gly Ile Met Ile Pro Leu Leu Pro Glu Thr Ser Glu Ser Gly
65                  70                  75                  80

Lys Asn Gln Ala Asp Lys Gly Lys Asn Gly Glu Thr Glu Phe Thr Arg
                85                  90                  95

Lys Phe Asp Tyr Thr Pro Glu Ser Asp Lys Lys Asp Thr Gln Ala Gly
            100                 105                 110

Thr Pro Thr Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr
        115                 120                 125

Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu
    130                 135                 140

Asn Tyr Leu Lys Tyr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn Thr
145                 150                 155                 160

Val Gly Ser Gly Asn Gly Ser Gln Ala Ala Ala Gln Thr Asp Ala Gln
                165                 170                 175

Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Ser
            180                 185                 190

Glu Gln Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Asn
        195                 200                 205

Gly Thr Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly Asn Arg
    210                 215                 220

Ala Glu Phe Thr Val Asp Phe Gly Ala Lys Lys Ile Asn Gly Lys Leu
225                 230                 235                 240

Thr Ala Glu Asn Arg Gln Ala Ala Thr Phe Thr Ile Glu Gly Asp Ile
                245                 250                 255

Glu Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala Glu Ser Gly Phe
            260                 265                 270

Asp Leu Asp Gln Ser Asn Thr Thr Arg Thr Pro Lys Ala Tyr Ile Thr
        275                 280                 285

Asp Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu
    290                 295                 300

Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Lys Asn Ala Thr
305                 310                 315                 320
```

```
Asn Ala Ser Gly Asn Ser Ser Ala Thr Val Val Phe Gly Ala Lys Arg
                325                 330                 335

Gln Gln Pro Val
            340
```

<210> 248

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 248

```
Thr Gln Asp Lys Asp Ala Asn Gly Asn Thr Glu Ala Ala Ser Gly Gly
1               5                  10                  15

Thr Gly Ala Ala Ala Ser Gly Gly Ala Ala Ala Met Pro Ser Glu Asn
            20                  25                  30

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

Lys Glu Val Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
    50                  55                  60

Val Asp Gly Ile Met Ile Pro Leu Leu Pro Glu Thr Ser Glu Ser Gly
65                  70                  75                  80

Lys Asn Gln Ala Asp Lys Gly Lys Asn Gly Glu Thr Glu Phe Thr Arg
                85                  90                  95

Lys Phe Asp Tyr Thr Pro Glu Ser Asp Lys Lys Asp Thr Gln Ala Gly
            100                 105                 110

Thr Pro Thr Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr
        115                 120                 125

Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu
    130                 135                 140

Asn Tyr Leu Lys Tyr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn Thr
145                 150                 155                 160

Val Gly Ser Gly Asn Gly Ser Gln Ala Ala Ala Gln Thr Asp Ala Gln
                165                 170                 175

Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Ser
            180                 185                 190

Glu Gln Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly Tyr Ile Ala Asn
        195                 200                 205

Asp Lys Ser Thr Ser Trp Ser Gly Asn Ala Ser Asn Ala Thr Ser Gly
    210                 215                 220

Asn Arg Ala Glu Phe Thr Val Asn Phe Ala Asp Lys Lys Ile Thr Gly
225                 230                 235                 240
```

```
Thr Leu Thr Ala Asp Asn Arg Gln Glu Ala Thr Phe Thr Ile Asp Gly
                245                 250                 255

Asn Ile Lys Asp Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala Glu Ser
            260                 265                 270

Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr Arg Thr Pro Lys Ala Tyr
        275                 280                 285

Ile Thr Asp Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu
    290                 295                 300

Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Lys Asn
305                 310                 315                 320

Ala Thr Asn Ala Ser Gly Asn Ser Ser Ala Thr Val Val Phe Gly Ala
                325                 330                 335

Lys Arg Gln Gln
            340
```

<210> 249

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 249

```
Thr Lys Asp Lys Thr Glu Asn Gly Ala Ala Ala Ser Gly Gly Ala Gly
1               5                   10                  15

Ala Ala Ala Ser Gly Gly Ala Ala Ala Met Pro Ser Glu Asn Gly Lys
            20                  25                  30

Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr His Gly Gly Thr Ala
        35                  40                  45

Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
    50                  55                  60

Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly His Asn
65                  70                  75                  80

Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
                85                  90                  95

Asp His Thr Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln
            100                 105                 110

Thr Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly
        115                 120                 125

Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
    130                 135                 140
```

```
Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln
145                 150                 155                 160

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

Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro
            180                 185                 190

Lys Glu Gln Gln Asp Ile Val Tyr Arg Gly Ser Trp Tyr Gly His Ile
        195                 200                 205

Ala Asn Asp Thr Ser Trp Ser Gly Asn Ala Ser Asp Arg Glu Gly Gly
    210                 215                 220

Asn Arg Ala Asp Phe Thr Val Asn Phe Gly Thr Lys Lys Ile Asn Gly
225                 230                 235                 240

Thr Leu Thr Ala Glu Asn Arg Gln Glu Ala Thr Phe Thr Ile Val Gly
                245                 250                 255

Asp Ile Lys Asp Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala Asp Ser
            260                 265                 270

Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr Arg Thr Pro Lys Ala Tyr
        275                 280                 285

Ile Thr Asp Ala Lys Val Lys Gly Gly Phe Tyr Gly Pro Lys Ala Glu
    290                 295                 300

Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Glu Lys
305                 310                 315                 320

Ala Thr Val Thr Ser Gly Asp Gly Asn Ser Ala Ser Ser Ala Thr Val
                325                 330                 335

Val Phe Gly Ala
            340
```

<210> 250

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 250

```
Thr Gln Asp Lys Pro Glu Asn Gly Ala Ala Ala Ser Gly Gly Thr Gly
1               5                   10                  15

Ala Ala Ala Ser Gly Gly Ala Ala Asp Met Pro Ser Glu Asn Gly Lys
            20                  25                  30

Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr His Gly Gly Thr Ala
        35                  40                  45

Ile Lys Lys Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
    50                  55                  60
```

```
Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly Asn Asn
65                  70                  75                  80

Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
                85                  90                  95

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

Ala Asn Gly Asp Gln Ala Ala Ser Asn Thr Ala Gly Asp Ala Asn Gly
        115                 120                 125

Lys Thr Lys Thr Tyr Ala Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
    130                 135                 140

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

Ser Gly Asn Gly Ser Pro Thr Ala Ala Ala Gln Thr Asp Ala Gln Ser
                165                 170                 175

Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Asn Asp
            180                 185                 190

Gln Asn Ile Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Asn Gly
        195                 200                 205

Thr Ser Trp Ser Gly Asn Ala Ser Asn Ala Thr Ser Gly Asn Lys Ala
    210                 215                 220

Asp Phe Thr Val Asn Phe Gly Glu Lys Lys Ile Asn Gly Thr Leu Thr
225                 230                 235                 240

Ala Glu Asn Arg Gln Ala Ala Thr Phe Thr Ile Glu Gly Met Ile Gln
                245                 250                 255

Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala Asp Leu Gly Phe Asp
            260                 265                 270

Leu Asp Gln Ser Asn Thr Thr Gly Thr Pro Lys Ala Tyr Ile Thr Asn
        275                 280                 285

Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly
    290                 295                 300

Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln Ala Gln Pro Pro Ala Ser
305                 310                 315                 320

Gly Ser Gly Ala Ser Ala Ala Asn Ser Ala Thr Val Val Phe Gly Ala
                325                 330                 335

Lys Arg Gln Gln
            340
```

<210> 251

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 251

```
Thr Gln Asp Lys Pro Gly Asn Gly Ala Ala Ala Ser Gly Gly Ala Gly
1               5                  10                  15

Ala Ala Ala Ser Gly Gly Ala Ala Asp Met Pro Ser Glu Asn Gly Lys
            20                  25                  30

Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr His Gly Gly Lys Ala
        35                  40                  45

Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
    50                  55                  60

Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly Asn Asn
65                  70                  75                  80

Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
                85                  90                  95

Ala His Thr Pro Asn Ser Asp Glu Lys Asp Thr Gln Ala Gly Thr Ala
            100                 105                 110

Glu Asn Gly Asn Pro Ala Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly
        115                 120                 125

Lys Thr Lys Thr Tyr Ala Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
    130                 135                 140

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

Gly Gly Asn Gly Ser Pro Thr Ala Ala Gln Thr Ala Gln Gly Ala Gln
                165                 170                 175

Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Lys
            180                 185                 190

Glu Gln Gln Asn Ile Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala
        195                 200                 205

Asn Gly Thr Ser Thr Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly
    210                 215                 220

Gly Asn Arg Ala Asp Phe Thr Val Asn Phe Gly Glu Lys Lys Ile Asn
225                 230                 235                 240

Gly Thr Leu Thr Ala Glu Asn Arg Gln Gln Ala Thr Phe Thr Ile Glu
                245                 250                 255

Gly Met Ile Gln Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala Asp
            260                 265                 270
```

```
Ser Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr Gly Thr Pro Lys Ala
        275                 280                 285

Tyr Ile Thr Asn Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala

    290                 295                 300

Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly Asp Asn Gln Ala Gln
305                 310                 315                 320

Pro Ser Ala Ser Gly Ser Gly Ala Ser Ala Ala Asn Ser Ala Thr Val
                325                 330                 335

Val Phe Gly Ala
            340
```

<210> 252

<211> 330

<212> PRT

<213> Neisseria meningitidis

<400> 252

```
Thr Gln Asp Lys Pro Gly Asn Gly Ala Ala Ala Ser Asp Gly Ala Gly
1               5                   10                  15

Ala Ala Ala Ser Gly Asp Ala Ala Asp Met Pro Ser Glu Asn Ser Lys
            20                  25                  30

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

Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
    50                  55                  60

Gly Ile Met Ile Pro Leu Leu Pro Glu Thr Ser Glu Ser Gly Lys Asn
65                  70                  75                  80

Gln Ala Asp Lys Gly Lys Asn Gly Glu Thr Glu Phe Thr Arg Lys Phe
                85                  90                  95

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

Thr Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly
        115                 120                 125

Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
    130                 135                 140

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

Ser Gly Asn Gly Ser Gln Ala Ala Ala Gln Thr Asp Ala Gln Ser Met
```

```
                165                 170                 175

Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Ser Glu Gln
            180                 185                 190

Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Asn Gly Thr
        195                 200                 205

Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly Asn Arg Ala Glu
    210                 215                 220

Phe Thr Val Asp Phe Gly Ala Lys Lys Ile Asn Gly Lys Leu Thr Ala
225                 230                 235                 240

Glu Asn Arg Gln Ala Ala Thr Phe Thr Ile Glu Gly Asp Ile Glu Gly
                245                 250                 255

Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala Glu Ser Gly Phe Asp Leu
            260                 265                 270

Asp Gln Ser Asn Thr Thr Arg Thr Pro Lys Ala Tyr Ile Thr Asp Ala
        275                 280                 285

Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly
    290                 295                 300

Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Lys Asn Ala Thr Asn Ala
305                 310                 315                 320

Ser Gly Asn Ser Ser Ala Thr Val Val Phe
                325                 330
```

<210> 253

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 253

```
Thr Lys Asp Lys Pro Ala Asn Gly Asn Thr Ala Glu Ala Ser Gly Gly
1               5                   10                  15

Thr Asp Ala Ala Ala Ser Gly Gly Thr Ala Gly Thr Pro Ser Glu Ser
            20                  25                  30

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

Lys Glu Val Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val

    50                  55                  60

Val Asp Gly Ile Met Ile Pro Leu Leu Pro Lys Asp Ser Glu Ser Gly
65                  70                  75                  80
```

```
Asn Asn Gln Ala Asp Lys Gly Lys Asn Gly Gly Thr Ala Phe Thr Tyr
                85                  90                  95

Thr Thr Thr Tyr Thr Pro Lys Ser Asp Lys Lys Asp Thr Gln Ala Gln
            100                 105                 110

Thr Val Thr Gly Gly Thr Gln Thr Ala Ser Gly Thr Glu Gly Val Asn
        115                 120                 125

Gly Gly Gln Ala Gly Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser
    130                 135                 140

Asn Leu Asn Tyr Leu Lys Tyr Gly Leu Leu Thr Arg Lys Thr Ala Gly
145                 150                 155                 160

Asn Thr Gly Glu Gly Gly Asn Gly Ser Pro Thr Ala Ala Ala Gln Met
                165                 170                 175

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

Lys Glu Ile Pro Ser Asp Gln Asn Val Val Tyr Arg Gly Ser Trp Tyr
        195                 200                 205

Gly His Ile Ala Asn Gly Thr Ser Trp Ser Gly Asn Ala Ser Asp Lys
    210                 215                 220

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

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

Ile Thr Ala Thr Ile Gln Gly Asn Gly Phe Glu Gly Thr Ala Lys Thr
            260                 265                 270

Gly Asp Asp Gly Phe Ala Leu Asp Thr Lys Asn Thr Val Glu Thr His
        275                 280                 285

Lys Ala His Ile Ala Asp Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro
    290                 295                 300

Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln
305                 310                 315                 320

Ala Gln Pro Ser Ala Ser Gly Ser Gly Thr Ser Ala Ala Asn Ser Ala
                325                 330                 335

Thr Val Val Phe
            340
```

<210> 254

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 254

```
Thr Lys Asp Lys Pro Ala Asn Gly Asn Thr Ala Glu Ala Ser Gly Gly
1               5                  10                  15

Thr Asp Ala Ala Ala Ser Gly Gly Thr Ala Gly Thr Pro Ser Glu Ser
            20                  25                  30

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

Lys Glu Val Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
    50                  55                  60

Val Asp Gly Ile Met Ile Pro Leu Leu Pro Glu Thr Ser Glu Ser Gly
65                  70                  75                  80

Ser Asn Gln Ala Asp Lys Gly Lys Asn Gly Glu Thr Glu Phe Thr Arg
                85                  90                  95

Lys Phe Asp His Thr Pro Lys Ser Asp Lys Lys Asp Ala Gln Ala Gly
            100                 105                 110

Thr Gln Thr Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr
        115                 120                 125

Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu
    130                 135                 140

Asn Tyr Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala
145                 150                 155                 160

Met Gln Ala Gly Glu Asn Gly Ser Gln Ala Asp Ala Lys Thr Glu Gln
                165                 170                 175

Val Glu Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu
            180                 185                 190

Ile Pro Ser Glu Gln Asn Ile Val Tyr Arg Gly Ser Trp Tyr Gly His
        195                 200                 205

Ile Ala Asn Gly Thr Ser Thr Ser Trp Ser Gly Asn Ala Ser Asp Lys
    210                 215                 220

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

Ile Asn Gly Thr Leu Thr Ala Glu Asn Arg Gln Gln Ala Thr Phe Thr
                245                 250                 255

Ile Glu Gly Met Ile Gln Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr
            260                 265                 270

Ala Asp Ser Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr Gly Thr Pro
        275                 280                 285

Lys Ala Tyr Ile Thr Asp Ala Lys Val Gln Glu Glu Phe Tyr Glu Pro
```

```
Lys Ala Tyr Ile Thr Asn Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro
    290                 295                 300

Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln
305                 310                 315                 320

Ala Gln Pro Pro Ala Ser Gly Ser Gly Ala Ser Ala Ala Asn Ser Ala
                325                 330                 335

Thr Val Val Phe
            340
```

<210> 255

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 255

```
Thr Lys Asp Lys Pro Ala Asn Gly Asn Thr Ala Glu Ala Ser Gly Gly
1               5                   10                  15

Thr Asp Ala Ala Ala Ser Gly Gly Thr Ala Gly Thr Pro Ser Glu Ser
            20                  25                  30

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

Lys Glu Val Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
    50                  55                  60

Val Asp Gly Ile Met Ile Pro Leu Leu Pro Lys Asp Ser Glu Ser Gly
65                  70                  75                  80

Gly Asn Gln Ala Asp Lys Ser Lys Asn Gly Glu Thr Ala Phe Thr Arg
                85                  90                  95

Lys Phe Asp His Thr Pro Lys Ser Asp Glu Lys Asp Thr Gln Ala Gly
            100                 105                 110

Thr Pro Thr Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr
        115                 120                 125

Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu
    130                 135                 140

Asn Tyr Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala
145                 150                 155                 160

Met Gln Ala Gly Gly Asn Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln
                165                 170                 175

Val Glu Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu
            180                 185                 190

Ile Pro Lys Glu Gln Gln Asp Ile Val Tyr Arg Gly Ser Trp Tyr Gly
        195                 200                 205
```

```
His Ile Ala Asn Gly Thr Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu
    210                 215                 220

Gly Gly Asn Arg Ala Glu Phe Thr Val Asn Phe Gly Asp Lys Lys Ile
225                 230                 235                 240

Thr Gly Thr Leu Thr Ala Glu Asn Arg Gln Ala Ala Thr Phe Thr Ile
                245                 250                 255

Glu Gly Asp Ile Glu Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala
            260                 265                 270

Glu Leu Gly Phe Asp Leu Asp Gln Ser Asp Asn Thr Arg Thr Pro Lys
        275                 280                 285

Ala Tyr Ile Thr Asp Ala Lys Val Lys Gly Gly Phe Tyr Gly Pro Lys
    290                 295                 300

Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Ser Asp Lys Gln Thr
305                 310                 315                 320

Lys Asn Ala Pro Asp Ala Ser Gly Asn Gly Asn Ser Ala Ser Ser Ala
                325                 330                 335

Thr Val Val Phe
            340
```

<210> 256

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 256

```
Thr Lys Asp Asn Thr Ala Asn Gly Asn Thr Ala Ala Ala Ser Gly Gly
1               5                   10                  15

Thr Gly Ala Ala Ala Ser Gly Gly Ala Ala Asp Met Pro Ser Glu Asn
            20                  25                  30

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

Thr Ala Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
    50                  55                  60

Val Asp Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly
65                  70                  75                  80

Asn Asn Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg
                85                  90                  95

Lys Phe Ala His Thr Pro Lys Ser Asp Glu Lys Asp Thr Gln Ala Gly
            100                 105                 110

Thr Ala Glu Asn Gly Asn Pro Ala Ala Ser Asn Thr Ala Gly Asp Thr
        115                 120                 125
```

```
        115                 120                 125

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

Asn Tyr Leu Lys Tyr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn Thr
145                 150                 155                 160

Gly Glu Gly Gly Asn Gly Ser Pro Thr Ala Ala Ala Gln Thr Ala Gln
                165                 170                 175

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

Ile Pro Ser Glu Gln Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His
        195                 200                 205

Ile Ala Asn Asp Thr Ser Thr Ser Trp Ser Gly Asn Ala Ser Asp Lys
    210                 215                 220

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

Ile Asn Gly Thr Leu Thr Ala Glu Asn Arg Gln Ala Ala Thr Phe Thr
                245                 250                 255

Ile Glu Gly Met Ile Gln Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr
            260                 265                 270

Ala Asp Leu Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr Gly Thr Pro
        275                 280                 285

Lys Ala Tyr Ile Thr Asn Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro
    290                 295                 300

Lys Ala Glu Glu Met Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln
305                 310                 315                 320

Thr Glu Asn Ala Thr Val Ala Ser Gly Asn Gly Asn Ser Ala Ser Ser
                325                 330                 335

Ala Thr Val Val
            340
```

<210> 257

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 257

```
Thr Lys Asp Lys Thr Glu Asn Gly Ala Ala Ala Ser Gly Gly Ala Gly
1               5                   10                  15

Ala Ala Ala Ser Gly Gly Ala Ala Ala Met Pro Ser Glu Asn Ser Lys
            20                  25                  30
```

```
Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr His Ser Gly Thr Ala
        35                  40                  45

Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
    50                  55                  60

Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly Asn Thr
65                  70                  75                  80

Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe Asp Tyr
                85                  90                  95

Thr Pro Asn Ser Asp Glu Lys Asp Thr Gln Ala Gly Thr Ala Glu Asn
            100                 105                 110

Gly Asn Pro Ala Ala Ser Asn Thr Ala Gly Asp Ala Asn Gly Lys Thr
        115                 120                 125

Lys Thr Tyr Ala Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys
    130                 135                 140

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

Asn Gly Ser Pro Thr Ala Ala Ala Gln Thr Ala Gln Gly Ala Gln Ser
                165                 170                 175

Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Ser Glu
            180                 185                 190

Gln Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Asn Gly
        195                 200                 205

Thr Ser Thr Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly Asn
    210                 215                 220

Arg Ala Glu Phe Thr Val Asn Phe Gly Asp Lys Lys Ile Thr Gly Thr
225                 230                 235                 240

Leu Thr Ala Asp Asn Arg Gln Ala Ala Thr Phe Thr Ile Glu Gly Asp
                245                 250                 255

Ile Glu Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr Asp Asn Leu Gly
            260                 265                 270

Phe Asp Leu Asp Gln Ser Asp Asn Thr Arg Thr Pro Lys Ala Tyr Ile
        275                 280                 285

Thr Asp Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu
    290                 295                 300

Leu Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Glu Lys Ala
305                 310                 315                 320

Thr Ala Thr Ser Ser Asp Gly Lys Ser Ala Ser Ser Ala Thr Val Val
                325                 330                 335
```

```
Phe Gly Ala Lys
            340
```

<210> 258

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 258

```
Thr Gln Asp Lys Ala Ala Asn Gly Asn Thr Ala Ala Ala Ser Asp Gly
1               5                   10                  15

Ala Gly Ala Ala Ala Ser Gly Ser Ala Ala Ala Met Pro Ser Glu Asn
            20                  25                  30

Gly Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr His Gly Gly
        35                  40                  45

Lys Ala Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
    50                  55                  60

Val Asp Gly Ile Met Ile Pro Leu Leu Pro Lys Asp Ser Glu Ser Gly
65                  70                  75                  80

Asn Asn Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg
                85                  90                  95

Lys Phe Asp His Thr Pro Gln Ser Asp Glu Lys Asp Ala Gln Ala Gly
            100                 105                 110

Thr Ala Ala Asn Gly Asp Gln Ala Ala Ser Asn Thr Ala Gly Asp Thr
        115                 120                 125

Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu
    130                 135                 140

Asn Tyr Leu Lys Tyr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn Thr
145                 150                 155                 160

Gly Glu Gly Gly Asn Gly Ser Gln Thr Ala Ala Gln Thr Ala Gln Gly
                165                 170                 175

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

Pro Ser Glu Gln Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile
        195                 200                 205

Ala Asn Asp Thr Ser Thr Ser Trp Ser Gly Asn Ala Ser Asn Ala Thr
    210                 215                 220

Ser Gly Asn Lys Ala Asp Phe Thr Val Asn Phe Gly Glu Lys Lys Ile
225                 230                 235                 240

Asn Gly Thr Leu Thr Ala Glu Asn Arg Gln Gln Ala Thr Phe Thr Ile
```

```
                245                 250                 255

Glu Gly Met Ile Gln Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala
            260                 265                 270

Asp Ser Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr Gly Thr Pro Lys
        275                 280                 285

Ala Tyr Ile Thr Asn Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys
    290                 295                 300

Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln Ala
305                 310                 315                 320

Gln Pro Pro Ala Ser Gly Ser Gly Ala Ser Ala Ala Asn Ser Ala Thr
                325                 330                 335

Val Val Phe Gly
            340
```

<210> 259

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 259

```
Thr Gln Asp Lys Asp Ala Asn Gly Asn Thr Glu Ala Ala Ser Gly Gly
1               5                   10                  15

Thr Gly Ala Ala Ala Ser Gly Gly Ala Ala Asp Met Pro Ser Glu Asn
            20                  25                  30

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

Thr Ala Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
    50                  55                  60

Val Asp Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly
65                  70                  75                  80

Asn Thr Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
                85                  90                  95

Ala His Thr Pro Lys Ser Asp Glu Lys Asp Thr Gln Ala Gly Thr Ala
            100                 105                 110

Ala Asn Gly Asp Gln Ala Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly
        115                 120                 125

Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
    130                 135                 140

Leu Lys Tyr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn Thr Gly Glu
145                 150                 155                 160
```

```
Gly Gly Asn Gly Ser Pro Thr Ala Ala Gln Thr Ala Gln Gly Ala Gln
                165                 170                 175

Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Asn Lys Ile Pro Ser
            180                 185                 190

Glu Gln Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Asn
        195                 200                 205

Gly Thr Ser Trp Ser Gly Asn Ala Ser Asn Ala Thr Ser Gly Asn Lys
    210                 215                 220

Ala Asp Phe Thr Val Asn Phe Gly Glu Lys Lys Ile Thr Gly Thr Leu
225                 230                 235                 240

Thr Ala Glu Asn Arg Gln Gln Ala Thr Phe Thr Ile Glu Gly Met Ile
                245                 250                 255

Gln Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala Asn Ser Gly Phe
            260                 265                 270

Asp Leu Asp Gln Ser Asn Thr Thr Gly Thr Pro Lys Ala Tyr Ile Thr
        275                 280                 285

Asn Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu

    290                 295                 300

Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Glu Asn Thr Thr
305                 310                 315                 320

Val Ala Ser Gly Asn Gly Asn Ser Ala Ser Ser Ala Thr Val Val Phe
                325                 330                 335

Gly Ala Lys Arg
            340
```

<210> 260

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 260

```
Thr Gln Asp Lys Asp Ala Asn Gly Asn Thr Glu Ala Ala Ser Gly Gly
1               5                   10                  15

Thr Gly Ala Ala Ala Ser Gly Gly Ala Ala Asp Met Pro Ser Glu Asn
            20                  25                  30

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

Thr Ala Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
    50                  55                  60
```

```
Val Asp Gly Ile Met Ile Pro Leu Leu Pro Lys Asp Ser Glu Ser Gly
65                  70                  75                  80

Asn Thr Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
                85                  90                  95

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

Ala Asn Gly Asp Gln Ala Ala Ser Asn Thr Ala Gly Asp Ala Asn Gly
        115                 120                 125

Lys Thr Lys Thr Tyr Ala Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
    130                 135                 140

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

Asp Gly Asn Gly Ser Pro Thr Ala Ala Ala Gln Thr Asp Ala Gln Ser

                165                 170                 175

Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Leu Asn Asp
            180                 185                 190

Gln Asn Ile Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Asn Gly
        195                 200                 205

Thr Ser Trp Ser Gly Asn Ala Ser Asn Ala Thr Ser Gly Asn Lys Ala
    210                 215                 220

Asp Phe Thr Val Asn Phe Gly Glu Lys Lys Ile Asn Gly Thr Leu Thr
225                 230                 235                 240

Ala Glu Asn Arg Gln Ala Ala Thr Phe Thr Ile Glu Gly Thr Ile Gln
                245                 250                 255

Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala Asp Ser Gly Phe Asp
            260                 265                 270

Leu Asp Gln Ser Asn Thr Thr Gly Thr Pro Lys Ala Tyr Ile Thr Asp
        275                 280                 285

Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly
    290                 295                 300

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

Gly Ser Gly Ala Ser Ala Ala Asn Ser Ala Thr Val Val Phe Gly Ala
                325                 330                 335

Lys Arg Gln Gln
            340
```

<210> 261

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 261

```
Thr Gln Asp Asn Thr Ala Asn Gly Asn Thr Ala Ala Ala Ser Gly Gly
1               5                  10                  15

Ala Gly Ala Ala Ala Ser Gly Gly Ala Ala Asp Met Pro Ser Glu Asn
            20                  25                  30

Ser Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr His Gly Asp

        35                  40                  45

Thr Ala Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
    50                  55                  60

Val Asp Gly Ile Met Ile Pro Leu Leu Pro Lys Asp Ser Glu Ser Gly
65                  70                  75                  80

Asn Asn Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg
                85                  90                  95

Lys Phe Ala His Thr Pro Lys Ser Asp Glu Lys Asp Ala Gln Ala Gly
            100                 105                 110

Thr Ala Ala Asn Gly Asp Gln Ala Ala Ser Asn Thr Ala Gly Asp Thr
        115                 120                 125

Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu
    130                 135                 140

Asn Tyr Leu Lys Tyr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn Thr
145                 150                 155                 160

Gly Glu Gly Gly Asn Gly Ser Pro Thr Ala Ala Ala Gln Thr Ala Gln
                165                 170                 175

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

Ile Pro Ser Glu Gln Asn Val Val Tyr Arg Gly Thr Trp Tyr Gly His
        195                 200                 205

Ile Ala Asn Asp Thr Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly
    210                 215                 220

Gly Asn Lys Ala Asp Phe Thr Val Asn Phe Gly Glu Lys Lys Ile Asn
225                 230                 235                 240

Gly Thr Leu Thr Ala Glu Asn Arg Gln Ala Ala Thr Phe Thr Ile Glu
                245                 250                 255
```

```
Gly Thr Ile Gln Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala Asp
            260                 265                 270

Ser Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr Arg Thr Pro Lys Ala
        275                 280                 285

Tyr Ile Thr Asn Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala
    290                 295                 300

Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly Asp Ser Gln Ala Gln
305                 310                 315                 320

Pro Ser Ala Ser Gly Ser Gly Thr Ser Ala Ala Asn Ser Ala Thr Val
                325                 330                 335

Val Phe Gly Ala
            340
```

<210> 262

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 262

```
Thr Lys Asp Lys Asp Ala Asn Gly Asn Thr Glu Ala Ala Ser Gly Gly
1               5                   10                  15

Thr Gly Ala Ala Ala Ser Gly Gly Ala Ala Asp Met Pro Ser Glu Asn
            20                  25                  30

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

Thr Ala Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
    50                  55                  60

Val Asp Gly Ile Met Ile Pro Leu Leu Ser Glu Thr Ser Glu Ser Gly
65                  70                  75                  80

Asn Thr Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
                85                  90                  95

Asn His Thr Pro Thr Ser Asp Glu Lys Asp Thr Gln Ala Gly Thr Ala
            100                 105                 110

Glu Asn Gly Asn Pro Ala Ala Ser Asn Thr Ala Gly Asp Ala Asn Gly
        115                 120                 125

Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
    130                 135                 140

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

Gly Gly Asn Gly Ser Gln Thr Ala Ala Gln Thr Asp Ala Gln Ser Met
```

```
                165                 170                 175

Phe Leu Gln Gly Glu Arg Thr Asp Glu Asn Lys Ile Pro Thr Asp Gln
            180                 185                 190

Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Asn Gly Thr
        195                 200                 205

Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly Asn Arg Ala Glu
    210                 215                 220

Phe Thr Val Asn Phe Ala Asp Lys Lys Leu Asp Gly Thr Leu Thr Ala
225                 230                 235                 240

Gly Glu Arg Thr Ser Pro Thr Phe Thr Ile Thr Ala Thr Ile Gln Gly
                245                 250                 255

Asn Gly Phe Glu Gly Thr Ala Lys Thr Gly Asp Gly Gly Phe Ala Leu
            260                 265                 270

Asp Thr Lys Asn Thr Val Glu Thr His Lys Ala His Ile Ser Asn Ala
        275                 280                 285

Lys Val Gln Gly Gly Phe Tyr Gly Ser Lys Ala Glu Glu Leu Gly Gly
    290                 295                 300

Trp Phe Ala Tyr Pro Gly Asp Ser Gln Ala Gln Pro Ser Ala Ser Gly
305                 310                 315                 320

Ser Gly Thr Ser Ala Ala Asn Ser Ala Thr Val Val Phe Gly Ala Lys
                325                 330                 335

Arg Gln Gln Leu
            340
```

<210> 263

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 263

```
Thr Lys Asp Lys Pro Ala Asn Gly Asn Thr Ala Ala Ala Ser Gly Gly
1               5                   10                  15

Thr Asp Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn
            20                  25                  30

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

Lys Glu Val Gln Lys Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
    50                  55                  60

Val Asp Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly
65                  70                  75                  80
```

```
Asn Asn Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg
                85                  90                  95

Lys Phe Asp His Thr Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly
            100                 105                 110

Thr Gln Thr Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr
        115                 120                 125

Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu
    130                 135                 140

Asn Tyr Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala
145                 150                 155                 160

Met Gln Ala Gly Glu Ser Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln
                165                 170                 175

Val Glu Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu
            180                 185                 190

Ile Pro Ser Glu Gln Asn Ile Val Tyr Arg Gly Ser Trp Tyr Gly Tyr
        195                 200                 205

Ile Ala Asn Asp Lys Ser Thr Ser Trp Ser Gly Asn Ala Ser Asn Ala
    210                 215                 220

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

Ile Thr Gly Thr Leu Thr Ala Asp Asn Arg Gln Glu Ala Thr Phe Thr
                245                 250                 255

Ile Asp Gly Asn Ile Lys Asp Asn Gly Phe Glu Gly Thr Ala Lys Thr
            260                 265                 270

Ala Glu Ser Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr Arg Thr Pro
        275                 280                 285

Lys Ala Tyr Ile Thr Asp Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro
    290                 295                 300

Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln
305                 310                 315                 320

Thr Lys Asn Ala Thr Asn Ala Ser Gly Asn Ser Ser Ala Thr Val Val
                325                 330                 335

Phe Gly Ala Lys
            340
```

<210> 264

<211> 350

<212> PRT

<213> Neisseria meningitidis

<400> 264

```
Thr Lys Asp Lys Pro Ala Asn Gly Asn Thr Ala Ala Ala Ser Gly Gly
1               5                  10                  15

Thr Asp Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn
            20                  25                  30

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

Lys Glu Val Gln Lys Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
    50                  55                  60

Val Asp Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly
65                  70                  75                  80

Ser Asn Gln Ala Asp Lys Gly Lys Lys Gly Lys Asn Gly Lys Asn Gly
                85                  90                  95

Gly Thr Asp Phe Thr Tyr Lys Thr Thr Tyr Thr Pro Lys Ser Asp Glu
            100                 105                 110

Lys Asp Thr Gln Ala Gln Thr Val Thr Gly Gly Thr Gln Thr Ala Ser
        115                 120                 125

Asn Thr Ala Gly Asp Ala Asn Gly Lys Thr Lys Thr Tyr Ala Val Glu
    130                 135                 140

Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr Gly Leu Leu Thr Arg
145                 150                 155                 160

Lys Thr Ala Gly Asn Thr Val Gly Ser Gly Asn Gly Ser Pro Thr Ala
                165                 170                 175

Ala Ala Gln Thr Ala Gln Gly Ala Gln Ser Met Phe Leu Gln Gly Glu
            180                 185                 190

Arg Thr Asp Glu Lys Glu Ile Pro Lys Glu Gln Asn Val Val Tyr Arg
        195                 200                 205

Gly Ser Trp Tyr Gly His Ile Ala Asn Gly Thr Ser Trp Ser Gly Asn
    210                 215                 220

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

Gly Glu Lys Lys Ile Asn Gly Thr Leu Thr Ala Glu Asn Arg Gln Ala
                245                 250                 255

Ala Thr Phe Thr Ile Glu Gly Thr Ile Gln Gly Asn Gly Phe Ser Gly
            260                 265                 270

Thr Ala Lys Thr Ala Asn Ser Gly Phe Asp Leu Asp Gln Ser Asn Thr
        275                 280                 285

Thr Glu Thr Pro Lys Ala Trp Ile Thr Asp Ala Lys Val Gln Glu Glu
```

```
Thr Gly Thr Pro Lys Ala Tyr Ile Thr Asp Ala Lys Val Gln Gly Gly
    290                 295                 300

Phe Tyr Gly Pro Glu Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro
305                 310                 315                 320

Gly Asp Ser Gln Ala Gln Pro Ser Ala Ser Gly Ser Gly Thr Ser Ala
                325                 330                 335

Ala Asn Ser Ala Thr Val Val Phe Gly Ala Lys Arg Gln Gln
            340                 345                 350
```

<210> 265

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 265

```
Thr Lys Asp Lys Pro Ala Asn Gly Asn Thr Ala Ala Ala Ser Gly Gly
1               5                   10                  15

Thr Asp Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn
            20                  25                  30

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

Lys Glu Val Gln Lys Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
    50                  55                  60

Val Asp Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly
65                  70                  75                  80

Asn Asn Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg
                85                  90                  95

Lys Phe Asp His Thr Pro Glu Ser Asp Glu Lys Asp Ala Gln Ala Gly
            100                 105                 110

Thr Gln Thr Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr
        115                 120                 125

Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu
    130                 135                 140

Asn Tyr Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala
145                 150                 155                 160

Met Gln Ala Gly Glu Ser Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln
                165                 170                 175

Val Glu Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu
            180                 185                 190

Ile Pro Ser Glu Gln Asn Ile Val Tyr Arg Gly Ser Trp Tyr Gly Tyr
        195                 200                 205
```

```
Ile Ala Asn Asp Lys Ser Thr Ser Trp Ser Gly Asn Ala Ser Asn Ala
    210                 215                 220

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

Ile Thr Gly Thr Leu Thr Ala Asp Asn Arg Gln Glu Ala Thr Phe Thr
                245                 250                 255

Ile Asp Gly Asn Ile Lys Asp Asn Gly Phe Glu Gly Thr Ala Lys Thr
            260                 265                 270

Ala Glu Ser Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr Arg Thr Pro
        275                 280                 285

Lys Ala Tyr Ile Thr Asp Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro
    290                 295                 300

Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln
305                 310                 315                 320

Thr Lys Asn Ala Thr Asn Ala Ser Gly Asn Ser Ser Ala Thr Val Val
                325                 330                 335

Phe Gly Ala Lys
            340
```

<210> 266

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 266

```
Thr Lys Asp Lys Pro Ala Asn Gly Asn Thr Ala Ala Ala Ser Gly Gly
1               5                   10                  15

Thr Asp Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn
            20                  25                  30

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

Lys Glu Val Gln Lys Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
    50                  55                  60

Val Asp Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly
65                  70                  75                  80

Asn Asn Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg
                85                  90                  95

Lys Phe Asp His Thr Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly
            100                 105                 110

Thr Gln Thr Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr
        115                 120                 125
```

```
        ---                 ---                 ---

Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu
    130                 135                 140

Asn Tyr Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala
145                 150                 155                 160

Met Gln Ala Gly Glu Ser Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln
                165                 170                 175

Val Glu Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu
            180                 185                 190

Ile Pro Ser Glu Gln Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His
        195                 200                 205

Ile Ala Asn Gly Thr Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly
    210                 215                 220

Gly Asn Arg Ala Glu Phe Thr Val Asp Phe Gly Ala Lys Lys Ile Asn
225                 230                 235                 240

Gly Lys Leu Thr Ala Glu Asn Arg Gln Ala Ala Thr Phe Thr Ile Glu
                245                 250                 255

Gly Asp Ile Glu Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala Glu
            260                 265                 270

Ser Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr Arg Thr Pro Lys Ala
        275                 280                 285

Tyr Ile Thr Asp Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala
    290                 295                 300

Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Lys
305                 310                 315                 320

Asn Ala Thr Asn Ala Ser Gly Asn Ser Ser Ala Thr Val Val Phe Gly
                325                 330                 335

Ala Lys Arg Gln
            340
```

<210> 267

<211> 330

<212> PRT

<213> Neisseria meningitidis

<400> 267

```
Thr Lys Asp Lys Pro Glu Asn Gly Ala Ala Ala Ser Gly Gly Thr Asp
1               5                   10                  15

Ala Ala Ala Ser Gly Gly Ala Ala Ala Met Pro Ser Glu Asn Gly Lys
            20                  25                  30
```

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

Val Lys Lys Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
    50                  55                  60

Gly Ile Met Ile Pro Leu Leu Pro Lys Asp Ser Glu Ser Gly Asn Asn
65                  70                  75                  80

Gln Ala Asp Lys Gly Lys Asn Gly Glu Thr Glu Phe Thr Arg Lys Phe
                85                  90                  95

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

Thr Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly
        115                 120                 125

Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
    130                 135                 140

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

Ser Gly Asn Gly Ser Gln Ala Ala Ala Gln Thr Asp Ala Gln Ser Met
                165                 170                 175

Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Ser Glu Gln
            180                 185                 190

Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Asn Gly Thr
        195                 200                 205

Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly Asn Arg Ala Glu
    210                 215                 220

Phe Thr Val Asp Phe Gly Ala Lys Lys Ile Asn Gly Lys Leu Thr Ala
225                 230                 235                 240

Glu Asn Arg Gln Ala Ala Thr Phe Thr Ile Glu Gly Asp Ile Glu Gly
                245                 250                 255

Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala Glu Ser Gly Phe Asp Leu
            260                 265                 270

Asp Gln Ser Asn Thr Thr Arg Thr Pro Lys Ala Tyr Ile Thr Asp Ala

        275                 280                 285

Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly
    290                 295                 300

Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Lys Asn Ala Thr Asn Ala
305                 310                 315                 320

Ser Gly Asn Ser Ser Ala Thr Val Val Phe
```

325 330

<210> 268

<211> 330

<212> PRT

<213> Neisseria meningitidis

<400> 268

```
Thr Gln Asp Lys Pro Glu Asn Gly Ala Ala Ala Leu Gly Gly Ala Gly
1               5                  10                  15

Ala Ala Ala Ser Gly Gly Val Ala Ala Met Pro Ser Glu Asn Gly Lys
            20                  25                  30

Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr His Gly Gly Thr Ala
        35                  40                  45

Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
    50                  55                  60

Gly Ile Met Ile Pro Leu Leu Pro Glu Thr Ser Glu Ser Gly Lys Asn
65                  70                  75                  80

Gln Ala Asp Lys Gly Lys Asn Gly Glu Thr Glu Phe Thr Arg Lys Phe
                85                  90                  95

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

Thr Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly
        115                 120                 125

Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
    130                 135                 140

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

Ser Gly Asn Gly Ser Gln Ala Ala Ala Gln Thr Asp Ala Gln Ser Met

                165                 170                 175

Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Ser Glu Gln
            180                 185                 190

Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Asn Gly Thr
        195                 200                 205

Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly Asn Arg Ala Glu
    210                 215                 220

Phe Thr Val Asp Phe Gly Ala Lys Lys Ile Asn Gly Lys Leu Thr Ala
225                 230                 235                 240
```

```
Glu Asn Arg Gln Ala Ala Thr Phe Thr Ile Glu Gly Asp Ile Glu Gly
                245                 250                 255

Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala Glu Ser Gly Phe Asp Leu
            260                 265                 270

Asp Gln Ser Asn Thr Thr Arg Thr Pro Lys Ala Tyr Ile Thr Asp Ala
        275                 280                 285

Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly
    290                 295                 300

Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Lys Asn Ala Thr Asn Ala
305                 310                 315                 320

Ser Gly Asn Ser Ser Ala Thr Val Val Phe
                325                 330
```

<210> 269

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 269

```
Thr Lys Asp Lys Asn Ala Asn Gly Asn Thr Pro Ala Ala Ser Ser Gly
1               5                   10                  15

Ala Gly Ala Ala Ala Ser Gly Gly Ala Ala Asp Thr Pro Ser Glu Ser
            20                  25                  30

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

Lys Glu Val Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val

    50                  55                  60

Val Asp Gly Ile Met Ile Pro Leu Leu Pro Lys Asp Ser Glu Ser Gly
65                  70                  75                  80

Asn Thr Gln Ala Asp Lys Gly Lys Asn Gly Gly Thr Lys Phe Thr Arg
                85                  90                  95

Lys Phe Glu His Thr Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly
            100                 105                 110

Thr Gln Thr Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr
        115                 120                 125

Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu
    130                 135                 140

Asn Tyr Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala
145                 150                 155                 160
```

```
Met Gln Ala Gly Glu Asn Gly Ser Gln Ala Asp Ala Lys Thr Glu Gln
                165                 170                 175

Val Glu Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu
            180                 185                 190

Ile Pro Lys Glu Gln Gln Asp Ile Val Tyr Arg Gly Ser Trp Tyr Gly
        195                 200                 205

His Ile Ala Gly Ser Thr Ser Trp Ser Gly Asn Ala Ser Asn Ala Thr
    210                 215                 220

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

Asn Gly Lys Leu Thr Ala Glu Asn Arg Gln Glu Ala Thr Phe Thr Ile
                245                 250                 255

Glu Gly Thr Ile Gln Asp Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala
            260                 265                 270

Asp Leu Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr Gly Thr Pro Lys
        275                 280                 285

Ala Tyr Ile Thr Asn Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys
    290                 295                 300

Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr
305                 310                 315                 320

Lys Asn Ala Thr Asn Ala Ser Gly Asn Ser Ser Ala Thr Val Val Phe
                325                 330                 335

Gly Ala Lys Arg
            340
```

<210> 270

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 270

```
Thr Lys Asp Lys Ala Glu Ser Gly Gly Gly Asn Gly Ala Ser Gly Gly
1               5                   10                  15

Thr Gly Ala Ala Ala Ser Gly Gly Ala Ala Asp Thr Pro Ser Glu Ser
            20                  25                  30

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

Lys Lys Val Glu Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
    50                  55                  60

Val Asp Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly
65                  70                  75                  80
```

```
Asn Thr Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
                85                  90                  95

Asp His Thr Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln
            100                 105                 110

Thr Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly
        115                 120                 125

Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
    130                 135                 140

Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln
145                 150                 155                 160

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

Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro
            180                 185                 190

Lys Glu Gln Gln Asp Ile Val Tyr Arg Gly Ser Trp Tyr Gly His Ile
        195                 200                 205

Ala Asn Asp Thr Ser Trp Ser Gly Asn Ala Ser Asp Arg Glu Gly Gly
    210                 215                 220

Asn Arg Ala Asp Phe Thr Val Asn Phe Gly Thr Lys Lys Ile Asn Gly
225                 230                 235                 240

Thr Leu Thr Ala Glu Asn Arg Gln Gln Ala Thr Phe Thr Ile Glu Gly
                245                 250                 255

Asp Ile Lys Asp Asn Gly Phe Glu Gly Thr Ala Lys Thr Asp Asp Leu
            260                 265                 270

Gly Phe Asp Leu Asp Gln Lys Asn Thr Thr Arg Thr Pro Lys Ala Tyr
        275                 280                 285

Ile Thr Asn Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu
    290                 295                 300

Glu Leu Gly Gly Trp Phe Ala Tyr Leu Gly Asp Lys Gln Thr Glu Lys
305                 310                 315                 320

Ala Thr Asp Ala Ser Gly Asn Gly Asn Ser Ala Ser Ser Ala Thr Val
                325                 330                 335

Val Phe Gly Ala
            340
```

<210> 271

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 271

```
Thr Lys Asp Lys Thr Glu Asn Gly Ala Val Ala Ser Gly Gly Thr Asp
1               5                  10                  15

Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys
            20                  25                  30

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

Val Gln Lys Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
    50                  55                  60

Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly Asn Asn
65                  70                  75                  80

Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
                85                  90                  95

Asp His Thr Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln
            100                 105                 110

Thr Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly
        115                 120                 125

Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
    130                 135                 140

Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln
145                 150                 155                 160

Ala Gly Glu Ser Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu
                165                 170                 175

Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro
            180                 185                 190

Ser Glu Gln Asn Ile Val Tyr Arg Gly Ser Trp Tyr Gly Tyr Ile Ala
        195                 200                 205

Asn Asp Lys Ser Thr Ser Trp Ser Gly Asn Ala Ser Asn Ala Thr Ser
    210                 215                 220

Gly Asn Arg Ala Glu Phe Thr Val Asn Phe Ala Asp Lys Lys Ile Thr
225                 230                 235                 240

Gly Thr Leu Thr Ala Asp Asn Arg Gln Glu Ala Thr Phe Thr Ile Asp
                245                 250                 255

Gly Asn Ile Lys Asp Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala Glu
            260                 265                 270

Ser Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr Arg Thr Pro Lys Ala
        275                 280                 285
```

```
Tyr Ile Thr Asp Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala
    290                 295                 300

Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Lys
305                 310                 315                 320

Asn Ala Thr Asn Ala Ser Gly Asn Ser Ser Ala Thr Val Val Phe Gly
                325                 330                 335

Ala Lys Arg Gln
            340
```

<210> 272

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 272

```
Thr Lys Asp Lys Leu Glu Asn Gly Ala Ala Ala Ser Gly Ser Thr Gly
1               5                   10                  15

Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys
            20                  25                  30

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

Val Gln Lys Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
    50                  55                  60

Gly Ile Met Ile Pro Leu Leu Pro Lys Ala Ser Glu Ser Gly Asn Asn
65                  70                  75                  80

Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Tyr Lys Thr
                85                  90                  95

Thr Tyr Thr Leu Glu Ser Asp Lys Lys Asp Thr Gln Ala Gln Thr Val
            100                 105                 110

Thr Asn Gly Thr Gln Thr Ala Ser Gly Thr Glu Ser Val Asn Gly Gly
        115                 120                 125

Gln Ala Gly Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu
    130                 135                 140

Asn Tyr Leu Lys Tyr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn Thr
145                 150                 155                 160

Gly Glu Gly Gly Asn Ser Ser Pro Thr Ala Ala Gln Thr Ala Gln Gly
                165                 170                 175

Ala Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Asn Lys Ile
            180                 185                 190

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

```
        195                 200                 205

Ala Asn Gly Thr Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly
    210                 215                 220

Asn Arg Ala Glu Phe Thr Val Asn Phe Asp Lys Lys Lys Ile Asn Gly
225                 230                 235                 240

Thr Leu Thr Ala Asp Asn Arg Gln Ala Ala Thr Phe Thr Ile Glu Gly
                245                 250                 255

Asp Ile Glu Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala Asp Ser
            260                 265                 270

Gly Phe Asp Leu Asp Gln Ser Asn Asn Thr Arg Thr Pro Lys Ala Tyr
        275                 280                 285

Ile Thr Asn Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu
    290                 295                 300

Glu Leu Gly Gly Trp Phe Ala Tyr Ser Asp Asp Lys Gln Thr Lys Asn
305                 310                 315                 320

Ala Thr Asp Ala Ser Gly Asn Gly Asn Ser Ala Ser Ser Ala Thr Val
                325                 330                 335

Val Phe Gly Ala
            340
```

<210> 273

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 273

```
Thr Lys Asp Lys Ala Glu Ser Gly Gly Gly Asn Gly Ala Ser Gly Gly
1               5                   10                  15

Thr Gly Ala Ala Ala Ser Asn Ser Ala Ala Ala Met Pro Ser Glu Asn
            20                  25                  30

Gly Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr His Gly Gly
        35                  40                  45

Thr Ala Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
    50                  55                  60

Val Asp Gly Ile Met Ile Pro Leu Leu Pro Lys Ala Ser Glu Ser Gly
65                  70                  75                  80

Asn Asn Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Tyr
                85                  90                  95

Lys Thr Thr Tyr Thr Leu Glu Ser Asp Lys Lys Asp Thr Gln Ala Gln
            100                 105                 110
```

```
Thr Val Thr Asn Gly Thr Gln Thr Ala Ser Gly Thr Glu Ser Val Asn
        115                 120                 125

Gly Gly Gln Ala Gly Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser
    130                 135                 140

Asn Leu Asn Tyr Leu Lys Tyr Gly Leu Leu Thr Arg Lys Thr Ala Gly
145                 150                 155                 160

Asn Thr Gly Glu Gly Gly Asn Ser Ser Pro Thr Ala Ala Gln Thr Ala
                165                 170                 175

Gln Gly Ala Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Asn
            180                 185                 190

Lys Ile Pro Thr Asp Gln Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly
        195                 200                 205

His Ile Ala Gly Ser Thr Ser Trp Ser Gly Asn Ala Ser Asn Ala Thr
    210                 215                 220

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

Asn Gly Lys Leu Thr Ala Glu Asn Arg Gln Ala Ala Thr Phe Thr Ile
                245                 250                 255

Val Gly Asp Ile Lys Asp Asn Gly Phe Glu Gly Thr Ala Lys Thr Asp
            260                 265                 270

Asn Leu Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr Gly Thr Pro Lys
        275                 280                 285

Ala Tyr Ile Thr Asn Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys
    290                 295                 300

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

Lys Asn Ala Thr Asp Ala Ser Gly Asn Gly Asn Ser Ala Ser Ser Ala
                325                 330                 335

Thr Val Val Phe
            340
```

<210> 274

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 274

```
Thr Lys Asp Lys Leu Glu Asn Gly Ala Ala Ala Ser Gly Ser Thr Gly
1               5                   10                  15

Ala Ala Ala Ser Gly Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys
            20                  25                  30
```

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

Val Gln Lys Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
    50                  55                  60

Gly Ile Met Ile Pro Leu Leu Pro Lys Asp Ser Glu Ser Gly Gly Asn
65                  70                  75                  80

Gln Ala Asp Lys Ser Lys Asn Gly Gly Thr Glu Phe Thr Arg Lys Phe
                85                  90                  95

Asp His Thr Pro Lys Ser Asp Asp Lys Asp Thr Lys Ala Gln Thr Gly
            100                 105                 110

Ala Ala Gly Ser Ser Gly Ala Gln Thr Asp Ser Gly Lys Ala Asp Val
        115                 120                 125

Asn Gly Gly Lys Ala Glu Thr Lys Thr Tyr Ala Val Glu Val Cys Cys
    130                 135                 140

Ser Asn Leu Asn Tyr Leu Lys Tyr Gly Leu Leu Thr Arg Lys Thr Ala
145                 150                 155                 160

Gly Asn Thr Val Gly Ser Gly Asn Ser Ser Gln Ala Ala Ala Gln Thr
                165                 170                 175

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

Lys Glu Ile Pro Thr Asp Gln Asn Val Val Tyr Arg Gly Ser Trp Tyr
        195                 200                 205

Gly His Ile Ala Asn Asp Thr Ser Trp Ser Gly Asn Ala Ser Asn Ala
    210                 215                 220

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

Ile Thr Gly Thr Leu Thr Ala Glu Asn Arg Gln Glu Ala Thr Phe Thr
                245                 250                 255

Ile Glu Gly Thr Ile Gln Asp Asn Gly Phe Glu Gly Thr Ala Lys Thr
            260                 265                 270

Ala Asp Leu Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr Gly Thr Pro
        275                 280                 285

Lys Ala Tyr Ile Thr Asn Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro
    290                 295                 300

Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln
305                 310                 315                 320
```

```
Thr Lys Asn Ala Thr Asn Ala Ser Gly Asn Ser Ser Ala Thr Val Val
                325                 330                 335

Phe Gly Ala Lys
            340
```

<210> 275

<211> 350

<212> PRT

<213> Neisseria meningitidis

<400> 275

```
Thr Lys Asp Lys Pro Ala Asn Gly Asn Thr Ala Ala Ala Ser Gly Gly
1               5                   10                  15

Thr Asp Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn
            20                  25                  30

Gly Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp
        35                  40                  45

Lys Lys Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
    50                  55                  60

Val Asp Gly Ile Met Ile Pro Leu Leu Pro Gln Asn Ser Thr Gly Glu
65                  70                  75                  80

Asn Asn Gln Pro Asp Gln Gly Lys Asn Gly Gly Thr Ala Phe Ile Tyr
                85                  90                  95

Lys Thr Thr Tyr Thr Pro Lys Asn Asp Asp Lys Asp Thr Lys Ala Gln
            100                 105                 110

Thr Gly Ala Ala Gly Ser Ser Gly Ala Gln Thr Ala Ser Gly Thr Glu
        115                 120                 125

Ser Val Thr Gly Gly Gln Ala Gly Thr Lys Thr Tyr Glu Val Glu Val
    130                 135                 140

Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr Gly Leu Leu Thr Arg Lys
145                 150                 155                 160

Thr Ala Gly Asn Thr Val Gly Ser Gly Asn Ser Ser Gln Ala Ala Ala
                165                 170                 175

Gln Thr Ala Gln Gly Ala Gln Ser Met Phe Leu Gln Gly Glu Arg Thr
            180                 185                 190

Asp Glu Lys Glu Ile Pro Lys Glu Gln Gln Asp Ile Val Tyr Arg Gly
        195                 200                 205

Ser Trp Tyr Gly His Ile Ala Asn Gly Thr Ser Trp Ser Gly Asn Ala
    210                 215                 220

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

```
Asp Lys Lys Ile Thr Gly Thr Leu Thr Ala Asp Asn Arg Gln Ala Ala
               245                 250                 255

Thr Phe Thr Ile Glu Gly Asp Ile Glu Gly Asn Gly Phe Ser Gly Thr
            260                 265                 270

Ala Lys Thr Asp Asn Leu Gly Phe Asp Leu Asp Gln Ser Asp Asn Thr
        275                 280                 285

Arg Thr Pro Lys Ala Tyr Ile Thr Asp Ala Lys Val Gln Gly Gly Phe

    290                 295                 300

Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly
305                 310                 315                 320

Asp Lys Gln Thr Glu Lys Ala Thr Val Ala Ser Gly Asp Gly Lys Ser
               325                 330                 335

Ala Ser Ser Ala Thr Val Val Phe Gly Ala Lys Arg Gln Gln
            340                 345                 350
```

<210> 276

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 276

```
Thr Gln Asp Lys Pro Gly Asn Gly Ala Ala Ala Ser Gly Gly Thr Gly
1               5                   10                  15

Ala Ala Ala Ser Gly Gly Ala Ala Asp Met Pro Ser Glu Asn Ser Lys
            20                  25                  30

Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr His Gly Gly Thr Ala
        35                  40                  45

Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
    50                  55                  60

Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly His Asn
65                  70                  75                  80

Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
               85                  90                  95

Asn His Thr Pro Thr Ser Asp Glu Lys Asp Thr Gln Ala Gly Thr Ala
            100                 105                 110

Ala Asn Gly Asn Gln Ala Ala Ser Asn Thr Ala Gly Asp Ala Asn Gly
        115                 120                 125

Lys Thr Lys Thr Tyr Ala Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
    130                 135                 140
```

```
Leu Lys Tyr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn Thr Gly Glu
145                 150                 155                 160

Gly Gly Asn Gly Ser Gln Thr Ala Ala Gln Thr Asp Ala Gln Ser Met

                165                 170                 175

Phe Leu Gln Gly Glu Arg Thr Asp Glu Asn Lys Ile Pro Thr Asp Gln
            180                 185                 190

Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Asn Gly Thr
        195                 200                 205

Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly Asn Arg Ala Glu
    210                 215                 220

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

Glu Asn Arg Gln Ala Ala Thr Phe Thr Ile Glu Gly Asp Ile Lys Asp
                245                 250                 255

Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala Asp Leu Gly Phe Asp Leu
            260                 265                 270

Asp Gln Ser Asn Thr Thr Gly Thr Pro Lys Ala Tyr Ile Thr Asn Ala
        275                 280                 285

Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Asp Glu Leu Gly Gly
    290                 295                 300

Trp Phe Ala Tyr Pro Gly Asp Asn Gln Ala Gln Pro Ser Ala Ser Gly
305                 310                 315                 320

Ser Gly Ala Ser Ala Ala Asn Ser Ala Thr Val Val Phe Gly Ala Lys
                325                 330                 335

Arg Gln Gln Leu
            340
```

<210> 277

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 277

```
Thr Lys Asp Asn Thr Ala Asn Gly Asn Thr Ala Ala Ala Ser Gly Gly
1               5                   10                  15

Thr Gly Ala Ala Ala Ser Gly Gly Ala Ala Asp Met Pro Ser Glu Asn
            20                  25                  30

Ser Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp
```

```
        35                  40                  45

Lys Lys Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
    50                  55                  60

Val Asp Gly Ile Met Ile Pro Leu Leu Pro Lys Asp Ser Glu Ser Gly
65                  70                  75                  80

Asn Asn Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg
                85                  90                  95

Lys Phe Asp His Thr Pro Lys Ser Asp Glu Lys Asp Thr Gln Ala Gly
            100                 105                 110

Thr Ala Ala Asn Gly Asp Gln Ala Ala Ser Asn Thr Ala Gly Asp Thr
        115                 120                 125

Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu
    130                 135                 140

Asn Tyr Leu Lys Tyr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn Thr
145                 150                 155                 160

Val Gly Ser Gly Asn Gly Ser Pro Thr Ala Ala Gln Thr Asp Ala Gln
                165                 170                 175

Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Asn
            180                 185                 190

Asp Gln Asn Ile Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Asn
        195                 200                 205

Gly Thr Ser Trp Ser Gly Asn Ala Ser Asn Ala Thr Ser Gly Asn Lys
    210                 215                 220

Ala Asp Phe Thr Val Asn Phe Gly Glu Lys Lys Ile Asn Gly Thr Leu
225                 230                 235                 240

Thr Ala Glu Asn Arg Gln Ala Ala Thr Phe Thr Ile Glu Gly Thr Ile
                245                 250                 255

Gln Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala Asp Ser Gly Phe
            260                 265                 270

Asp Leu Asp Gln Ser Asn Thr Thr Gly Thr Pro Lys Ala Tyr Ile Thr
        275                 280                 285

Asn Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Met
    290                 295                 300

Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln Ala Gln Pro Ser Ala
305                 310                 315                 320

Ser Gly Ser Gly Ala Ser Ala Ala Asn Ser Ala Thr Val Val Phe Gly
                325                 330                 335
```

```
Ala Lys Arg Gln
            340
```

<210> 278

<211> 340

<212> PRT

<213> Neisseria meningitidis

<400> 278

```
Thr Gln Asp Lys Pro Glu Asn Gly Ala Ala Ala Leu Gly Gly Ala Gly
1               5                  10                  15

Ala Ala Ala Ser Gly Gly Val Ala Ala Met Pro Ser Glu Asn Gly Lys
            20                  25                  30

Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr His Gly Gly Thr Ala
        35                  40                  45

Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
    50                  55                  60

Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly Asn Asn
65                  70                  75                  80

Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
                85                  90                  95

Asp His Thr Pro Lys Ser Asp Glu Lys Asp Thr Gln Ala Gly Thr Ala
            100                 105                 110

Ala Asn Gly Asp Gln Ala Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly
        115                 120                 125

Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
    130                 135                 140

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

Gly Gly Asn Gly Ser Pro Thr Ala Ala Gln Thr Ala Gln Gly Ala Gln
                165                 170                 175

Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Asn Lys Ile Pro Ser
            180                 185                 190

Glu Gln Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Asn
        195                 200                 205

Gly Thr Ser Trp Ser Gly Asn Ala Ser Asn Ala Thr Ser Gly Asn Lys
    210                 215                 220

Ala Asp Phe Thr Val Asn Phe Gly Glu Lys Lys Ile Thr Gly Thr Leu
225                 230                 235                 240

Thr Ala Glu Asn Arg Gln Gln Ala Thr Phe Thr Ile Glu Gly Met Ile
```

```
                245                 250                 255

Gln Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala Asp Ser Gly Phe
            260                 265                 270

Asp Leu Asp Gln Ser Asn Thr Thr Gly Thr Pro Lys Ala Tyr Ile Thr
        275                 280                 285

Asn Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu
    290                 295                 300

Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln Ala Gln Pro Ser Ala
305                 310                 315                 320

Ser Gly Ser Gly Ala Ser Ala Ala Asn Ser Ala Thr Val Val Phe Gly
                325                 330                 335

Ala Lys Arg Gln
            340
```

<210> 279

<211> 539

<212> PRT

<213> Neisseria meningitidis

<400> 279

```
Asn Ser Gly Ala Ala Tyr Gly Phe Ala Val Lys Leu Pro Arg Arg Asn
1               5                   10                  15

Ala His Phe Asn Pro Lys Tyr Lys Glu Lys His Lys Pro Leu Gly Ser
            20                  25                  30

Met Asp Trp Lys Lys Leu Gln Arg Gly Glu Pro Asn Ser Phe Ser Glu
        35                  40                  45

Arg Asp Glu Leu Glu Lys Lys Arg Gly Ser Ser Glu Leu Ile Glu Ser
    50                  55                  60

Lys Trp Glu Asp Gly Gln Ser Arg Val Val Gly Tyr Thr Asn Phe Thr
65                  70                  75                  80

Tyr Val Arg Ser Gly Tyr Val Tyr Leu Asn Lys Asn Asn Ile Asp Ile
                85                  90                  95

Lys Asn Asn Ile Val Leu Phe Gly Pro Asp Gly Tyr Leu Tyr Tyr Lys
            100                 105                 110

Gly Lys Glu Pro Ser Lys Glu Leu Pro Ser Glu Lys Ile Thr Tyr Lys
        115                 120                 125

Gly Thr Trp Asp Tyr Val Thr Asp Ala Met Glu Lys Gln Arg Phe Glu
    130                 135                 140

Gly Leu Gly Ser Ala Ala Gly Gly Asp Lys Ser Gly Ala Leu Ser Ala
145                 150                 155                 160
```

```
Leu Glu Glu Gly Val Leu Arg Asn Gln Ala Glu Ala Ser Ser Gly His
                165                 170                 175

Thr Asp Phe Gly Met Thr Ser Glu Phe Glu Val Asp Phe Ser Asp Lys
            180                 185                 190

Thr Ile Lys Gly Thr Leu Tyr Arg Asn Asn Arg Ile Thr Gln Asn Asn
        195                 200                 205

Ser Glu Asn Lys Gln Ile Lys Thr Thr Arg Tyr Thr Ile Gln Ala Thr
    210                 215                 220

Leu His Gly Asn Arg Phe Lys Gly Lys Ala Leu Ala Ala Asp Lys Gly
225                 230                 235                 240

Ala Thr Asn Gly Ser His Pro Phe Ile Ser Asp Ser Asp Ser Leu Glu
                245                 250                 255

Gly Gly Phe Tyr Gly Pro Lys Gly Glu Glu Leu Ala Gly Lys Phe Leu
            260                 265                 270

Ser Asn Asp Asn Lys Val Ala Ala Val Phe Gly Ala Lys Gln Lys Asp
        275                 280                 285

Lys Lys Asp Gly Glu Asn Ala Ala Gly Pro Ala Thr Glu Thr Val Ile
    290                 295                 300

Asp Ala Tyr Arg Ile Thr Gly Glu Glu Phe Lys Lys Glu Gln Ile Asp
305                 310                 315                 320

Ser Phe Gly Asp Val Lys Lys Leu Leu Val Asp Gly Val Glu Leu Ser
                325                 330                 335

Leu Leu Pro Ser Glu Gly Asn Lys Ala Ala Phe Gln His Glu Ile Glu
            340                 345                 350

Gln Asn Gly Val Lys Ala Thr Val Cys Cys Ser Asn Leu Asp Tyr Met
        355                 360                 365

Ser Phe Gly Lys Leu Ser Lys Glu Asn Lys Asp Asp Met Phe Leu Gln
    370                 375                 380

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

Ala Lys Tyr Arg Gly Thr Trp Tyr Gly Tyr Ile Ala Asn Gly Thr Ser
                405                 410                 415

Trp Ser Gly Glu Ala Ser Asn Gln Glu Gly Gly Asn Arg Ala Glu Phe
            420                 425                 430

Asp Val Asp Phe Ser Thr Lys Lys Ile Ser Gly Thr Leu Thr Ala Lys
        435                 440                 445

Asp Arg Thr Ser Pro Ala Phe Thr Ile Thr Ala Met Ile Lys Asp Asn
    450                 455                 460
```

```
Gly Phe Ser Gly Val Ala Lys Thr Gly Glu Asn Gly Phe Ala Leu Asp
465                 470                 475                 480

Pro Gln Asn Thr Gly Asn Ser His Tyr Thr His Ile Glu Ala Thr Val
                485                 490                 495

Ser Gly Gly Phe Tyr Gly Lys Asn Ala Ile Glu Met Gly Gly Ser Phe
            500                 505                 510

Ser Phe Pro Gly Asn Ala Pro Glu Gly Lys Gln Glu Lys Ala Ser Val
        515                 520                 525

Val Phe Gly Ala Lys Arg Gln Gln Leu Val Gln
    530                 535
```

<210> 280

<211> 280

<212> PRT

<213> Neisseria meningitidis

<400> 280

```
Asn Ser Gly Ala Ala Tyr Gly Phe Ala Val Lys Leu Pro Arg Arg Asn
1               5                   10                  15

Ala His Phe Asn Pro Lys Tyr Lys Glu Lys His Lys Pro Leu Gly Ser
            20                  25                  30

Met Asp Trp Lys Lys Leu Gln Arg Gly Glu Pro Asn Ser Phe Ser Glu
        35                  40                  45

Arg Asp Glu Leu Glu Lys Lys Arg Gly Ser Ser Glu Leu Ile Glu Ser
    50                  55                  60

Lys Trp Glu Asp Gly Gln Ser Arg Val Val Gly Tyr Thr Asn Phe Thr
65                  70                  75                  80

Tyr Val Arg Ser Gly Tyr Val Tyr Leu Asn Lys Asn Asn Ile Asp Ile
                85                  90                  95

Lys Asn Asn Ile Val Leu Phe Gly Pro Asp Gly Tyr Leu Tyr Tyr Lys
            100                 105                 110

Gly Lys Glu Pro Ser Lys Glu Leu Pro Ser Glu Lys Ile Thr Tyr Lys
        115                 120                 125

Gly Thr Trp Asp Tyr Val Thr Asp Ala Met Glu Lys Gln Arg Phe Glu
    130                 135                 140

Gly Leu Gly Ser Ala Ala Gly Gly Asp Lys Ser Gly Ala Leu Ser Ala
145                 150                 155                 160

Leu Glu Glu Gly Val Leu Arg Asn Gln Ala Glu Ala Ser Ser Gly His
                165                 170                 175

Thr Asp Phe Gly Met Thr Ser Glu Phe Glu Val Asp Phe Ser Asp Lys
            180                 185                 190
```

Thr Ile Lys Gly Thr Leu Tyr Arg Asn Asn Arg Ile Thr Gln Asn Asn
195 200 205

Ser Glu Asn Lys Gln Ile Lys Thr Thr Arg Tyr Thr Ile Gln Ala Thr
210 215 220

Leu His Gly Asn Arg Phe Lys Gly Lys Ala Leu Ala Ala Asp Lys Gly
225 230 235 240

Ala Thr Asn Gly Ser His Pro Phe Ile Ser Asp Ser Asp Ser Leu Glu
245 250 255

Gly Gly Phe Tyr Gly Pro Lys Gly Glu Glu Leu Ala Gly Lys Phe Leu
260 265 270

Ser Asn Asp Asn Lys Val Ala Ala
275 280

<210> 281

<211> 654

<212> PRT

<213> Neisseria meningitidis

<400> 281

Gln Gly Gly Tyr Gly Phe Ala Met Arg Leu Lys Arg Arg Asn Trp Tyr
1 5 10 15

Pro Gly Ala Glu Glu Ser Glu Val Lys Leu Asn Glu Ser Asp Trp Glu
20 25 30

Ala Thr Gly Leu Pro Thr Lys Pro Lys Glu Leu Pro Lys Arg Gln Lys
35 40 45

Ser Val Ile Glu Lys Val Glu Thr Asp Gly Asp Ser Asp Ile Tyr Ser
50 55 60

Ser Pro Tyr Leu Thr Pro Ser Asn His Gln Asn Gly Ser Ala Gly Asn
65 70 75 80

Gly Val Asn Gln Pro Lys Asn Gln Ala Thr Gly His Glu Asn Phe Gln
85 90 95

Tyr Val Tyr Ser Gly Trp Phe Tyr Lys His Ala Ala Ser Glu Lys Asp
100 105 110

Phe Ser Asn Lys Lys Ile Lys Ser Gly Asp Asp Gly Tyr Ile Phe Tyr
115 120 125

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

Tyr Lys Gly Val Trp His Phe Val Thr Asp Thr Lys Lys Gly Gln Asp
145 150 155 160

```
Phe Arg Glu Ile Ile Gln Pro Ser Lys Lys Gln Gly Asp Arg Tyr Ser
                165                 170                 175

Gly Phe Ser Gly Asp Gly Ser Glu Glu Tyr Ser Asn Lys Asn Glu Ser
            180                 185                 190

Thr Leu Lys Asp Asp His Glu Gly Tyr Gly Phe Thr Ser Asn Leu Glu
        195                 200                 205

Val Asp Phe Gly Asn Lys Lys Leu Thr Gly Lys Leu Ile Arg Asn Asn
    210                 215                 220

Ala Ser Leu Asn Asn Asn Thr Asn Asn Asp Lys His Thr Thr Gln Tyr
225                 230                 235                 240

Tyr Ser Leu Asp Ala Gln Ile Thr Gly Asn Arg Phe Asn Gly Thr Ala
                245                 250                 255

Thr Ala Thr Asp Lys Lys Glu Asn Glu Thr Lys Leu His Pro Phe Val
            260                 265                 270

Ser Asp Ser Ser Ser Leu Ser Gly Gly Phe Phe Gly Pro Gln Gly Glu
        275                 280                 285

Glu Leu Gly Phe Arg Phe Leu Ser Asp Asp Gln Lys Val Ala Val Val
    290                 295                 300

Gly Ser Ala Lys Thr Lys Asp Lys Leu Glu Asn Gly Ala Ala Ala Ser
305                 310                 315                 320

Gly Ser Thr Gly Ala Ala Ala Ser Gly Gly Ala Ala Gly Thr Ser Ser
                325                 330                 335

Glu Asn Ser Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Leu
            340                 345                 350

Asn Asp Lys Lys Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln
        355                 360                 365

Leu Val Val Asp Gly Ile Met Ile Pro Leu Leu Pro Lys Asp Ser Glu
    370                 375                 380

Ser Gly Asn Thr Gln Ala Asp Lys Gly Lys Asn Gly Gly Thr Glu Phe
385                 390                 395                 400

Thr Arg Lys Phe Glu His Thr Pro Glu Ser Asp Lys Lys Asp Ala Gln

                405                 410                 415

Ala Gly Thr Gln Thr Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly
            420                 425                 430

Asp Thr Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser
        435                 440                 445

Asn Leu Asn Tyr Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys
```

```
    450                 455                 460

Ser Ala Met Gln Ala Gly Gly Asn Ser Ser Gln Ala Asp Ala Lys Thr
465                 470                 475                 480

Glu Gln Val Glu Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu
                485                 490                 495

Lys Glu Ile Pro Thr Asp Gln Asn Val Val Tyr Arg Gly Ser Trp Tyr
            500                 505                 510

Gly His Ile Ala Asn Gly Thr Ser Trp Ser Gly Asn Ala Ser Asp Lys
        515                 520                 525

Glu Gly Gly Asn Arg Ala Glu Phe Thr Val Asn Phe Ala Asp Lys Lys
    530                 535                 540

Ile Thr Gly Lys Leu Thr Ala Glu Asn Arg Gln Ala Gln Thr Phe Thr
545                 550                 555                 560

Ile Glu Gly Met Ile Gln Gly Asn Gly Phe Glu Gly Thr Ala Lys Thr
                565                 570                 575

Ala Glu Ser Gly Phe Asp Leu Asp Gln Lys Asn Thr Thr Arg Thr Pro
            580                 585                 590

Lys Ala Tyr Ile Thr Asp Ala Lys Val Lys Gly Gly Phe Tyr Gly Pro
        595                 600                 605

Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln
    610                 615                 620

Thr Glu Lys Ala Thr Ala Thr Ser Ser Asp Gly Asn Ser Ala Ser Ser
625                 630                 635                 640

Ala Thr Val Val Phe Gly Ala Lys Arg Gln Gln Pro Val Gln
                645                 650
```

<210> 282

<211> 303

<212> PRT

<213> Neisseria meningitidis

<400> 282

```
Gln Gly Gly Tyr Gly Phe Ala Met Arg Leu Lys Arg Arg Asn Trp Tyr
1               5                   10                  15

Pro Gly Ala Glu Glu Ser Glu Val Lys Leu Asn Glu Ser Asp Trp Glu
            20                  25                  30

Ala Thr Gly Leu Pro Thr Lys Pro Lys Glu Leu Pro Lys Arg Gln Lys
        35                  40                  45

Ser Val Ile Glu Lys Val Glu Thr Asp Gly Asp Ser Asp Ile Tyr Ser
    50                  55                  60
```

```
Ser Pro Tyr Leu Thr Pro Ser Asn His Gln Asn Gly Ser Ala Gly Asn
65                  70                  75                  80

Gly Val Asn Gln Pro Lys Asn Gln Ala Thr Gly His Glu Asn Phe Gln
                85                  90                  95

Tyr Val Tyr Ser Gly Trp Phe Tyr Lys His Ala Ala Ser Glu Lys Asp
            100                 105                 110

Phe Ser Asn Lys Lys Ile Lys Ser Gly Asp Asp Gly Tyr Ile Phe Tyr
        115                 120                 125

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

Tyr Lys Gly Val Trp His Phe Val Thr Asp Thr Lys Lys Gly Gln Asp
145                 150                 155                 160

Phe Arg Glu Ile Ile Gln Pro Ser Lys Lys Gln Gly Asp Arg Tyr Ser
                165                 170                 175

Gly Phe Ser Gly Asp Gly Ser Glu Glu Tyr Ser Asn Lys Asn Glu Ser
            180                 185                 190

Thr Leu Lys Asp Asp His Glu Gly Tyr Gly Phe Thr Ser Asn Leu Glu
        195                 200                 205

Val Asp Phe Gly Asn Lys Lys Leu Thr Gly Lys Leu Ile Arg Asn Asn
    210                 215                 220

Ala Ser Leu Asn Asn Asn Thr Asn Asn Asp Lys His Thr Thr Gln Tyr
225                 230                 235                 240

Tyr Ser Leu Asp Ala Gln Ile Thr Gly Asn Arg Phe Asn Gly Thr Ala
                245                 250                 255

Thr Ala Thr Asp Lys Lys Glu Asn Glu Thr Lys Leu His Pro Phe Val
            260                 265                 270

Ser Asp Ser Ser Ser Leu Ser Gly Gly Phe Phe Gly Pro Gln Gly Glu
        275                 280                 285

Glu Leu Gly Phe Arg Phe Leu Ser Asp Asp Gln Lys Val Ala Val
    290                 295                 300
```

<210> 283

<211> 513

<212> PRT

<213> Haemophilus parasuis

<400> 283

```
Glu Tyr Lys Asp Val Glu Thr Asp Lys Lys Val Lys Glu Gln Leu Gly
1               5                   10                  15

Glu Leu Met Glu Pro Ala Leu Gly Tyr Val Val Lys Val Pro Val Ser
```

```
                20                  25                  30

Gln Ser Gly Val Lys Arg Thr Glu Ile Ser Asn Pro Glu Ala Ile Thr
        35                  40                  45

Asp Glu Asp Leu Asn Lys Ile Pro Asn Tyr Glu Ile Ile Lys Gly Val
    50                  55                  60

Ala Tyr Pro Asn Tyr Gly Glu Leu Val Asp Lys Thr Ala Ala Glu Thr
65                  70                  75                  80

Met Lys Tyr Val Arg Ser Gly Tyr Val Ile Asp Val Tyr His Ser Gly
                85                  90                  95

Thr Arg Asp Lys Gly Tyr Val Phe Tyr Lys Gly Ile Thr Pro Ser Lys
            100                 105                 110

Glu Leu Pro Gln Gly Pro Ala Leu Thr Tyr Gln Gly Glu Trp Asp Phe
        115                 120                 125

Thr Ser Asp Ala Asn Leu Asn Asn Glu Glu Gly Arg Pro Thr Tyr Leu
    130                 135                 140

Asn Asp Asp Tyr Tyr Thr Thr Trp Ile Gly Lys Arg Ala Gly Leu Val
145                 150                 155                 160

Ser Gly Asp Ala Lys Pro Ser Lys His Lys Tyr Thr Ser Gln Phe Lys
                165                 170                 175

Val Asp Phe Ala Thr Lys Lys Met Thr Gly Lys Leu Ser Asp Lys Glu
            180                 185                 190

Lys Thr Ile Tyr Thr Val Asn Ala Asp Ile Arg Gly Asn Arg Phe Thr
        195                 200                 205

Gly Ser Ala Thr Ala Ser Asp Lys Asp Lys Gly Lys Gly Ala Ser Tyr
    210                 215                 220

Asn Phe Phe Ser Val Asp Ser Gln Ser Leu Glu Gly Gly Phe Tyr Gly
225                 230                 235                 240

Pro Lys Ala Glu Glu Met Ala Gly Lys Phe Val Ala Asp Asp Lys Ser
                245                 250                 255

Leu Phe Ala Val Phe Ser Ala Lys His Asn Ala Ser Asn Val Asn Thr
            260                 265                 270

Val Arg Ile Ile Asp Ala Ser Lys Ile Asp Leu Thr Asn Phe Ser Ile
        275                 280                 285

Ser Glu Leu Thr Asn Phe Gly Asp Ala Ser Val Leu Ile Ile Asp Gly
    290                 295                 300

Lys Lys Met Glu Leu Ala Gly Ser Glu Phe Thr Asn Lys His Thr Ile
305                 310                 315                 320
```

```
Asp Ile Asn Gly Lys Lys Met Val Ala Val Ala Cys Cys Ser Asn Leu
                325                 330                 335

Glu Tyr Met Lys Phe Gly Gln Leu Trp Gln Gln Thr Glu Gly Glu Lys
            340                 345                 350

Gln Val Lys Asp Asn Ser Leu Phe Leu Gln Gly Glu Arg Thr Ala Thr
        355                 360                 365

Asp Lys Met Pro Lys Asp Gly Asn Tyr Lys Tyr Ile Gly Thr Trp Asp
    370                 375                 380

Ala Gln Val Ser Lys Glu Asn Asn Tyr Trp Val Ala Thr Ala Asp Asp
385                 390                 395                 400

Asp Arg Lys Ala Gly Tyr Arg Thr Glu Phe Asp Val Asp Phe Gly Ser
                405                 410                 415

Lys Asn Leu Ser Gly Lys Leu Phe Asp Lys Asn Gly Val Asn Pro Val
            420                 425                 430

Phe Thr Val Asn Ala Lys Ile Asp Gly Asn Gly Phe Thr Gly Glu Ala
        435                 440                 445

Lys Thr Ser Asp Ala Gly Phe Val Leu Asp Pro Gly Ser Leu Arg His
    450                 455                 460

Asp Asn Val Lys Phe Ser Asp Val Ala Val Ser Gly Gly Phe Tyr Gly
465                 470                 475                 480

Pro Thr Ala Ala Glu Leu Gly Gly Gln Phe Arg Tyr Gln Ser Asp Asn
                485                 490                 495

Gly Ser Val Gly Val Gly Ala Val Phe Gly Ala Lys Gln Gln Val Lys
            500                 505                 510

Lys
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<210> 284

<211> 2114

<212> DNA

<213> Neisseria meningitidis

<400> 284

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tgtatcggcg gcaatttcgg cgtgcagcct gttgtcgaat caacgccgac gtcactttca       60

agtctaagga cgttcccact ccgccccctg ccaaaccttc tatagaaatc acgccggtca      120

accggcccgc cgtcggtgcg gcaatgcggc tgccaaggcg gaatactgct tttcatcgtg      180

aagatggcac ggaaattcca aatagcaaac aagcagaaga aaagctgtcg tttcaagaag      240

gtgatgttct gtttttatac ggttcaaaag gaaataaact tcaacaactt aaaagcgaaa      300

ttcataaacg tgattccgat gtagaaatta ggacatcaga aaaggaaaat aaaaaatatg      360

attataaatt tgtagatgca ggttatgtat atgtaaaggg aaaagatgaa attaagtgga      420

cttcagatta caagcagttt tccaaccgct taggttatga cggttttgta tattattccg      480
```

```
gagaacgtcc ttcccaatct ttaccgagtg cgggaacggt ggaatatttt ggtaactggc      540
aatatatgac cgatgccaaa cgtcatcgag caggtaaggc ggttggcatt gacaatttgg      600
gttattacac attttatggt aacgatgttg gtgcaacttc ttatgcggct aaggatgtcg      660
acgaaaggga aaaacatcct gctaaatata cggtagattt cggtaacaaa accctgacgg      720

gcgagctgat taaaaaccaa tatgtcaaac ccagtgagaa gcaaaaaccg ctgaccattt      780
acaacatcac tgccgattta aacggcaacc gctttaccgg cagtgccaag gtcaatcctg      840
atttagcgaa aagccatgcc aataaggagc atttgttttt ccatgccgat gccgatcagc      900
ggcttgaggg cggttttttc ggcgataagg gggaagagct tgccggacgg tttatcagca      960
acgacaacag cgtattcggt gtattcgcag gcaaacaaaa tagccccgtg ccgtctggaa     1020
aacacaccaa aatcttggat tctctgaaaa tttccgttga tgaggcaagt ggtgaaaatc     1080
cccgaccgtt tgccatttct cctatgcccg attttggtca tcccgacaaa cttcttgtcg     1140
aagggcatga aattcctttg gttagccaag agaaaaccat cgagcttgcc gacggcagga     1200
aaatgaccgt cagtgcttgt tgcgactttt tgacctatgt gaaactcgga cggataaaaa     1260
ccgaacgtcc cgccgccaaa ccgaaggcgc aggacgaaga ggattcggac attgataatg     1320
gcgaagaaag cgaagacgaa atcggcgatg aagaagaagg caccgaagat gcagccgcag     1380
gagatgaagg cagcgaagaa gacgaagcca cagaaaacga agacggcgaa gaagacgaag     1440
ctgaagaacc tgaagaagaa tcgtcggcag aaggcaacgg cagttcaaac gccatcctgc     1500
ctgtcccgga agcctctaaa ggcagggata tcgacctttt cctgaaaggt atccgcacgg     1560
cagaaacgaa tattccgcaa actggagaag cacgctatac cggcacttgg gaagcgcgta     1620
tcggcaaacc cattcaatgg gacaatcatg cggataaaga agcggcaaaa gcagtattta     1680
ccgttgattt cggcaagaaa tcgatttccg gaacgctgac ggagaaaaac ggtgtagaac     1740
ctgctttccg tattgaaaac ggcgtgattg agggcaacgg tttccatgcg acagcgcgca     1800
ctcgggatga cggcatcgac ctttccgggc agggttcgac caaaccgcag atcttcaaag     1860
ctaatgatct tcgtgtagaa ggaggatttt acggcccgaa ggcggaggaa ttgggcggta     1920
ttattttcaa taatgatggg aaatctcttg gtataactga aggtactgaa aataaagttg     1980
aagctgatgt tgatgttgat gttgatgttg atgttgatgt tgatgctgat gttgaacagt     2040
taaaacctga agttaaaccc caattcggcg tggtattcgg tgcgaagaaa gataataaag     2100
aggtggaaaa atga                                                       2114
```

<210> 285
<211> 707
<212> PRT
<213> Neisseria meningitidis

<400> 285

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Cys Ile Gly Gly Asn Phe Gly Val Gln Pro Val Val Glu Ser Thr Pro
1               5                  10                  15

Thr Ala Tyr Pro Val Thr Phe Lys Ser Lys Asp Val Pro Thr Pro Pro
            20                  25                  30
```

```
Pro Ala Lys Pro Ser Ile Glu Ile Thr Pro Val Asn Arg Pro Ala Val
        35                  40                  45

Gly Ala Ala Met Arg Leu Pro Arg Arg Asn Thr Ala Phe His Arg Glu
    50                  55                  60

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

Phe Gln Glu Gly Asp Val Leu Phe Leu Tyr Gly Ser Lys Gly Asn Lys
                85                  90                  95

Leu Gln Gln Leu Lys Ser Glu Ile His Lys Arg Asp Ser Asp Val Glu
            100                 105                 110

Ile Arg Thr Ser Glu Lys Glu Asn Lys Lys Tyr Asp Tyr Lys Phe Val
        115                 120                 125

Asp Ala Gly Tyr Val Tyr Val Lys Gly Lys Asp Glu Ile Lys Trp Thr
    130                 135                 140

Ser Asp Tyr Lys Gln Phe Ser Asn Arg Leu Gly Tyr Asp Gly Phe Val
145                 150                 155                 160

Tyr Tyr Ser Gly Glu Arg Pro Ser Gln Ser Leu Pro Ser Ala Gly Thr
                165                 170                 175

Val Glu Tyr Phe Gly Asn Trp Gln Tyr Met Thr Asp Ala Lys Arg His
            180                 185                 190

Arg Ala Gly Lys Ala Val Gly Ile Asp Asn Leu Gly Tyr Tyr Thr Phe
        195                 200                 205

Tyr Gly Asn Asp Val Gly Ala Thr Ser Tyr Ala Ala Lys Asp Val Asp
    210                 215                 220

Glu Arg Glu Lys His Pro Ala Lys Tyr Thr Val Asp Phe Gly Asn Lys
225                 230                 235                 240

Thr Leu Thr Gly Glu Leu Ile Lys Asn Gln Tyr Val Lys Pro Ser Glu
                245                 250                 255

Lys Gln Lys Pro Leu Thr Ile Tyr Asn Ile Thr Ala Asp Leu Asn Gly
            260                 265                 270

Asn Arg Phe Thr Gly Ser Ala Lys Val Asn Pro Asp Leu Ala Lys Ser
        275                 280                 285

His Ala Asn Lys Glu His Leu Phe Phe His Ala Asp Ala Asp Gln Arg
    290                 295                 300

Leu Glu Gly Gly Phe Phe Gly Asp Lys Gly Glu Glu Leu Ala Gly Arg
305                 310                 315                 320

Phe Ile Ser Asn Asp Asn Ser Val Phe Gly Val Phe Ala Gly Lys Gln
                325                 330                 335
```

```
Asn Ser Pro Val Pro Ser Gly Lys His Thr Lys Ile Leu Asp Ser Leu
            340                 345                 350

Lys Ile Ser Val Asp Glu Ala Ser Gly Glu Asn Pro Arg Pro Phe Ala
        355                 360                 365

Ile Ser Pro Met Pro Asp Phe Gly His Pro Asp Lys Leu Leu Val Glu
    370                 375                 380

Gly His Glu Ile Pro Leu Val Ser Gln Glu Lys Thr Ile Glu Leu Ala
385                 390                 395                 400

Asp Gly Arg Lys Met Thr Val Ser Ala Cys Cys Asp Phe Leu Thr Tyr
                405                 410                 415

Val Lys Leu Gly Arg Ile Lys Thr Glu Arg Pro Ala Ala Lys Pro Lys
            420                 425                 430

Ala Gln Asp Glu Glu Asp Ser Asp Ile Asp Asn Gly Glu Glu Ser Glu
        435                 440                 445

Asp Glu Ile Gly Asp Glu Glu Glu Gly Thr Glu Asp Ala Ala Ala Gly
    450                 455                 460

Asp Glu Gly Ser Glu Glu Asp Glu Ala Thr Glu Asn Glu Asp Gly Glu
465                 470                 475                 480

Glu Asp Glu Ala Glu Glu Pro Glu Glu Glu Ser Ser Ala Glu Gly Asn
                485                 490                 495

Gly Ser Ser Asn Ala Ile Leu Pro Val Pro Glu Ala Ser Lys Gly Arg
            500                 505                 510

Asp Ile Asp Leu Phe Leu Lys Gly Ile Arg Thr Ala Glu Thr Asn Ile
        515                 520                 525

Pro Gln Thr Gly Glu Ala Arg Tyr Thr Gly Thr Trp Glu Ala Arg Ile

    530                 535                 540

Gly Lys Pro Ile Gln Trp Asp Asn His Ala Asp Lys Glu Ala Ala Lys
545                 550                 555                 560

Ala Val Phe Thr Val Asp Phe Gly Lys Lys Ser Ile Ser Gly Thr Leu
                565                 570                 575

Thr Glu Lys Asn Gly Val Glu Pro Ala Phe Arg Ile Glu Asn Gly Val
            580                 585                 590

Ile Glu Gly Asn Gly Phe His Ala Thr Ala Arg Thr Arg Asp Asp Gly
        595                 600                 605

Ile Asp Leu Ser Gly Gln Gly Ser Thr Lys Pro Gln Ile Phe Lys Ala
    610                 615                 620
```

```
Asn Asp Leu Arg Val Glu Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu
625                 630                 635                 640

Leu Gly Gly Ile Ile Phe Asn Asn Asp Gly Lys Ser Leu Gly Ile Thr
                645                 650                 655

Glu Gly Thr Glu Asn Lys Val Glu Ala Asp Val Asp Val Asp Val Asp
            660                 665                 670

Val Asp Val Asp Val Asp Ala Asp Val Glu Gln Leu Lys Pro Glu Val
        675                 680                 685

Lys Pro Gln Phe Gly Val Val Phe Gly Ala Lys Lys Asp Asn Lys Glu
    690                 695                 700

Val Glu Lys
705
```

<210> 286

<211> 15

<212> PRT

<213> Neisseria meningitidis

<400> 286

```
Tyr Gly Thr Asp Glu Ala Glu Lys Phe Arg Asp Lys Ser Gly Val
1               5                   10                  15
```

<210> 287

<211> 15

<212> PRT

<213> Neisseria meningitidis

<400> 287

```
Leu Asn Arg Trp Val Lys Glu Arg Ile Glu Gln Asn Gln Pro Leu
1               5                   10                  15
```

<210> 288

<211> 852

<212> DNA

<213> Haemophilus somnus

<400> 288

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gaaacccgct ttgatgccgt taaaatcagc acggatagta ataaattaga aaaagaaacg       60

atggatacgt tcggcaatgc ggcgtattta gtgttggacg gcagacagtt tcctttggtg      120

ccggaaagta atgccggtac gacgggcgct ggcaacacag gcaagaatga gtttatcagc      180

accatagacg gtagccattt aaacaaaaca aatcatgaaa accacaaaaa atacaaagtt      240

accgtatgtt gcagtaattt ggtgtatgtg aaattcggca gctatgggga acaaacaaca      300

gcaaacgatg cttcaaacag cactgccggt gcagcaacta cgcataacag cacattaaca      360

aacggacacc ttttcctaac aggtgaacgt acttcgctta ctgatatggc gaagcaaagt      420

ggtgcagcaa agtatattgg cacatggcaa gccaactttt taagtagcaa aggacaggtt      480
```

```
ggcagtgttg acgccggtga tccgcgtaac gatagtggta aaagccgtgc tgaatttgat      540

gttaattttg gtggtaagac agttacaggc aagtttttg atgccgacgg tattcaaccc      600

gccctcacaa tggatagtac caagattgaa ggtaacggct tctcgggtac agctaagaca      660

actggtagtt tgcaattaga taaaggcagt acaggtgcgg gtataacagt aaccttcacc      720

gatgctaaag tcgatggcgc attctacggt ccgaatgcag aagaaatcgg cggtaccatc      780

acatcgaatg gcacgggcga taaagtcggt ggggtgttcg gtgcgaaacg ccaagaacta      840

tcgcaacaga aa                                                          852
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<210> 289

<211> 284

<212> PRT

<213> Haemophilus somnus

<400> 289

```
Glu Thr Arg Phe Asp Ala Val Lys Ile Ser Thr Asp Ser Asn Lys Leu
1               5                   10                  15

Glu Lys Glu Thr Met Asp Thr Phe Gly Asn Ala Ala Tyr Leu Val Leu
            20                  25                  30

Asp Gly Arg Gln Phe Pro Leu Val Pro Glu Ser Asn Ala Gly Thr Thr
        35                  40                  45

Gly Ala Gly Asn Thr Gly Lys Asn Glu Phe Ile Ser Thr Ile Asp Gly

    50                  55                  60

Ser His Leu Asn Lys Thr Asn His Glu Asn His Lys Lys Tyr Lys Val
65                  70                  75                  80

Thr Val Cys Cys Ser Asn Leu Val Tyr Val Lys Phe Gly Ser Tyr Gly
                85                  90                  95

Glu Gln Thr Thr Ala Asn Asp Ala Ser Asn Ser Thr Ala Gly Ala Ala
            100                 105                 110

Thr Thr His Asn Ser Thr Leu Thr Asn Gly His Leu Phe Leu Thr Gly
        115                 120                 125

Glu Arg Thr Ser Leu Thr Asp Met Ala Lys Gln Ser Gly Ala Ala Lys
    130                 135                 140

Tyr Ile Gly Thr Trp Gln Ala Asn Phe Leu Ser Ser Lys Gly Gln Val
145                 150                 155                 160

Gly Ser Val Asp Ala Gly Asp Pro Arg Asn Asp Ser Gly Lys Ser Arg
                165                 170                 175

Ala Glu Phe Asp Val Asn Phe Gly Gly Lys Thr Val Thr Gly Lys Phe
            180                 185                 190
```

```
Phe Asp Ala Asp Gly Ile Gln Pro Ala Leu Thr Met Asp Ser Thr Lys
        195                 200                 205

Ile Glu Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr Thr Gly Ser Leu
    210                 215                 220

Gln Leu Asp Lys Gly Ser Thr Gly Ala Gly Ile Thr Val Thr Phe Thr
225                 230                 235                 240

Asp Ala Lys Val Asp Gly Ala Phe Tyr Gly Pro Asn Ala Glu Glu Ile
                245                 250                 255

Gly Gly Thr Ile Thr Ser Asn Gly Thr Gly Asp Lys Val Gly Gly Val
            260                 265                 270

Phe Gly Ala Lys Arg Gln Glu Leu Ser Gln Gln Lys
        275                 280
```

<210> 290

<211> 272

<212> PRT

<213> Haemophilus influenzae

<400> 290

```
Thr Lys Lys Pro Asp Ala Thr Thr Ser Thr Thr Ala Asn Ala Lys Thr
1               5                   10                  15

Asp Ala Thr Thr Asn Ala Glu Asn Phe Thr Thr Lys Asp Ile Ser Ser
            20                  25                  30

Phe Gly Glu Ala Asp Tyr Leu Leu Ile Asp Asn Tyr Pro Val Pro Leu
        35                  40                  45

Leu Pro Glu Thr Glu Asn Ser Gly Asp Phe Ala Thr Ser Lys His Tyr
    50                  55                  60

Glu Val Arg Asp Lys Thr Tyr Lys Val Glu Ala Cys Cys Lys Asn Leu
65                  70                  75                  80

Ser Tyr Val Lys Phe Gly Met Tyr Tyr Glu Asp Asn Lys Lys Asn Asn
                85                  90                  95

Lys Asn Glu Thr Glu Gln Tyr His Gln Phe Leu Leu Gly Leu Arg Thr
            100                 105                 110

Ala Ser Ser Lys Ile Pro Thr Thr Gly Asn Val Lys Tyr Arg Gly Ser
        115                 120                 125

Trp Phe Gly Tyr Ile Ser Asp Gly Glu Thr Ser Tyr Ser Thr Thr Gly
    130                 135                 140

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

Ala Glu Lys Thr Leu Lys Gly Ser Leu Lys Arg Ala Asp Ser Gln Asn
```

```
                165                 170                 175

Pro Val Phe Ser Ile Glu Ala Asn Phe Lys Asn Gly Gly Asn Ala Phe
            180                 185                 190

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

Gln Thr Lys Asn Thr Pro Ile Asn Ile Thr Thr Lys Val Asn Gly Ala
    210                 215                 220

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

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

Asn Ser Glu Lys Ala Arg Ala Ala Val Val Phe Gly Ala Lys Lys Gln
            260                 265                 270
```

<210> 291

<211> 254

<212> PRT

<213> Moraxella bovis

<400> 291

```
Val Gln Thr Gln Phe Asp Ala Thr Ala Ile Asp Ser Lys Thr Leu Thr
1               5                   10                  15

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

Gly Lys Leu Val Ser Leu Leu Pro Glu Gly Val Ser Ser Phe Ala Asp
        35                  40                  45

Met Lys Phe Ile Asn Thr His Gln Ile Ala His Gly Asp Lys Lys Leu
    50                  55                  60

Ser Ile Thr Val Cys Cys Asn Asn Leu Asp Tyr Val Lys Phe Gly Gly
65                  70                  75                  80

Tyr Gly Thr Val Gly Gly Thr Ala Asp Thr Pro Val Leu Ser Asp Gly
                85                  90                  95

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

Ser Gly Thr Ala His Tyr Arg Gly Thr Trp Glu Gly Tyr Ile Asp Ser
        115                 120                 125

Lys Asp Gly Arg Arg Trp Ala Ser Ser Ala Ser Asn Leu Thr Thr Gly
    130                 135                 140

Thr Arg Ser Arg Phe Asp Val Asp Phe Gly Ser Lys Ser Leu Ile Gly
145                 150                 155                 160
```

```
Lys Leu Ile Ala Asp Asn Gly Leu Glu Asp Asn Pro Val Leu Thr Leu
                165                 170                 175

Asn Gly Thr Ile Thr Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr Gly
            180                 185                 190

Val Asn Gly Phe Asn Leu Asp Pro Asn Ser Thr Gly Ala Ser Ala Ile
        195                 200                 205

Ala His Ile Asn Ala Asp Phe His Gly Gly Phe Tyr Gly Val Asn Ala
    210                 215                 220

Ser Glu Leu Gly Gly Val Ile His His Asp Lys Val Gly Glu Asp Lys
225                 230                 235                 240

Ile Gly Val Val Phe Gly Gly Lys Arg Gln Thr Asn Thr Pro
                245                 250
```

<210> 292

<211> 232

<212> PRT

<213> Bibersteinia trehalosi

<400> 292

```
Leu Lys Asp Leu Ser Lys Ser Glu Met Asp Thr Phe Gly Asn Ala Thr
1               5                   10                  15

His Leu Ile Ile Asn Asn Lys Gln Leu Pro Leu Ile Ala Glu Gly Lys
            20                  25                  30

Gln Ser Phe Ala Asp Met Gln Phe Asn Asp Thr Val Thr His Asn Ile
        35                  40                  45

Gly Gly Lys Thr Tyr Arg Val Ser Val Cys Cys Asn Asn Leu Asp Tyr
    50                  55                  60

Val Lys Phe Gly Thr Tyr Ser Glu Glu Asp Asn Lys Asp Ser Ala His
65                  70                  75                  80

Leu Tyr Leu Val Gly Glu Arg Thr Ala Val Ser Asp Leu Pro Ser Gly
                85                  90                  95

Lys Ala Gln Tyr Arg Gly Thr Trp Asn Gly Val Ile His Ser His Ser
            100                 105                 110

Gly Thr Val Gly Gly Glu Ser Pro Ser Asn Ser Glu Ser Gly Thr Arg
        115                 120                 125

Ser Leu Phe Asp Val Asp Phe Ala Asn Lys Lys Ile Asn Gly Lys Leu
    130                 135                 140

Ile Ala Asn Asp Gly Val Glu Glu Arg Pro Met Leu Ser Leu Glu Gly
145                 150                 155                 160

Glu Ile Lys Ala Asn Gly Phe Ser Gly Ser Ala Lys Thr His Asp Ser
```

```
                165                 170                 175

Gly Phe Asn Ile Asp Pro Lys Ser Thr Ala Gly Gly Thr Glu Val His
            180                 185                 190

Leu Asp Ser Arg Phe Glu Gly Ala Phe Tyr Gly Lys Asn Ala Leu Glu
        195                 200                 205

Leu Gly Gly Ile Val His Asp Ser His Ser Lys Asp Lys Val Ser Ile
    210                 215                 220

Thr Phe Ala Gly Lys Arg Gln Ile
225                 230
```

<210> 293

<400> 293

000

<210> 294

<211> 243

<212> PRT

<213> Haemophilus parasuis

<400> 294

```
Asn Thr Val Arg Ile Ile Asp Ala Ser Lys Ile Asp Leu Thr Asn Phe
1               5                   10                  15

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

Asp Gly Lys Lys Met Glu Leu Ala Gly Ser Glu Phe Thr Asn Lys His
        35                  40                  45

Thr Ile Asp Ile Asn Gly Lys Lys Met Val Ala Val Ala Cys Cys Ser
    50                  55                  60

Asn Leu Glu Tyr Met Lys Phe Gly Gln Leu Trp Gln Gln Thr Glu Gly
65                  70                  75                  80

Glu Lys Gln Val Lys Asp Asn Ser Leu Phe Leu Gln Gly Glu Arg Thr
                85                  90                  95

Ala Thr Asp Lys Met Pro Lys Asp Gly Asn Tyr Lys Tyr Ile Gly Thr
            100                 105                 110

Trp Asp Ala Gln Val Ser Lys Glu Asn Asn Tyr Trp Val Ala Thr Ala
        115                 120                 125

Asp Asp Asp Arg Lys Ala Gly Tyr Arg Thr Glu Phe Asp Val Asp Phe
    130                 135                 140

Gly Ser Lys Asn Leu Ser Gly Lys Leu Phe Asp Lys Asn Gly Val Asn
145                 150                 155                 160
```

```
Pro Val Phe Thr Val Asn Ala Lys Ile Asp Gly Asn Gly Phe Thr Gly
                165                 170                 175

Glu Ala Lys Thr Ser Asp Ala Gly Phe Val Leu Asp Pro Gly Ser Leu
            180                 185                 190

Arg His Asp Asn Val Lys Phe Ser Asp Val Ala Val Ser Gly Gly Phe
        195                 200                 205

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

Asp Asn Gly Ser Val Gly Val Gly Ala Val Phe Gly Ala Lys Gln Gln
225                 230                 235                 240

Val Lys Lys
```

<210> 295

<211> 50

<212> PRT

<213> Neisseria meningitidis

<400> 295

```
Asp Asn His Ala Asp Lys Glu Ala Ala Lys Ala Val Phe Thr Val Asp
1               5                   10                  15

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

Glu Pro Ala Phe Arg Ile Glu Asn Gly Val Ile Glu Gly Asn Gly Phe
        35                  40                  45

His Ala
    50
```

REFERENCES CITED IN THE DESCRIPTION

Cited references

This list of references cited by the applicant is for the reader's convenience only. It does not form part of the European patent document. Even though great care has been taken in compiling the references, errors or omissions cannot be excluded and the EPO disclaims all liability in this regard.

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Patentkrav

1. Immunogen sammensætning, som omfatter et transferrinbindende protein B (TbpB)-polypeptid, der kan opnås fra en gramnegativ patogen bakterieart, hvor TbpB-polypeptidet omfatter sekvensen ifølge SEQ ID NO: 174.

2. Vaccinesammensætning, som omfatter en immunogen sammensætning ifølge krav 1.

3. Fremgangsmåde til fremstilling af en immunogen sammensætning, som omfatter:
(a) tilvejebringelse af en kimær nukleinsyresekvens, der som operabelt koblede bestanddele omfatter:
(i) en nukleinsyresekvens, der koder for et TbpB-polypeptid, der kan opnås fra en gramnegativ patogen bakterieart, hvor TbpB-polypeptidet omfatter sekvensen ifølge SEQ ID NO: 174; og
(ii) en nukleinsyresekvens, der kan kontrollere ekspressionen i en rekombinant værtscelle;
(b) indførelse af den kimære nukleinsyresekvens i en værtscelle og dyrkning af værtscellen til frembringelse af TbpB-polypeptidet;
(c) indvinding af TbpB-polypeptidet fra værtscellen; og
(d) fremstilling af en immunogen sammensætning.

4. Ekspressionsvektor, som omfatter en nukleinsyresekvens, der koder for et TbpB-polypeptid, der kan opnås fra en gramnegativ patogen bakterieart, hvor TbpB-polypeptidet omfatter sekvensen ifølge SEQ ID NO: 174.

DRAWINGS

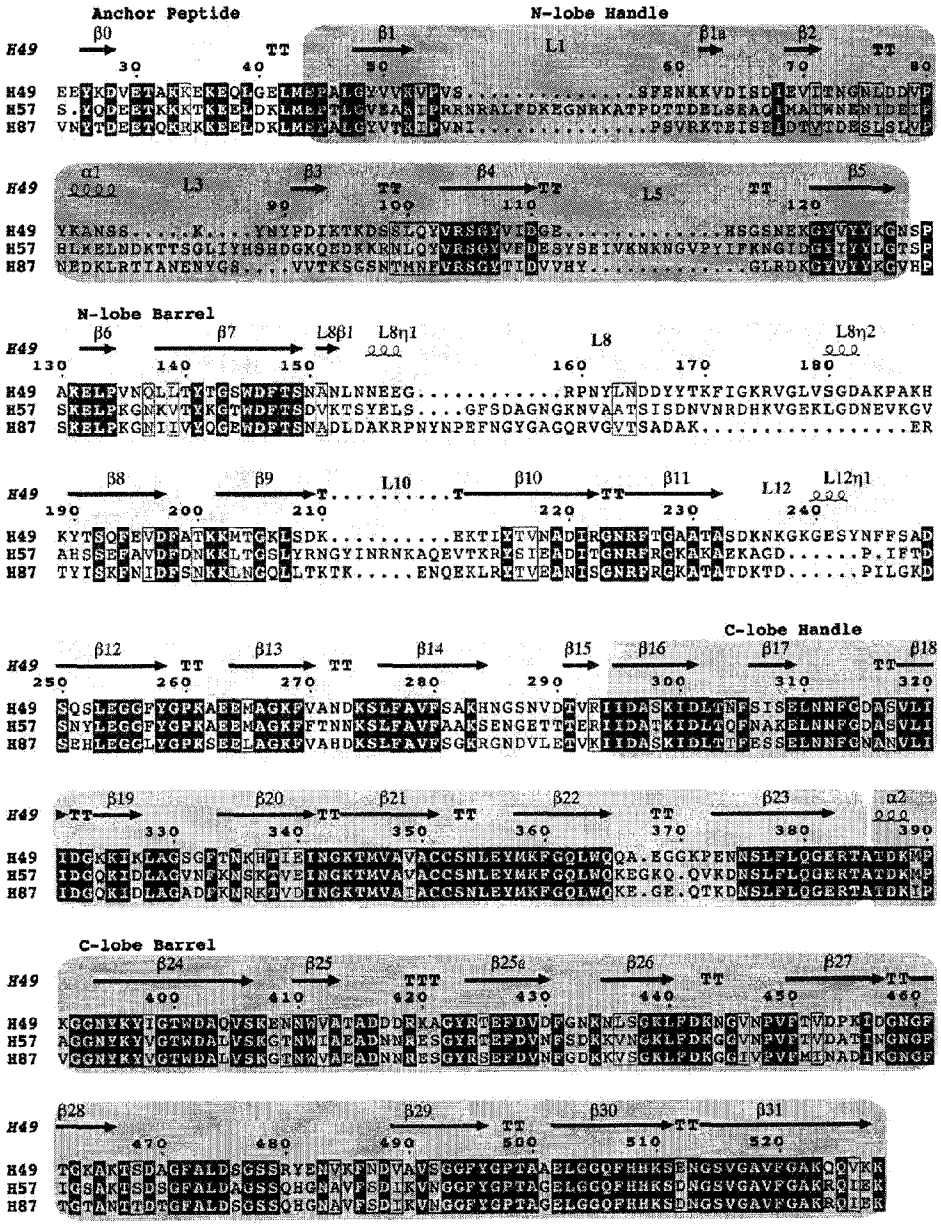


FIGURE 1

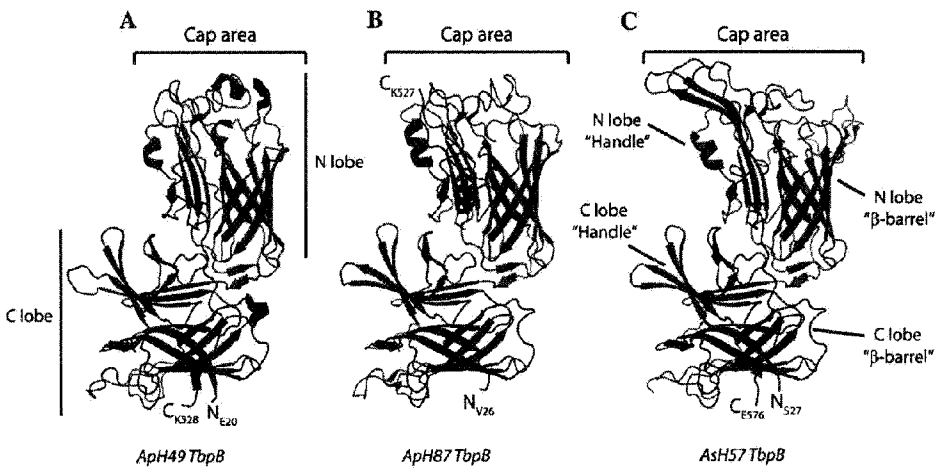


FIGURE 1 - CONTINUED

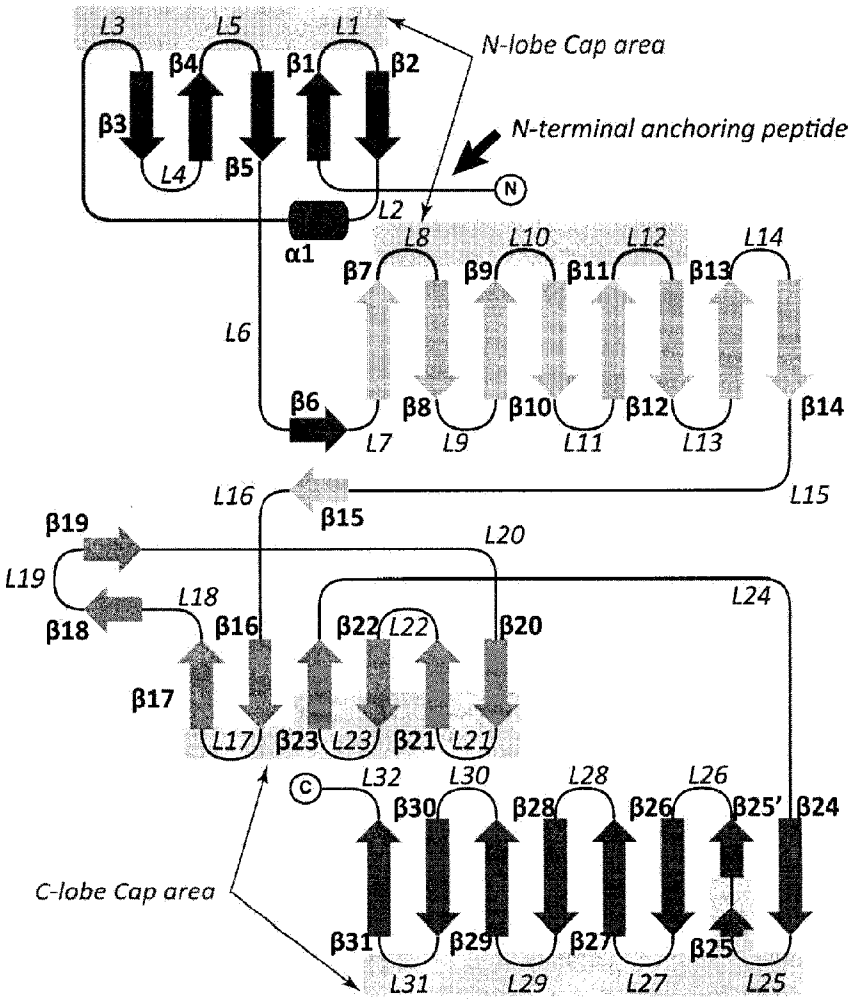

L3
L5
L1
N-lobe Cap area
β4
β1
β2
β3
N-terminal anchoring peptide
L4
β5
N
L2
α1
L8
L10
L12
L14
β7
β9
β11
β13
L6
β6
β8
β10
β12
β14
L7
L9
L11
L13
L16
L15
β15
β19
L20
L19
L24
L18
β18
β16
β22
L22
β20
β17
L17
β23
L23
β21
L21
C
L32
L30
L28
L26
β30
β28
β26
β25'
β24
C-lobe Cap area
β31
β29
β27
β25
L31
L29
L27
L25

FIGURE 2

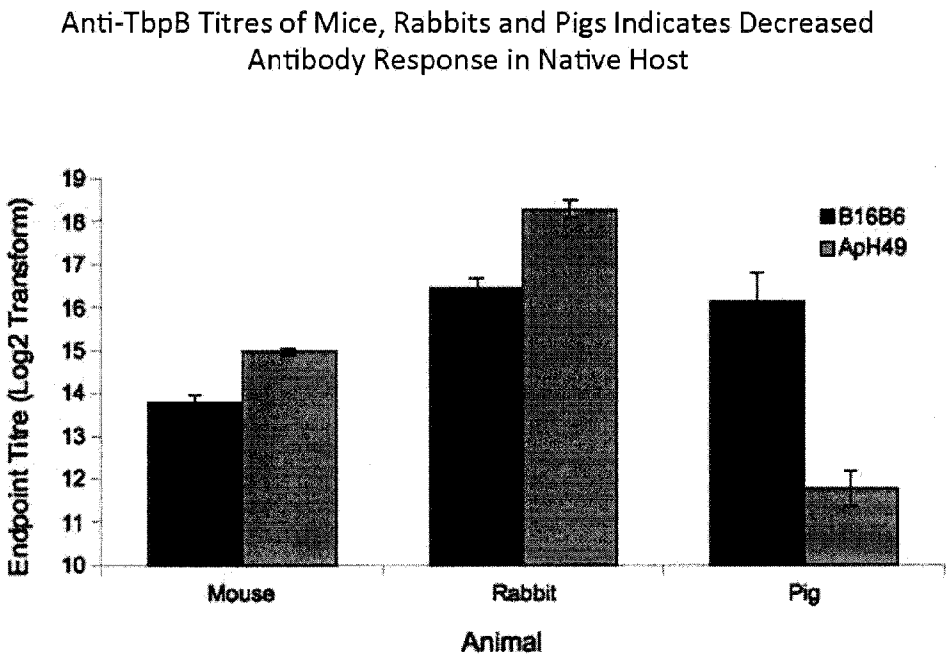

Anti-TbpB Titres of Mice, Rabbits and Pigs Indicates Decreased Antibody Response in Native Host
Endpoint Titre (Log2 Transform)
19
18
17
16
15
14
13
12
11
10
B16B6
ApH49
Mouse
Rabbit
Pig
Animal

FIGURE 3A

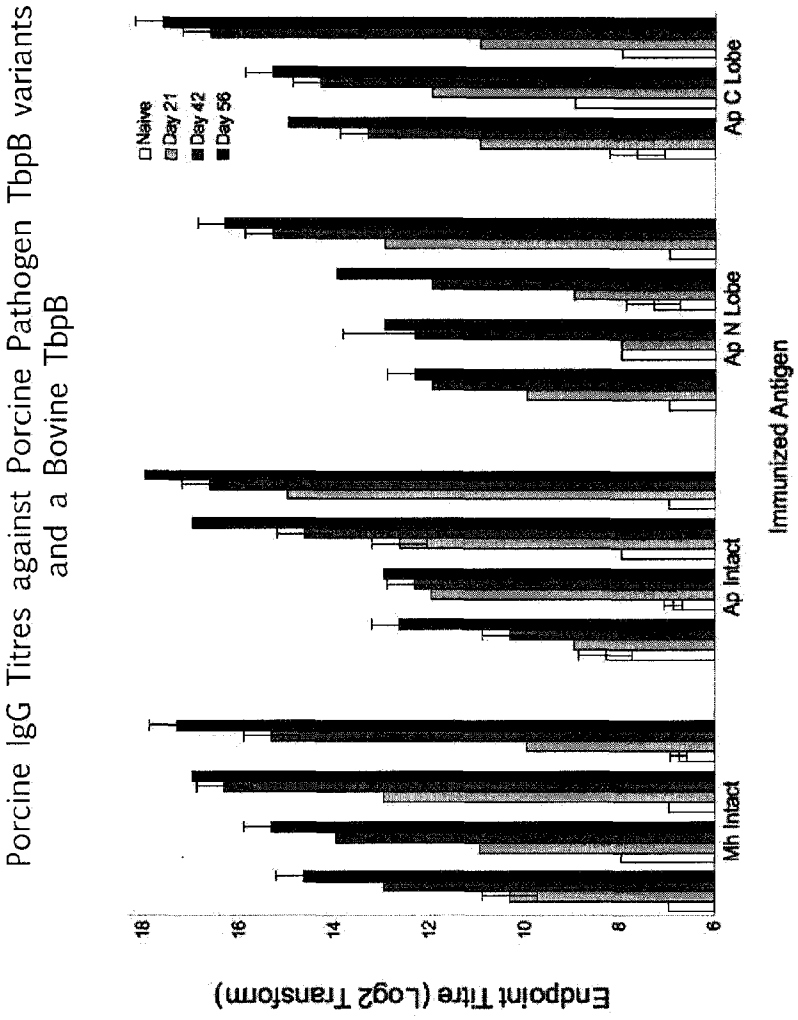

Porcine IgG Titres against Porcine Pathogen TbpB variants and a Bovine TbpB
Naive
Day 21
Day 42
Day 56
Mh Intact
Ap Intact
Ap N Lobe
Ap C Lobe
Immunized Antigen
Endpoint Titre (Log2 Transform)
6
8
10
12
14
16
18

FIGURE 3B

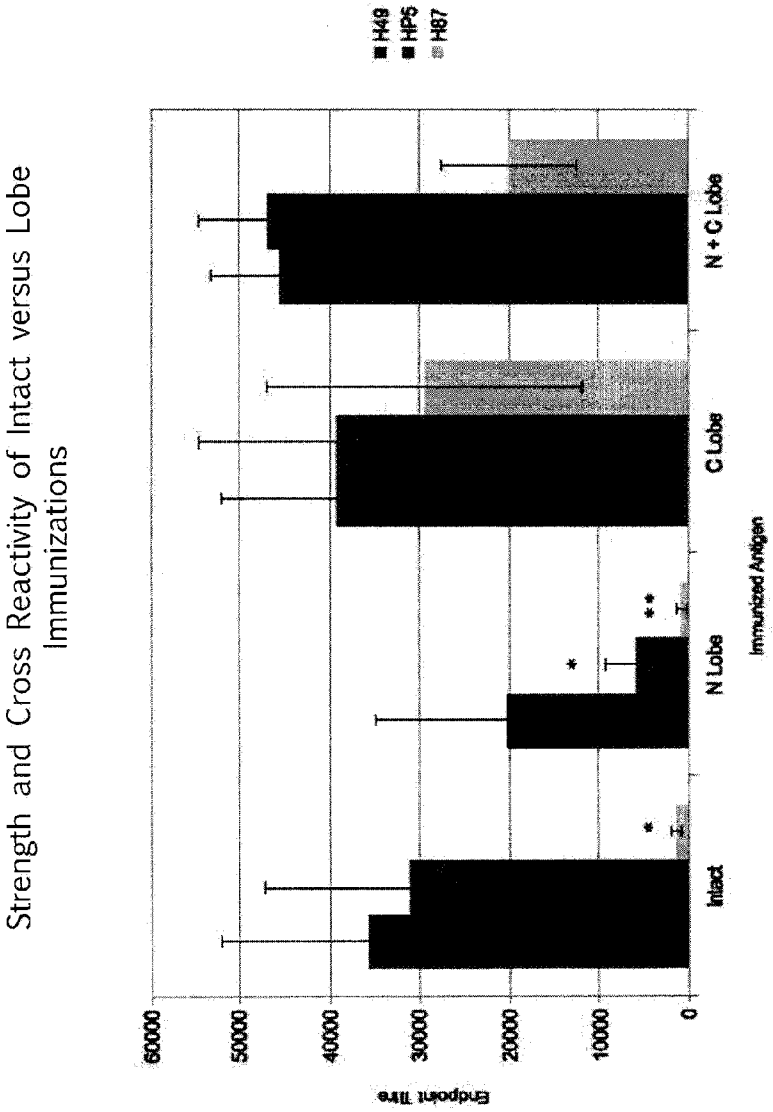

Strength and Cross Reactivity of Intact versus Lobe Immunizations
H49
HP5
H87
Endpoint Titre
60000
50000
40000
30000
20000
10000
0
Intact
N Lobe
C Lobe
N + C Lobe
Immunized Antigen
*
*
**

FIGURE 3C

Sequence Diversity of TbpBs from Porcine Pathogens

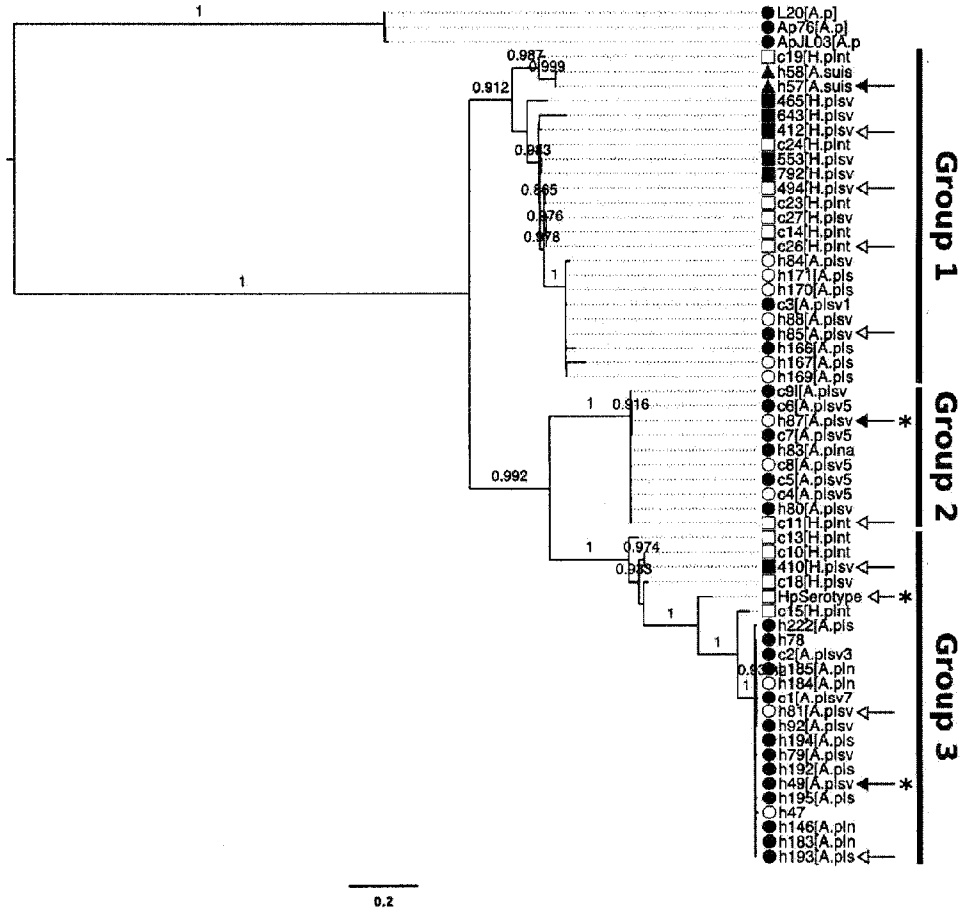
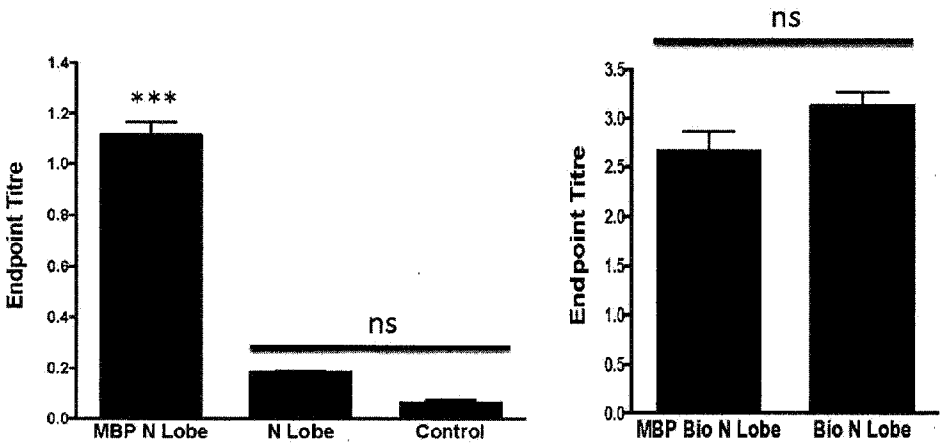


FIGURE 4

Panel A



Panel B

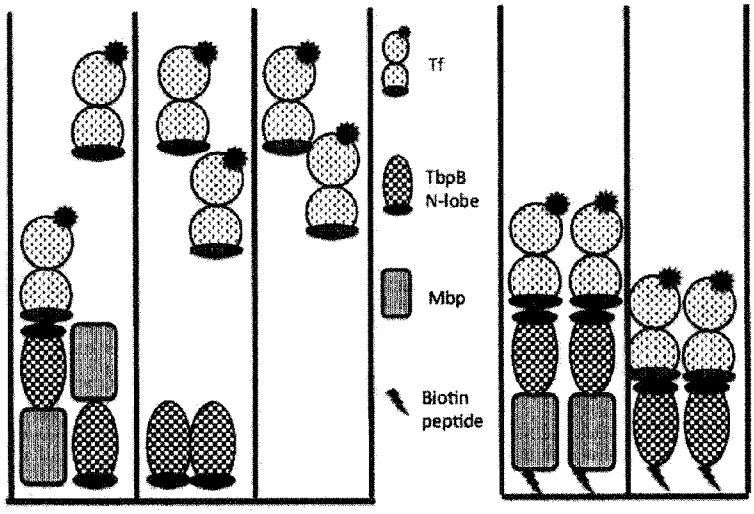


FIGURE 5

Panel A

```
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▸ D  T  V  R  I  I  D  A  S  K  I  D  L  T  N  F  S  I  S  E  L  N  N  F  G  D  A  S  V  L  I  I
TGATGGGAAAAAAATAAAGCTAGCTGGTAGCGGGTTTACAAATAAGCACACTATTGAAATCAATGGCAAAACAATGGTAGCCGTAGCCTGCTGTA
▸  D  G  K  K  I  K  L  A  G  S  G  F  T  N  K  H  T  I  E  I  N  G  K  T  M  V  A  V  A  C  C
GTAATCTGGAATATATGAAGTTTGGTCAATTATGGCAACAAGCAGAGGGCGGAAAACCCGAGAATAATAGTTTATTCCTACAAGGCGAACGTACC
▸S  N  L  E  Y  M  K  F  G  Q  L  W  Q  Q  A  E  G  G  K  P  E  N  N  S  L  F  L  Q  G  E  R  T
GCAACAGATAAGATGCCAAAAGGCGGAAACTATAAATATATTGGTACTTGGGATGCTCAGGTTTCAAAAGAAAATAACTGGGTTGCTACGGCAGA
▸ A  T  D  K  M  P  K  G  G  N  Y  K  Y  I  G  T  W  D  A  Q  V  S  K  E  N  N  W  V  A  T  A  D
TGATGATAGAAAAGCTGGCTATCGCACAGAATTTGATGTTGATTTTGGCAACAAAAATTTAAGTGGTAAGTTATTTGATAAAAACGGTGTAAATC
▸  D  D  R  K  A  G  Y  R  T  E  F  D  V  D  F  G  N  K  N  L  S  G  K  L  F  D  K  N  G  V  N
CTGTGTTTACCGTAGATGCAAAAATTGATGGTAATGGTTTTACTGGCAAAGCTAAAACCTCAGATGCTGGTTTCGCTCTAGATTCAGGTAGTTCA
▸P  V  F  T  V  D  A  K  I  D  G  N  G  F  T  G  K  A  K  T  S  D  A  G  F  A  L  D  S  G  S  S
CGTTATGAGAATGTGAAATTTAACGATGTAGCAGTTAGTGGTGGCTTCTATGGTCCAACGGCAGCAGAGCTTGGCGGACAATTCCACCATAAATC
▸ R  Y  E  N  V  K  F  N  D  V  A  V  S  G  G  F  Y  G  P  T  A  A  E  L  G  G  Q  F  H  H  K  S
AGAAAATGGCAGTGTAGGTGCTGTCTTTGGTGCAAAACAACAAGTAAAAAAACTTGAAACAGTCAAGATCATTGATGCCTCAAAAATTGATTTAA
▸  E  N  G  S  V  G  A  V  F  G  A  K  Q  Q  V  K  K
                                                  ▸ L  E  T  V  K  I  I  D  A  S  K  I  D  L
CTACTTTTGAATCATCGGAACTCAACAATTTCGGCAACGCTAATGTGTTAATTATTGATGGACAGAAAATAGATCTAGCAGGTGCAGATTTTAAA

▸T  T  F  E  S  S  E  L  N  N  F  G  N  A  N  V  L  I  I  D  G  Q  K  I  D  L  A  G  A  D  F  K
AATAGAAAAACCGTTGATATCAATGGTAAGACAATGGTAGCCATAGCTTGCTGTAGTAATTTGGAATATATGAAATTTGGTCAATTATGGCAAAA

▸ N  R  K  T  V  D  I  N  G  K  T  M  V  A  I  A  C  C  S  N  L  E  Y  M  K  F  G  Q  L  W  Q  K
AGAGGGCGAACAAACTAAAGATAATAGCTTATTCCTGCAAGGTGAGCGTACTGCCACAGATAAAATACCCGTAGGTGGAAACTATAAATATGTAG

▸  E  G  E  Q  T  K  D  N  S  L  F  L  Q  G  E  R  T  A  T  D  K  I  P  V  G  G  N  Y  K  Y  V
GAACCTGGGATGCACTCGTTTCAAAAGGAACGAACTGGGTAGCTGAGGCGGATAATAATCGAGAATCGGGCTATCGCTCAGAATTTGATGTTAAT

▸G  T  W  D  A  L  V  S  K  G  T  N  W  V  A  E  A  D  N  N  R  E  S  G  Y  R  S  E  F  D  V  N
TTTGGTGATAAAAAAGTAAGCGGCAAGTTATTTGATAAAGGGGGCATAGTACCTGTCTTTATGATCAACGCAGATATTAAAGGTAACGGCTTTAC

▸ F  G  D  K  K  V  S  G  K  L  F  D  K  G  G  I  V  P  V  F  M  I  N  A  D  I  K  G  N  G  F  T
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▸  G  T  A  N  T  T  D  T  G  F  A  L  D  S  G  S  S  Q  H  G  N  A  V  F  S  D  I  K  V  N  G
GCTTCTATGGTCCAACCGCTGGAGAACTTGGCGGACAATTCCATCATAAATCAGACAATGGCAGTGTTGGCGCTGTCTTTGGTGCAAAACGACAA

▸G  F  Y  G  P  T  A  G  E  L  G  G  Q  F  H  H  K  S  D  N  G  S  V  G  A  V  F  G  A  K  R  Q
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        ▸ T  T  T  E  R  I  I  D  A  T  K  I  D  L  T  Q  F  N  A  K  E  L  N  N  F  G  D  A  S
▸ I  E  K
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▸  V  L  I  I  D  G  Q  K  I  D  L  A  G  V  N  F  K  N  S  K  T  V  E  I  N  G  K  T  M  V  A
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▸V  A  C  C  S  N  L  E  Y  M  K  F  G  Q  L  W  Q  K  E  G  K  Q  Q  V  K  D  N  S  L  F  L  Q
GGTGAACGTACTGCAACGGATAAAATGCCCGCAGGAGGTAACTATAAGTATGTTGGAACTTGGGATGCACTCGTATCTAAAGGGACGAACTGGAT
▸ G  E  R  T  A  T  D  K  M  P  A  G  G  N  Y  K  Y  V  G  T  W  D  A  L  V  S  K  G  T  N  W  I
AGCGGAAGCAGATAATAATCGAGAATCGGGCTATCGCACTGAATTTGATGTTAATTTTAGTGATAAAAAAGTAAACGGTAAGTTATTTGATAAAG
▸  A  E  A  D  N  N  R  E  S  G  Y  R  T  E  F  D  V  N  F  S  D  K  K  V  N  G  K  L  F  D  K
GCGGTGTAAATCCTGTATTTACCGTAGATGCGACAATTAATGGTAATGGCTTTATCGGCAGTGCGAAAACCTCTGATAGTGGCTTTGCTTTAGAT
▸G  G  V  N  P  V  F  T  V  D  A  T  I  N  G  N  G  F  I  G  S  A  K  T  S  D  S  G  F  A  L  D
GCAGGCTCTAGCCAACACGGAAATGCGGTATTTAGTGATATAAAAGTCAATGGTGGCTTCTATGGTCCAACCGCTGGAGAACTTGGCGGACAATT
▸ A  G  S  S  Q  H  G  N  A  V  F  S  D  I  K  V  N  G  G  F  Y  G  P  T  A  G  E  L  G  G  Q  F
CCATCATAAATCAGACAATGGCAGTGTTGGCGCTGTCTTTGGTGCAAAACGACAAATAGAAAAA
▸  H  H  K  S  D  N  G  S  V  G  A  V  F  G  A  K  R  Q  I  E  K
```

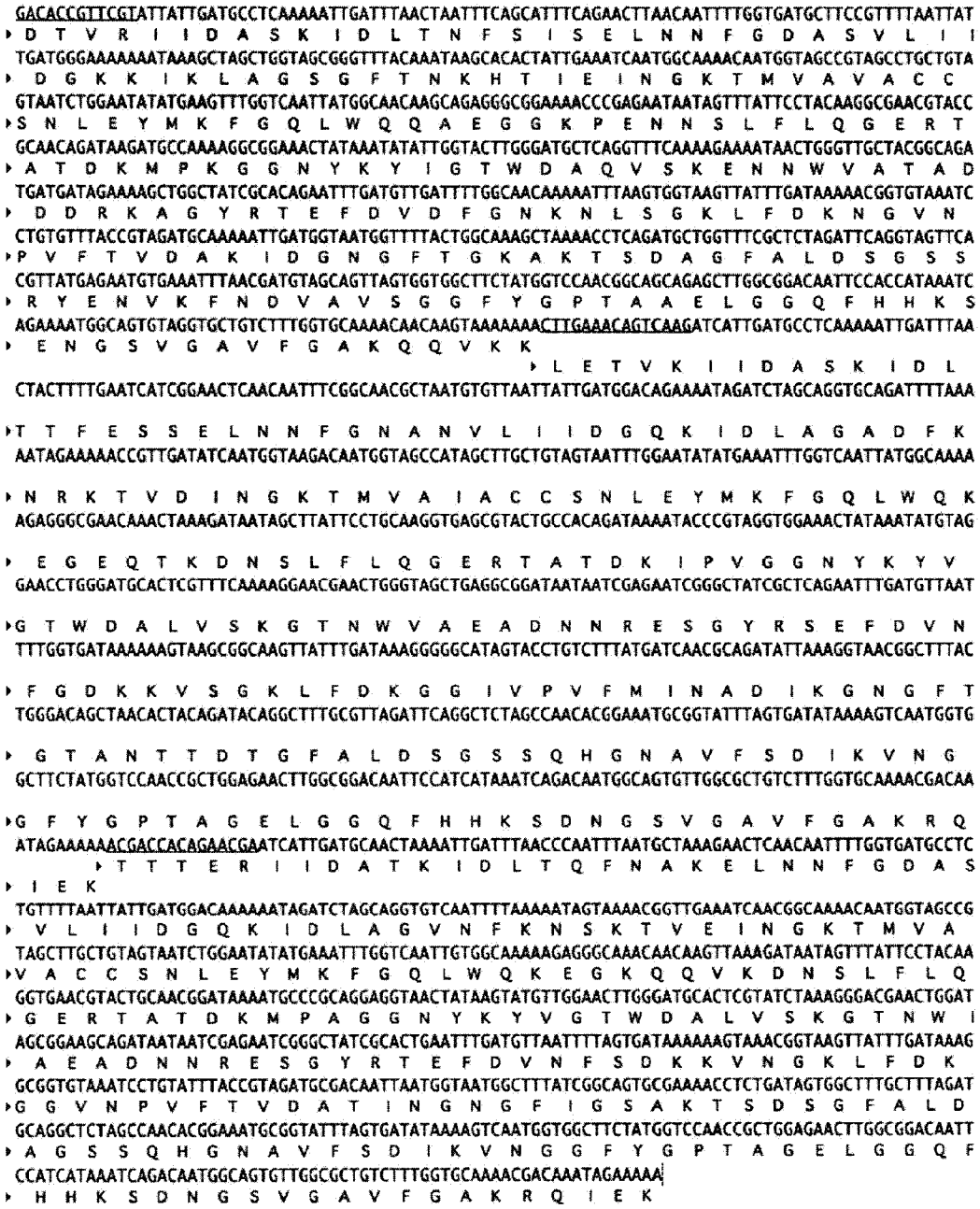


FIGURE 6

Panel B

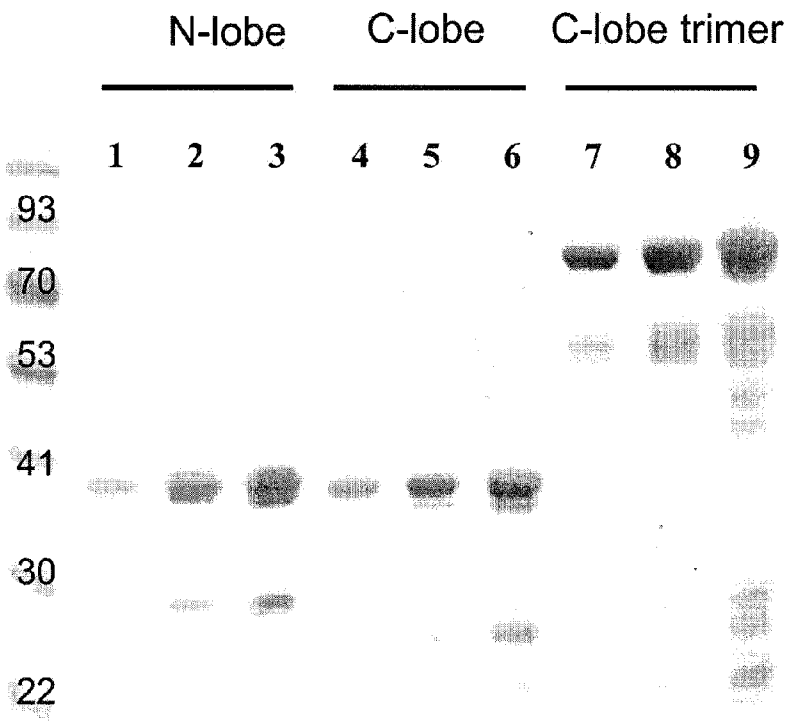


FIGURE 6 - CONTINUED

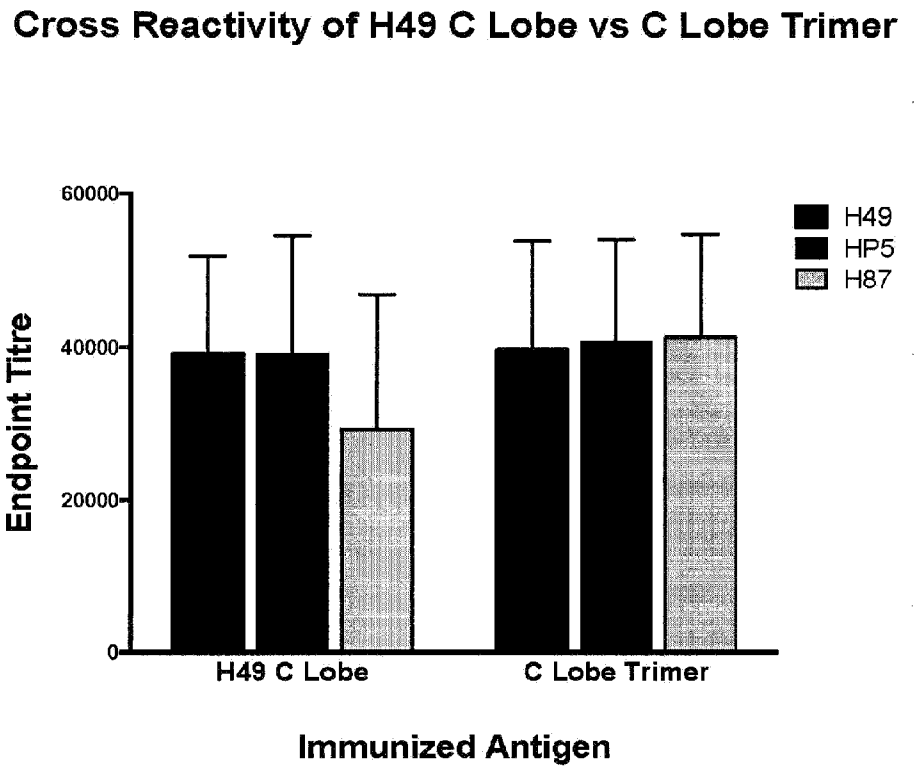
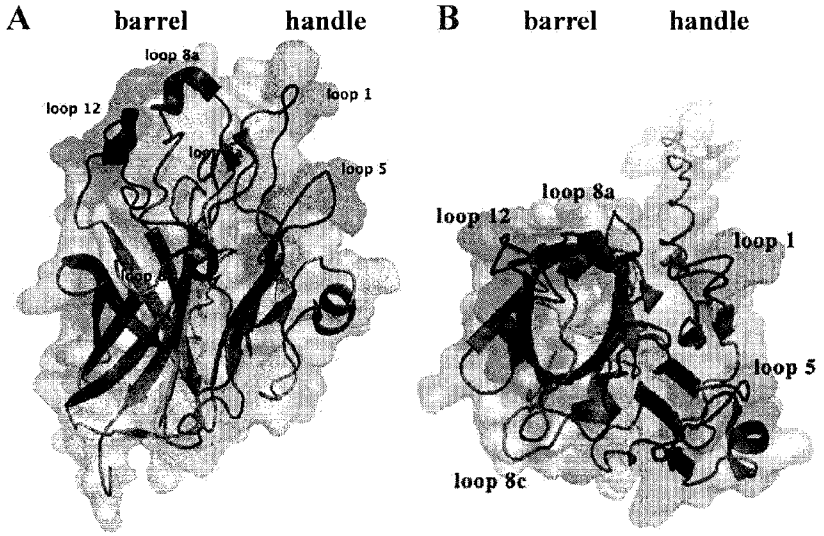

Cross Reactivity of H49 C Lobe vs C Lobe Trimer
60000
40000
20000
0
Endpoint Titre
H49
HP5
H87
H49 C Lobe
C Lobe Trimer
Immunized Antigen

FIGURE 7



C

% matched: 89		10	20	30	40
ApTbpBN-lobe	1	GVSKEEYKDV	ETAKKEKEQL	GELGELMEPA	LGYVVKVPVS
ApTbpN-lobe ver1	1	GVSKEEYKDV	ETAKKEKEQL	GELGELMEPA	LGYVVKVPVS
ApTbpBN-lobe	51	DIEVITNGNL	DDVPYKANSS	KYNYPDIKTK	DSSLQYVRSG
ApTbpN-lobe ver1	49	DIEVITNGNL	DDVPYKANSS	KYNYPDIKTK	DSSLQYVRSG
ApTbpBN-lobe	101	NEKGYVYYKG	NSPAKELPVN	QLLTYTGSWD	FTSNANLNNE
ApTbpN-lobe ver1	93	PDGGYVYYKG	NSPAKELPVN	QLLTYTGSWD	FTSNANLN
ApTbpBN-lobe	151	YYTKFIGKRV	GLVSGDAKPA	KHKYTSQFEV	DFATKKMTGK
ApTbpN-lobe ver1	135		GLVSGDAK	ERKYTSQFEV	DFATKKMTGK
ApTbpBN-lobe	201	VNADIRGNRF	TGAATASDKN	KGKGESYNFF	SADSQSLEGG
ApTbpN-lobe ver1	180	VNADIRGNRF	TGAATASDKN	D	SADSQSLEGG
ApTbpBN-lobe	251	GKFVANDKSL	FAVFSAKHNG	SNV	
ApTbpN-lobe ver1	224	GKFVANDKSL	FAVFSAKHNG	SNV	

FIGURE 8

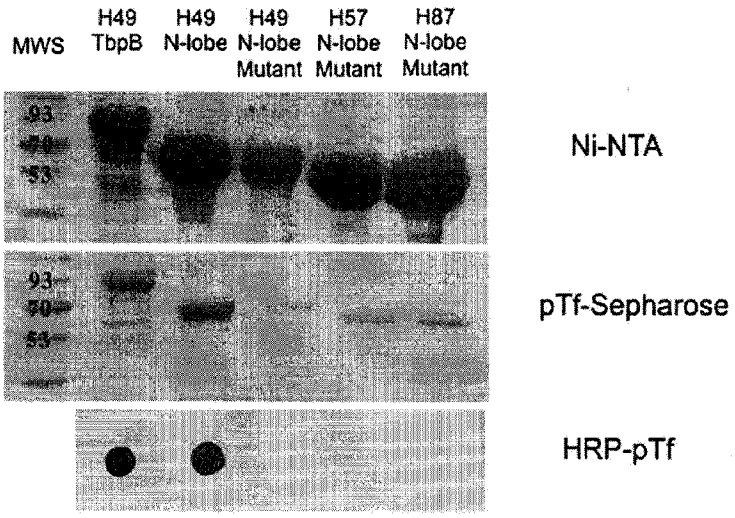

MWS
H49 TbpB
H49 N-lobe
H49 N-lobe Mutant
H57 N-lobe Mutant
H87 N-lobe Mutant
93
53
Ni-NTA
93
50
53
pTf-Sepharose
HRP-pTf

FIGURE 9

Sequence Diversity of *Neisseria meningitidis* TbpBs

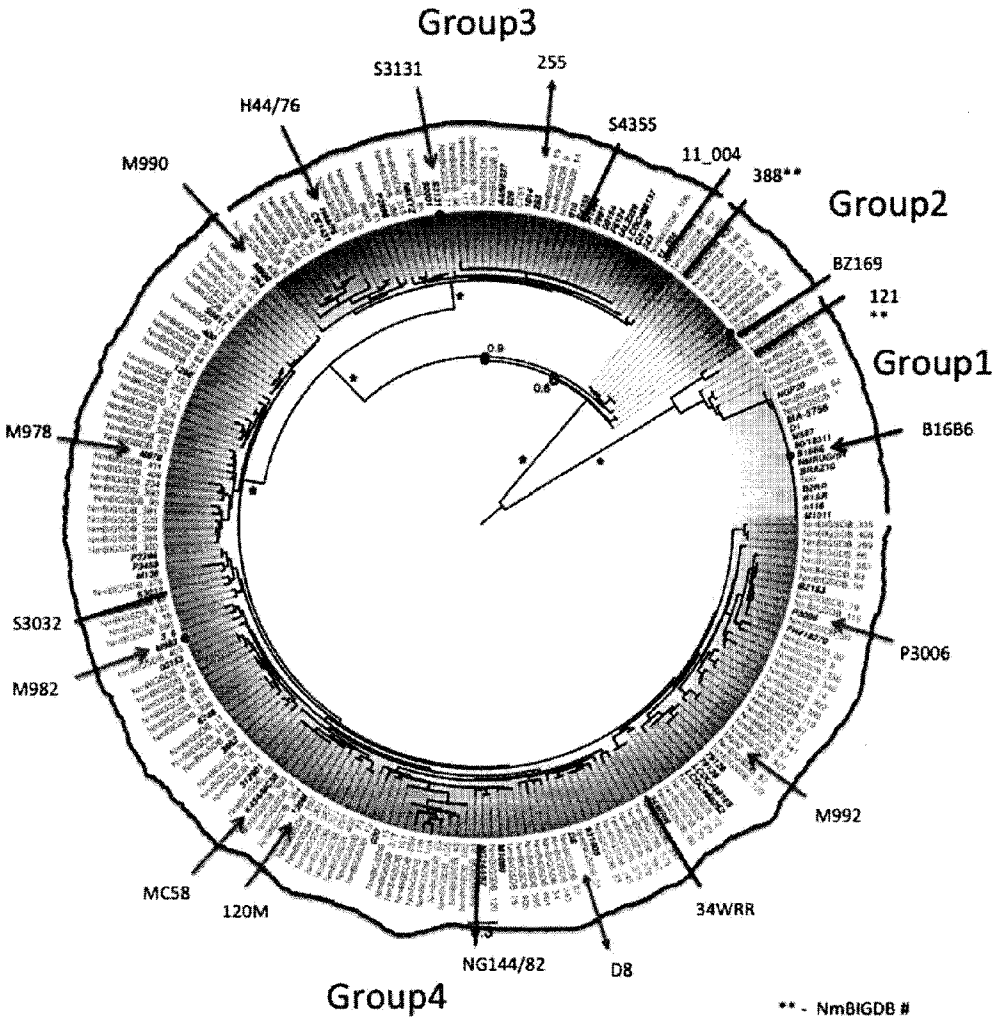


Figure 10A

Sequence Diversity of *Neisseria meningitidis* TbpB C-lobes

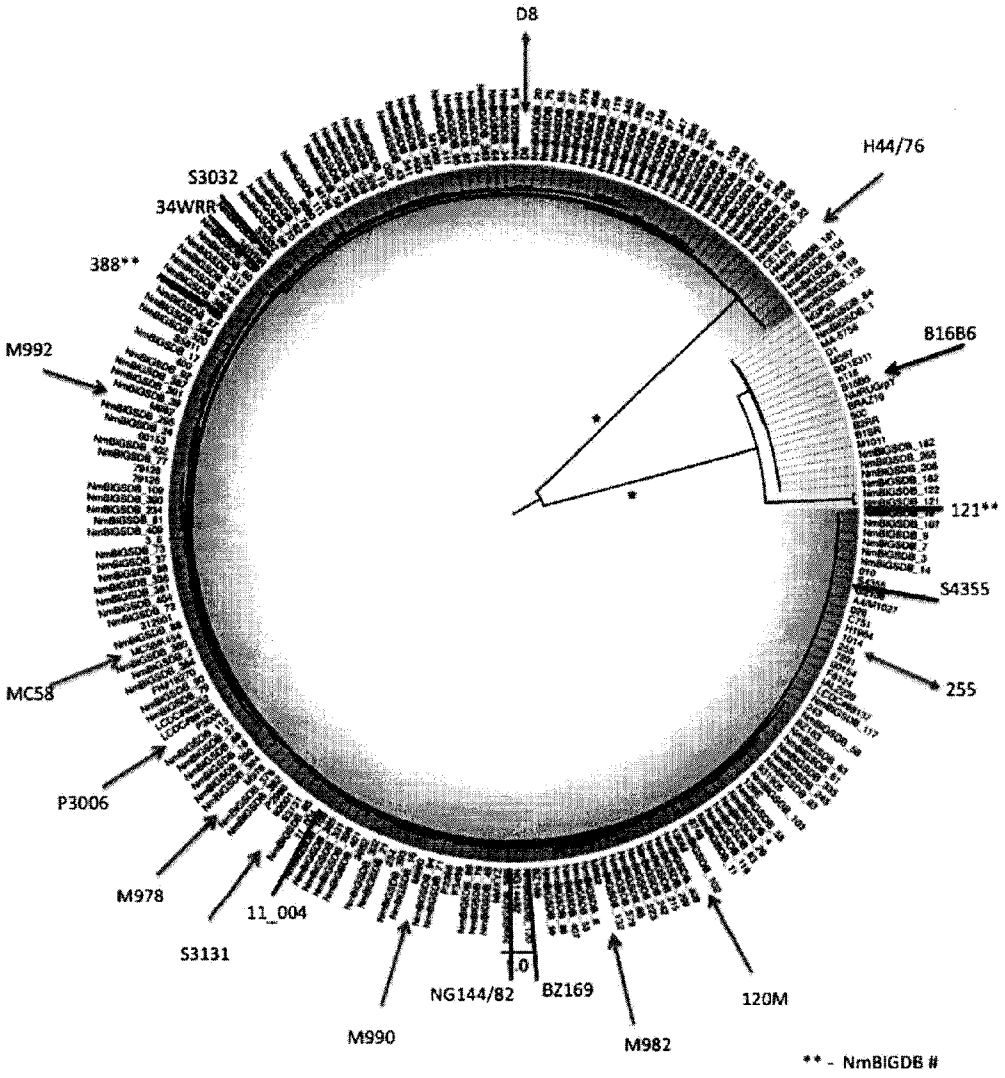


Figure 10B

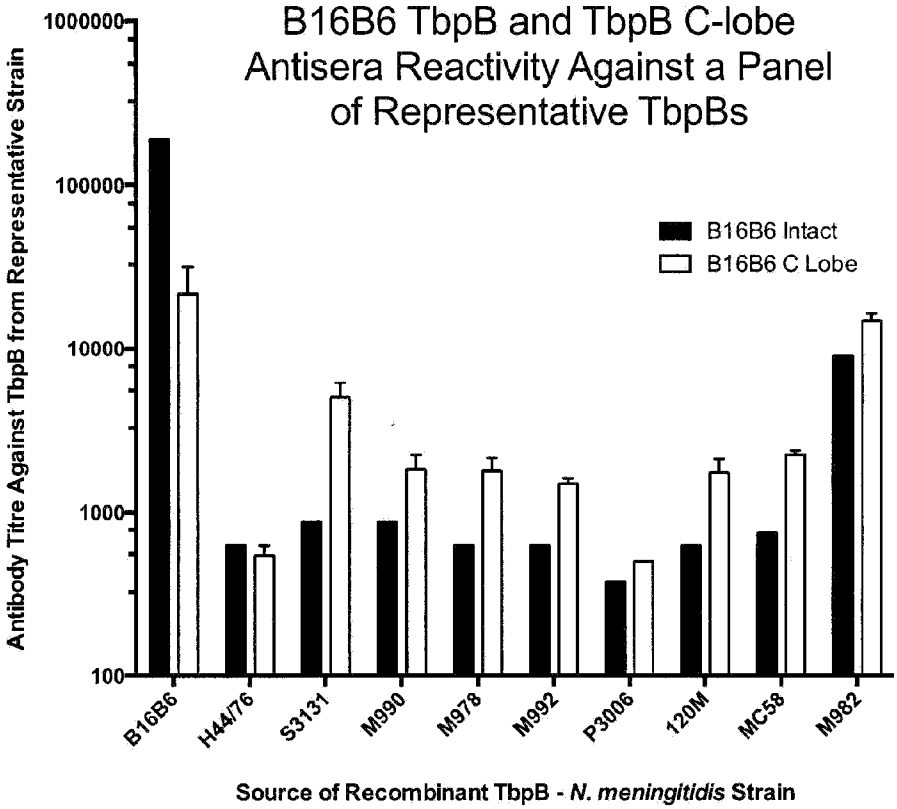

B16B6 TbpB and TbpB C-lobe
Antisera Reactivity Against a Panel
of Representative TbpBs
B16B6 Intact
B16B6 C Lobe
Antibody Titre Against TbpB from Representative Strain
1000000
100000
10000
1000
100
B16B6
H44/76
S3131
M990
M978
M992
P3006
120M
MC58
M982
Source of Recombinant TbpB - N. meningitidis Strain

FIGURE 11

Panel A

GGATCTTCTGAAAACAGTAAGCTGACCACGGTTTTGGATGCGGTTGAATTGACACTAAACGACAAGAAAATCAAAAATCTCGACAACTTCAGCAATGCCGC
▸ G S S E N S K L T T V L D A V E L T L N D K K I K N L D N F S N A A
CCAACTGGTTGTCGACGGCATTATGATTCCGCTCCTGCCCAAGGATTCCGAAAGCGGGAACACTCAGGCAGATAAAGGTAAAAACGGCGGAACAGAATTTA
▸ Q L V V D G I M I P L L P K D S E S G N T Q A D K G K N G G T E F
CCCGCAAATTTGAACACACGCCGGAAAGTGATAAAAAAGACGCCCAAGCAGGTACGCAGACGAATGGGGCGCAAACCGCTTCAAATACGGCAGGTGATACC
▸T R K F E H T P E S D K K D A Q A G T Q T N G A Q T A S N T A G D T
AATGGCAAAACAAAAACCTATGAAGTCGAAGTCTGCTGTTCCAACCTCAATTATCTGAAATACGGAATGTTGACGCGCAAAAACAGCAAGTCCGCGATGCA
▸ N G K T K T Y E V E V C C S N L N Y L K Y G M L T R K N S K S A M Q
GGCAGGAGGAAACAGTAGTCAAGCTGATGCTAAAACGGAACAAGTTGAACAAAGTATGTTCCTCCAAGGCGAGCGTACCGATGAAAAAGAGATTCCAACCG
▸ A G G N S S Q A D A K T E Q V E Q S M F L Q G E R T D E K E I P T
ACCAAAACGTCGTTTATCGGGGGTCTTGGTACGGGCATATTGCCAACGGCACAAGCTGGAGCGGCAATGCTTCTGATAAAGAGGGCGGCAACAGGGCGGAA
▸D Q N V V Y R G S W Y G H I A N G T S W S G N A S D K E G G N R A E
TTTACTGTGAATTTTGCCGATAAAAAAATTACCGGCAAGTTAACCGCTGAAAACAGGCAGGCGCAAACCTTTACCATTGAGGGAATGATTCAGGGCAACGG
▸ F T V N F A D K K I T G K L T A E N R Q A Q T F T I E G M I Q G N G
CTTTGAAGGTACGGCGAAAACTGCTGAGTCAGGTTTTGATCTCGATCAAAAAAATACCACCCGCACGCCTAAGGCATATATCACAGATGCCAAGGTAAAGG
▸ F E G T A K T A E S G F D L D Q K N T T R T P K A Y I T D A K V K
GCGGTTTTTACGGGCCTAAAGCCGAAGAGTTGGGCGGATGGTTTGCCTATCCGGGCGATAAACAAACGGAAAAGGCAACAGCTACATCCAGCGATGGAAAT
▸G G F Y G P K A E E L G G W F A Y P G D K Q T E K A T A T S S D G N
TCAGCAAGCAGCGCGACCGTGGTATTCGGTGCGAAACGCCAACAGCCTGTGCAAGGGGAAAACGCGGCAGGGCCTGCAACGGAAACCGTGATAGATGC
▸ S A S S A T V V F G A K R Q Q P V Q G E N A A G P A T E T V I D A
ATACCGTATTACCGGCGAGGAGTTTAAGAAAGAGCAAATAGACAGTTTTGGAGATGTGAAAAAGCTGCTGGTTGACGGAGTGGAGCTTTCACTGCTGCCGT
▸ Y R I T G E E F K K E Q I D S F G D V K K L L V D G V E L S L L P
CTGAGGGCAATAAGGCGGCATTTCAGCACGAGATTGAGCAAAACGGCGTGAAGGCAACGGTGTGTTGTTCCAACTTGGATTACATGAGTTTTGGGAAGCTG
▸S E G N K A A F Q H E I E Q N G V K A T V C C S N L D Y M S F G K L
TCAAAAGAAAATAAAGACGATATGTTCCTGCAAGGTGTCCGCACTCCAGTATCCGATGTGGCGGCAAGGACGGAGGCAAACGCCAAATATCGCGGTACTTG
▸ S K E N K D D M F L Q G V R T P V S D V A A R T E A N A K Y R G T W
GTACGGATATATTGCCAACGGCACAAGCTGGAGCGGCGAAGCCTCCAATCAGGAAGGTGGTAATAGGGCAGAGTTTGACGTGGATTTTTCCACTAAAAAAA
▸ Y G Y I A N G T S W S G E A S N Q E G G N R A E F D V D F S T K K
TCAGTGGCACACTGACGGCAAAAGACCGTACGTCTCCTGCGTTTACTATTACTGCCATGATTAAGGACAACGGTTTTTCAGGTGTGGCGAAAACCGGTGAA
▸I S G T L T A K D R T S P A F T I T A M I K D N G F S G V A K T G E
AACGGCTTTGCGCTGGATCCGCAAAATACCGGAAATTCCCACTATACGCATATTGAAGCCACTGTATCCGGCGGTTTCTACGGCAAAAACGCCATCGAGAT
▸N G F A L D P Q N T G N S H Y T H I E A T V S G G F Y G K N A I E M
GGGCGGATCGTTCTCATTTCCGGGAAATGCACCAGAGGGAAAACAAGAAAAAGCATCGGTGGTATTCGGTGCGAAACGCCAACAGCTTGTGCAA
▸ G G S F S F P G N A P E G K Q E K A S V V F G A K R Q Q L V Q

Panel B

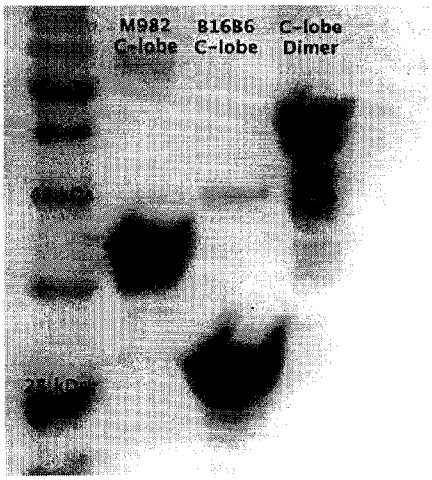


FIGURE 12

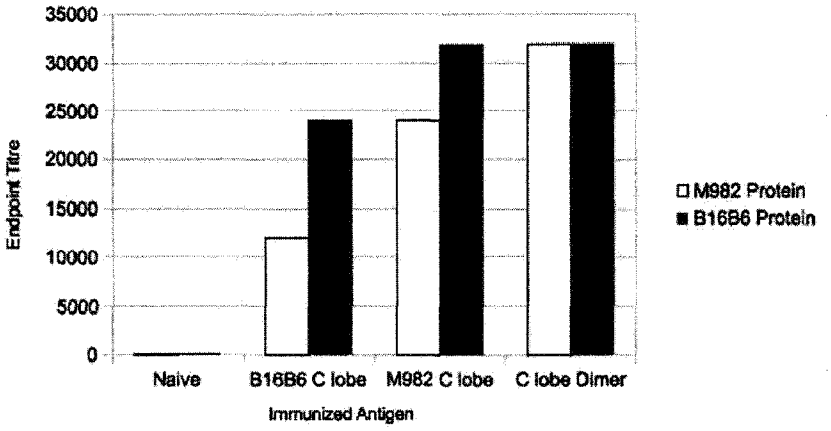
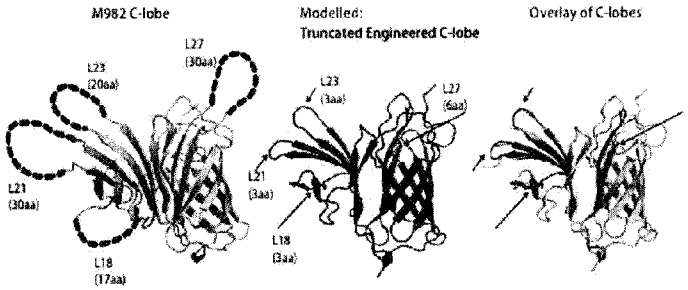

35000
30000
25000
20000
15000
10000
5000
0
Endpoint Titre
Naive
B16B6 C lobe
M982 C lobe
C lobe Dimer
Immunized Antigen
M982 Protein
B16B6 Protein

FIGURE 13

Panel A



Panel B

```
                         10        20        30        40        50        60        70
wt          1  SSSENSKLTT VLDAVELTLN DKKIKNLDNF SNAAQLVVDG IMIPLLPKDS ESGNTQADKG KNGGTEFTRK
loop1       1  SSSENSKLTT VLDAVELTLN DKKIKNLDNF SNAAQLVVDG IMIDL--loop 18----- --AGTEFTRK
loop2       1  SSSENSKLTT VLDAVELTLN DKKIKNLDNF SNAAQLVVDG IMIPLLPKDS ESGNTQADKG KNGGTEFTRK
loop3       1  SSSENSKLTT VLDAVELTLN DKKIKNLDNF SNAAQLVVDG IMIPLLPKDS ESGNTQADKG KNGGTEFTRK
loop4       1  SSSENSKLTT VLDAVELTLN DKKIKNLDNF SNAAQLVVDG IMIPLLPKDS ESGNTQADKG KNGGTEFTRK
loopless    1  SSSENSKLTT VLDAVELTLN DKKIKNLDNF SNAAQLVVDG IMIDL---loop 18---- --AGTEFTRK
wt         71  FEHTPESDKK DAQAGTQTNG AQTASNTAGD TNGKTKTYEV EVCCSNLNYL KYGMLTRKNS KSAMQAGGNS
loop1      54  FEHTPESDKK DAQAGTQTNG AQTASNTAGD TNGKTKTYEV EVCCSNLNYL KYGMLTRKNS KSAMQAGGNS
loop2      71  FEHT------ -loop 21 ---------- INGKT--YEV EVCCSNLNYL KYGMLTRKNS KSAMQAGGNS
loop3      71  FEHTPESDKK DAQAGTQTNG AQTASNTAGD TNGKTKTYEV EVCCSNLNYL KYGMLTRKG- loop 23-
loop4      71  FEHTPESDKK DAQAGTQTNG AQTASNTAGD TNGKTKTYEV EVCCSNLNYL KYGMLTRKNS KSAMQAGGNS
loopless   54  FEHT------ -loop 21 ---------- INGKT--YEV EVCCSNLNYL KYGMLTRKG- loop 23-
wt        141  SQADAKTEQV EQSMFLQGER TDEKEIPTDQ NVVYRGSWYG HIANGTSWSG NASDKEGGNR AEFTVNFADK
loop1     124  SQADAKTEQV EQSMFLQGER TDEKEIPTDQ NVVYRGSWYG HIANGTSWSG NASDKEGGNR AEFTVNFADK
loop2     113  SQADAKTEQV EQSMFLQGER TDEKEIPTDQ NVVYRGSWYG HIANGTSWSG NASDKEGGNR AEFTVNFADK
loop3     130  -------KQV EQSMFLQGER TDEKEIPTDQ NVVYRGSWYG HIANGTSWSG NASDKEGGNR AEFTVNFADK
loop4     141  SQADAKTEQV EQSMFLQGER TDEKEIPTDQ NVVYRGSWYG HIANGTSWSG NASDKEGGNR AEFTVNFADK
loopless   85  -------KQV EQSMFLQGER TDEKEIPTDQ NVVYRGSWYG HIANGTSWSG NASDKEGGNR AEFTVNFADK
wt        211  KITGKLTAEN RQAQTFTIEG MIQGNGFEGT AKTAESGFDL DQKNTTRTPK AYITDAKVKG GFYGPKAEEL
loop1     194  KITGKLTAEN RQAQTFTIEG MIQGNGFEGT AKTAESGFDL DQKNTTRTPK AYITDAKVKG GFYGPKAEEL
loop2     183  KITGKLTAEN RQAQTFTIEG MIQGNGFEGT AKTAESGFDL DQKNTTRTPK AYITDAKVKG GFYGPKAEEL
loop3     193  KITGKLTAEN RQAQTFTIEG MIQGNGFEGT AKTAESGFDL DQKNTTRTPK AYITDAKVKG GFYGPKAEEL
loop4     211  KITGKLTAEN RQAQTFTIEG MIQGNGFEGT AKTAESGFDL DQKNTTRTPK AYITDAKVKG GFYGPKAEEL
loopless  148  KITGKLTAEN RQAQTFTIEG MIQGNGFEGT AKTAESGFDL DQKNTTRTPK AYITDAKVKG GFYGPKAEEL
wt        281  GGWFAYPGDK QTEKATATSS DGNSASSATV VFGAKRQQPV Q
loop1     264  GGWFAYPGDK QTEKATATSS DGNSASSATV VFGAKRQQPV Q
loop2     253  GGWFAYPGDK QTEKATATSS DGNSASSATV VFGAKRQQPV Q
loop3     263  GGWFAYPGDK QTEKATATSS DGNSASSATV VFGAKRQQPV Q
loop4     281  GGWFAY--loop 27-HKSD NG----SATV VFGAKRQQPV Q
loopless  218  GGWFAY--loop 27-HKSD NG----SATV VFGAKRQQPV Q
```

FIGURE 14

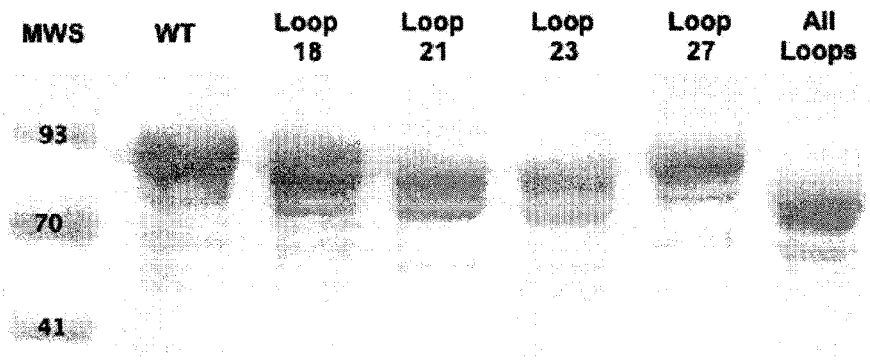


FIGURE 15

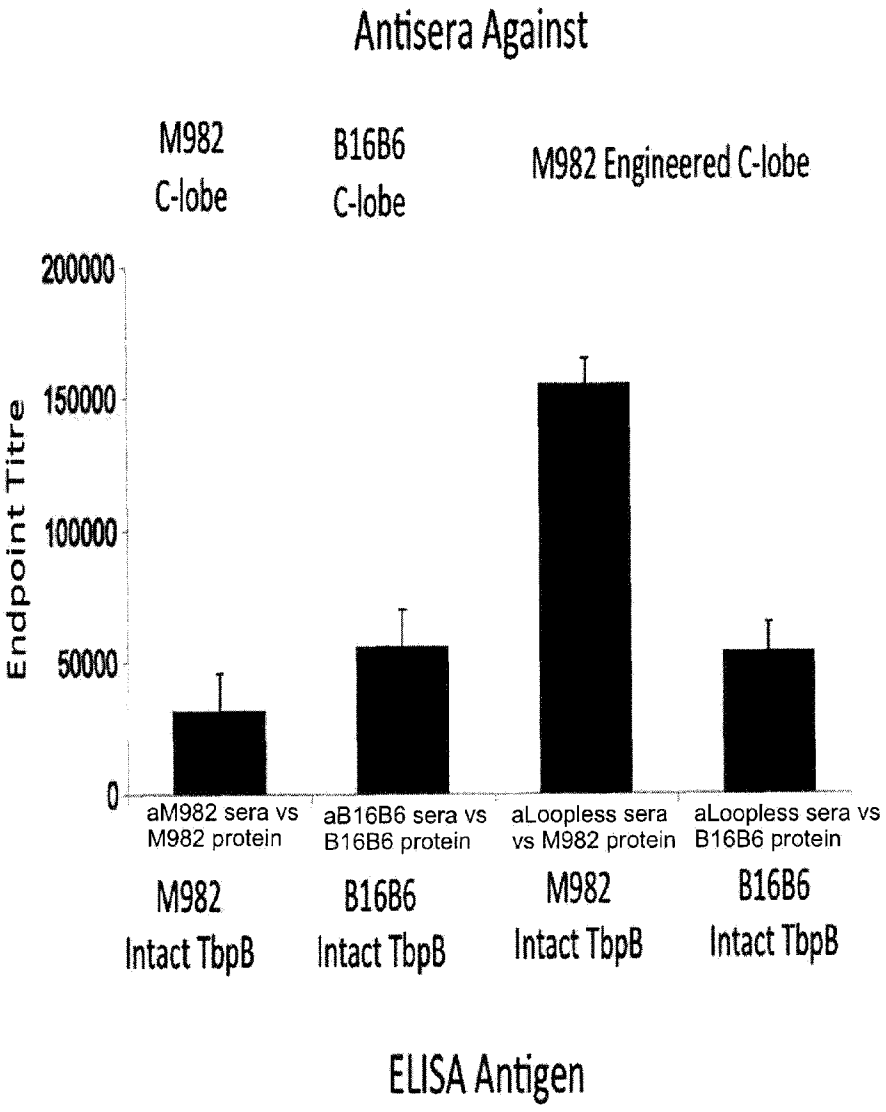
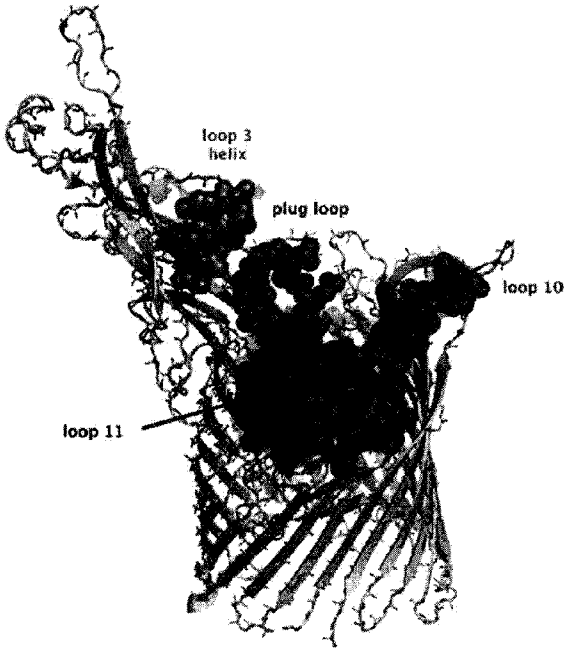

Antisera Against
M982 C-lobe
B16B6 C-lobe
M982 Engineered C-lobe
Endpoint Titre
200000
150000
100000
50000
0
aM982 sera vs M982 protein
aB16B6 sera vs B16B6 protein
aLoopless sera vs M982 protein
aLoopless sera vs B16B6 protein
M982 Intact TbpB
B16B6 Intact TbpB
M982 Intact TbpB
B16B6 Intact TbpB
ELISA Antigen

FIGURE 16

Panel A



Panel B

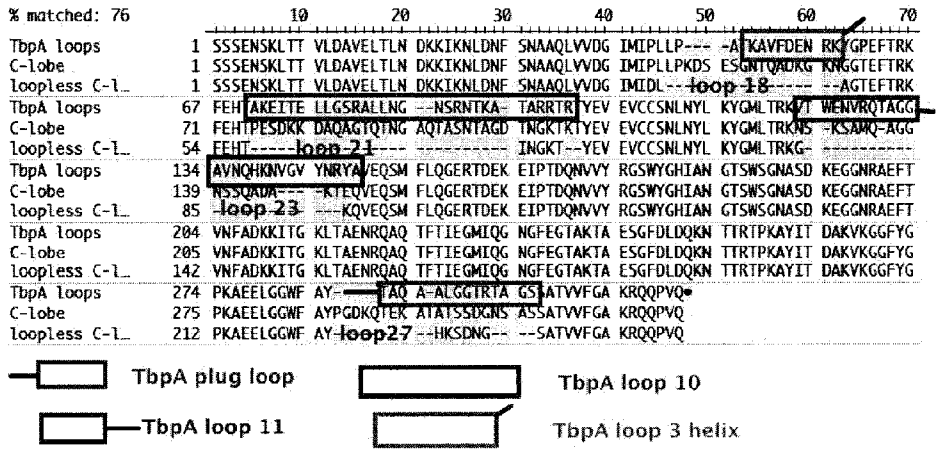


FIGURE 17

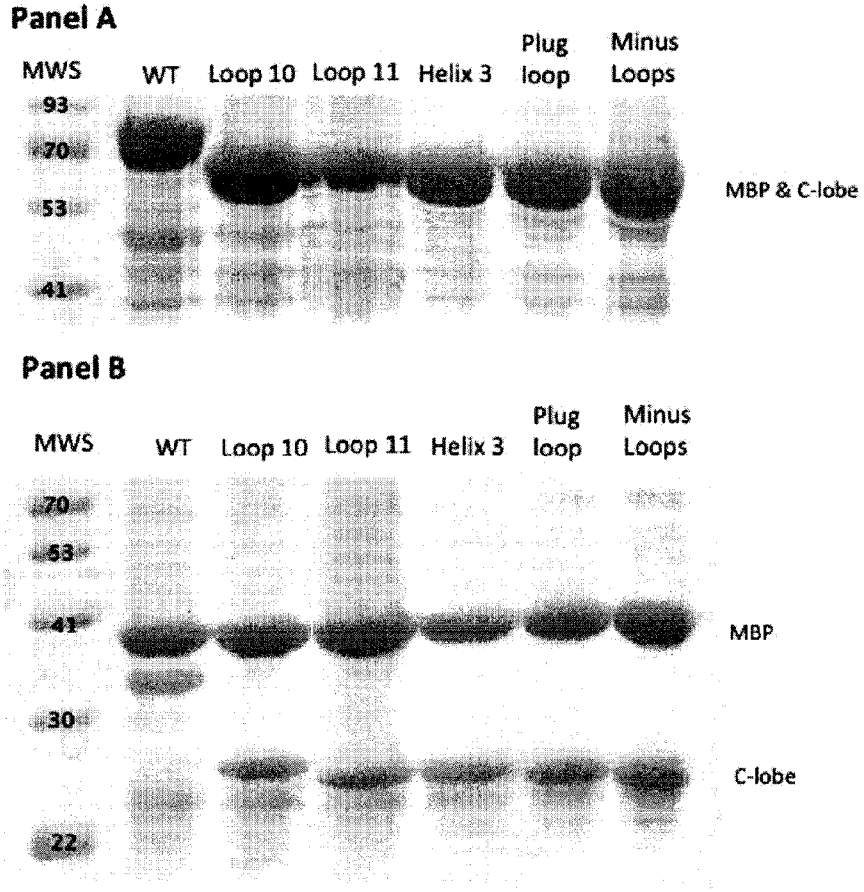

Panel A
MWS
WT
Loop 10
Loop 11
Helix 3
Plug loop
Minus Loops
93
70
53
41
MBP & C-lobe
Panel B
MWS
WT
Loop 10
Loop 11
Helix 3
Plug loop
Minus Loops
70
53
41
30
22
MBP
C-lobe

FIGURE 18

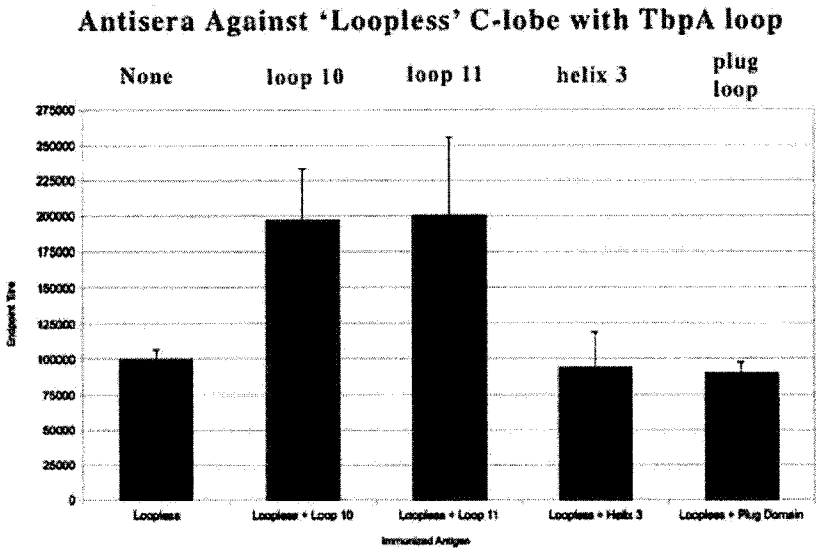
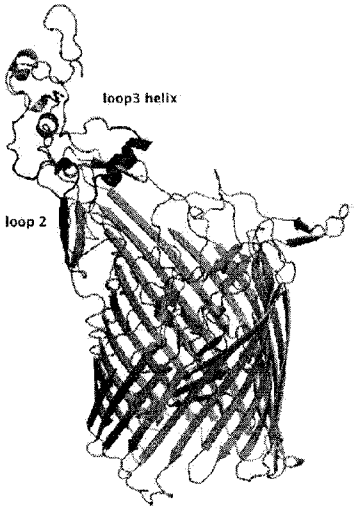

Antisera Against 'Loopless' C-lobe with TbpA loop
None
loop 10
loop 11
helix 3
plug loop
275000
250000
225000
200000
175000
150000
125000
100000
75000
50000
25000
0
Loopless
Loopless + Loop 10
Loopless + Loop 11
Loopless + Helix 3
Loopless + Plug Domain
ELISA Antigen for all samples is the C-lobe with all four TbpA loops

FIGURE 19

Panel A



Panel B

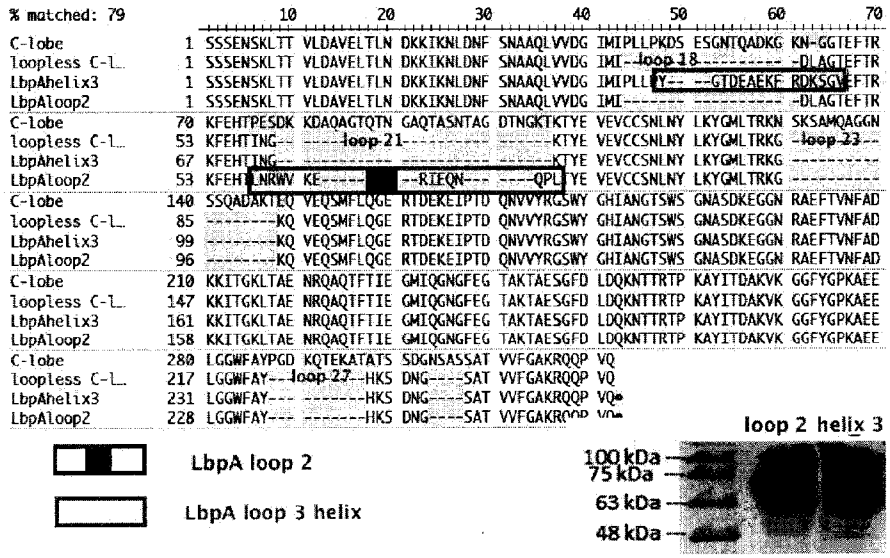
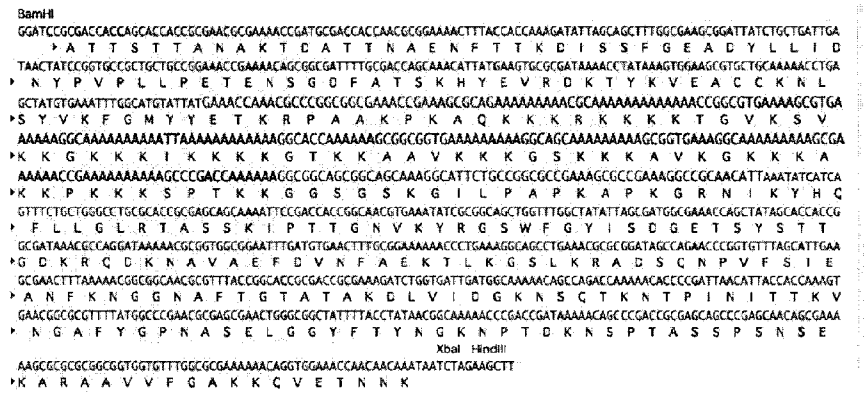


FIGURE 20

A



B

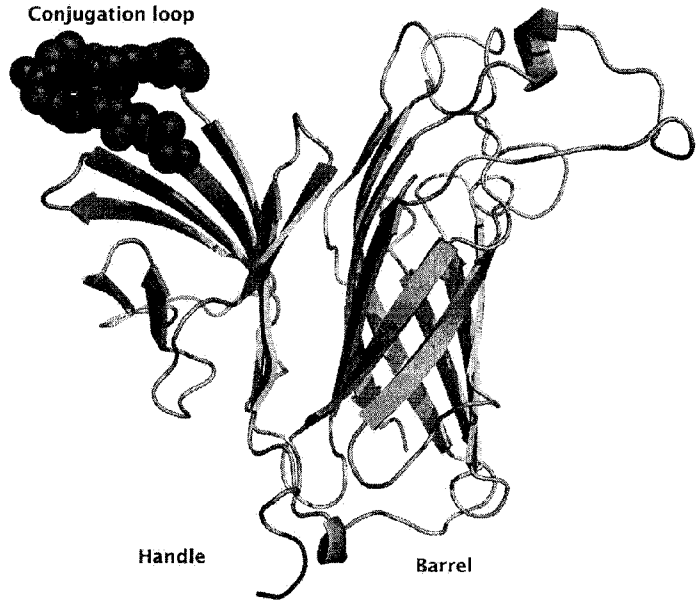


FIGURE 21

Affinity binding constants for wild-type and mutant TbpBs

Protein	Mutation	Loop	Kd	Method
ApH49 TbpB	WT		55 nM	ITC
ApH49 TbpB	F171A	L8	NDB	ITC
ApH49 TbpB	WT		44 nM	SPR
ApH49 TbpB	F171A	L8	TBD	SPR
ApH87 TbpB	WT		60 nM	SPR
ApH87 TbpB	Y95A	L3	585 nM	SPR
ApH87 TbpB	Y121A	L5	203 nM	SPR
ApH87 TbpB	Y174A	L8	8.9 uM	SPR
ApH87 TbpB	R179E	L8	6.1 uM	SPR
AsH57 TbpB	WT		120 nM	SPR
AsH57 TbpB	F63A	L1	326 nM	SPR
AsH57 TbpB	F152A	L5	495 nM	SPR
*Hp*5 TbpB	WT		21 nM	BLI
*Hp*5 TbpB	Y93 A	L3	TBD	BLI
*Hp*5 TbpB	Y117A	L5	TBD	BLI
*Hp*5 TbpB (e4535)	Y167A	L8	40uM	BLI
*Hp*5 TbpB	W176A	L8	TBD	BLI
Hp5 TbpB (e4597)	Y167A, W176A	L8	NDB	BLI

TBD – To Be Determined
NDB – No Detectable Binding
ITC – isothermal titration calorimetry
SPR – surface plasmon resonances
BLI – biolayer interferometry

FIGURE 22

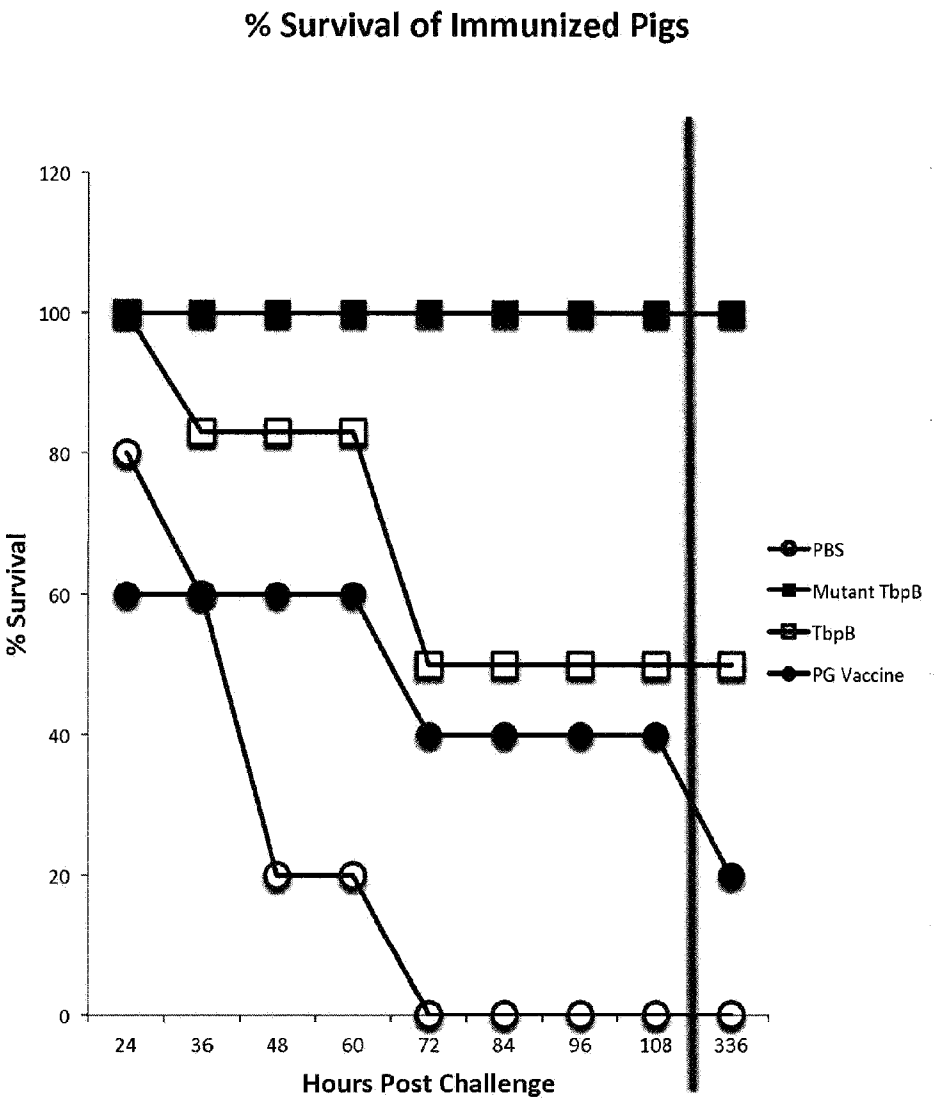

% Survival of Immunized Pigs
120
100
80
60
40
20
0
% Survival
24
36
48
60
72
84
96
108
336
Hours Post Challenge
PBS
Mutant TbpB
TbpB
PG Vaccine

FIGURE 23

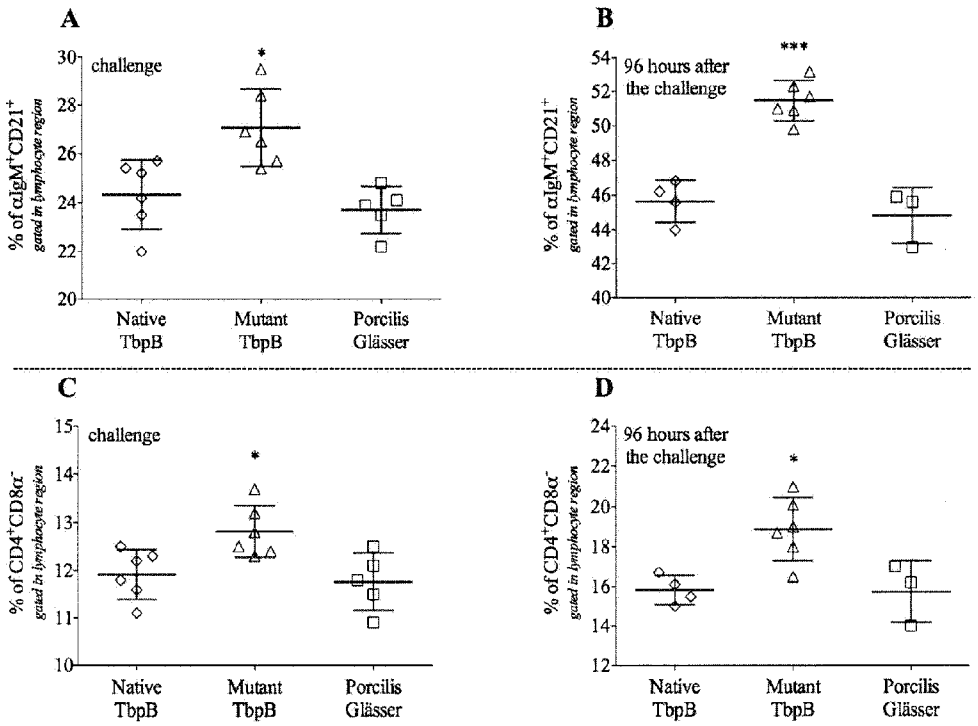

A
challenge
% of αIgM+CD21+ gated in lymphocyte region
Native TbpB
Mutant TbpB
Porcilis Glässer
B
96 hours after the challenge
% of αIgM+CD21+ gated in lymphocyte region
Native TbpB
Mutant TbpB
Porcilis Glässer
C
challenge
% of CD4+CD8α- gated in lymphocyte region
Native TbpB
Mutant TbpB
Porcilis Glässer
D
96 hours after the challenge
% of CD4+CD8α- gated in lymphocyte region
Native TbpB
Mutant TbpB
Porcilis Glässer

FIGURE 24

TbpB and TbpB C-lobe Induce Sterilizing Mucosal Immunity

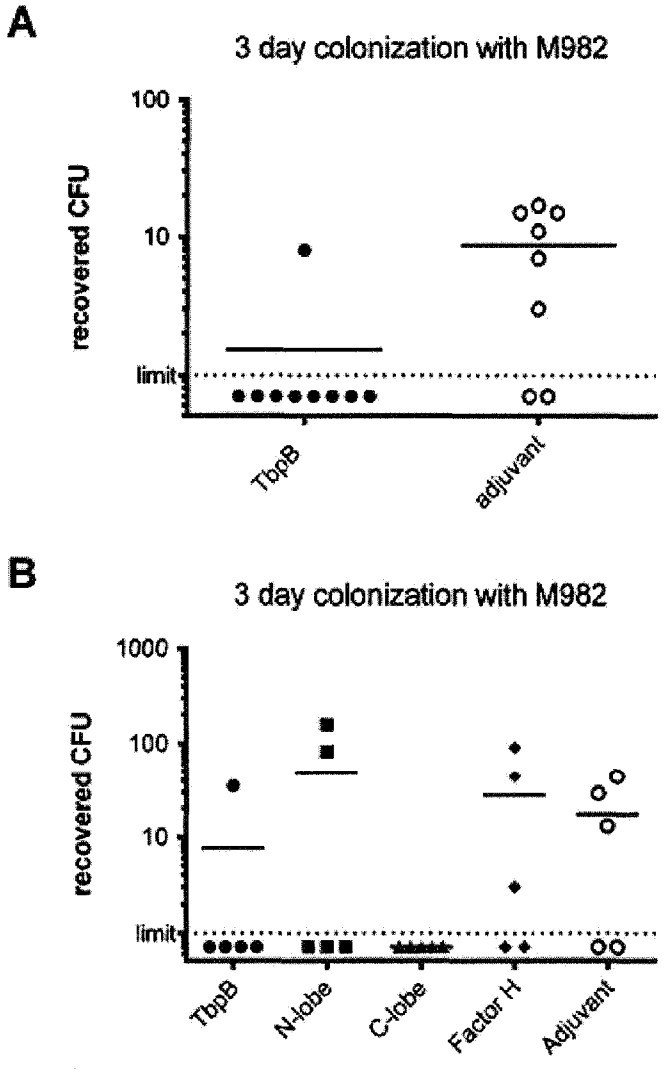


FIGURE 25

Sequence Diversity of Intact TbpBs from *N. meningitidis* and *N. gonorrhoeae*

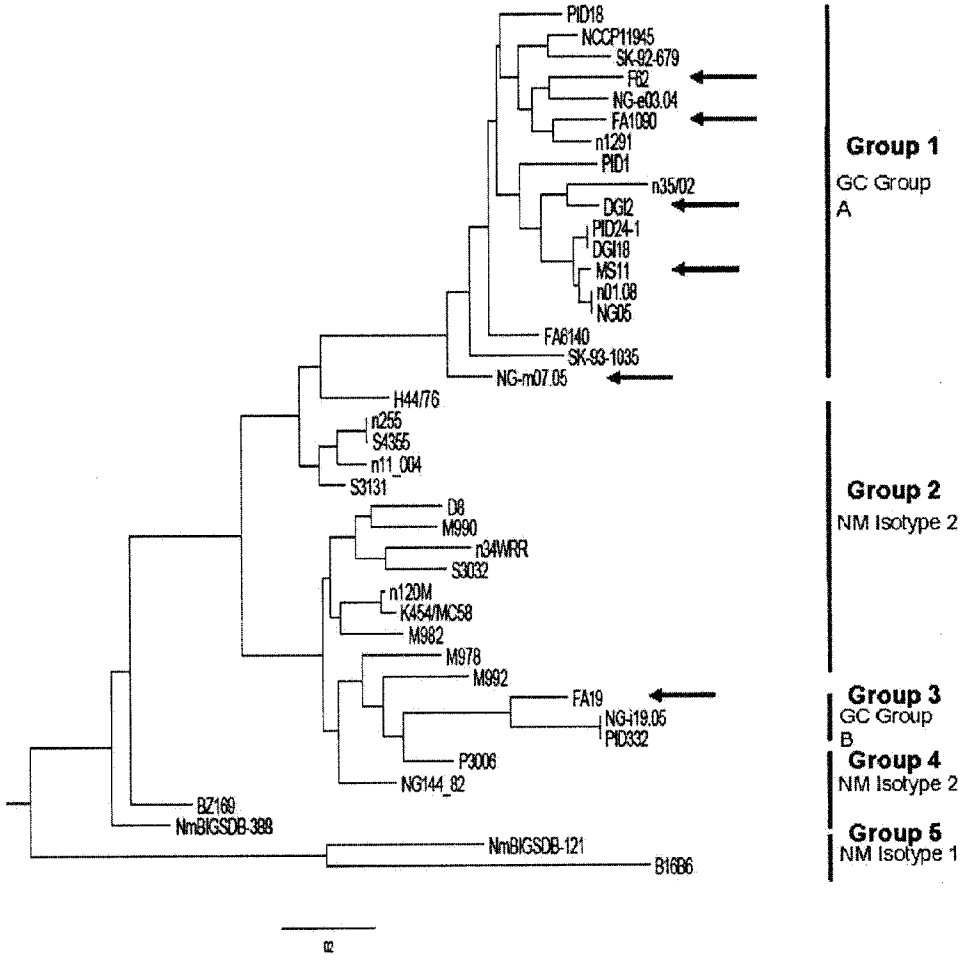


FIGURE 26A

Sequence Diversity of TbpB Lobes from *N. meningitidis* and *N. gonorrhoeae*

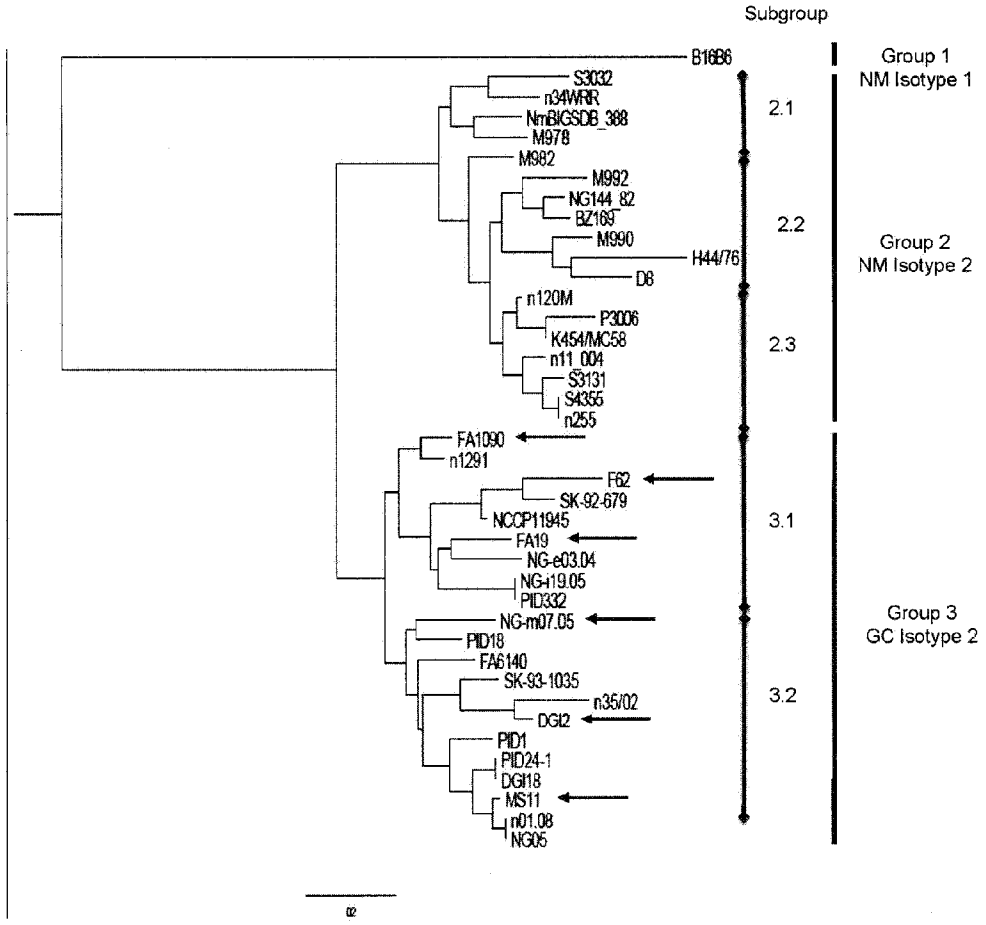


FIGURE 26B

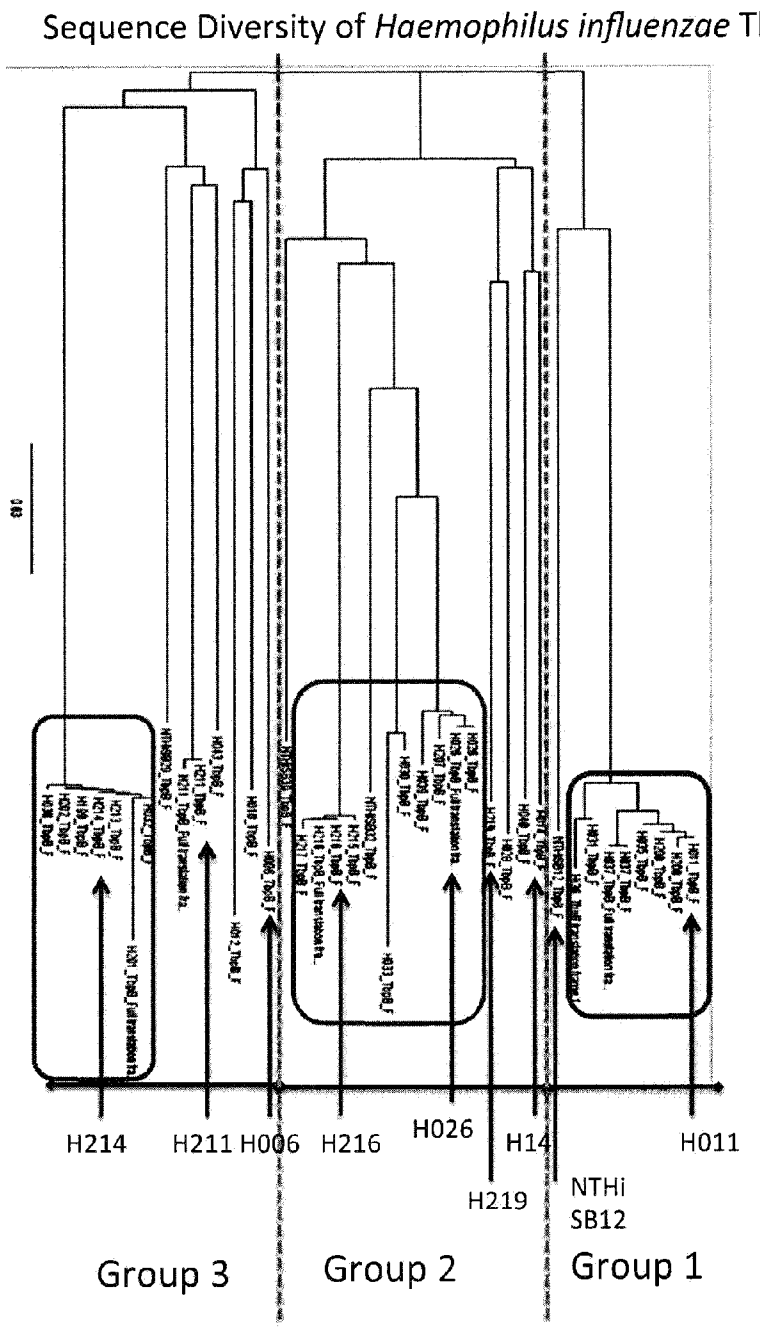

Sequence Diversity of *Haemophilus influenzae* TbpBs
0.03
H214
H211
H006
H216
H026
H14
H011
H219
NTHi
SB12
Group 3
Group 2
Group 1

Figure 27A

Sequence Diversity of *Haemophilus* TbpB C-lobes

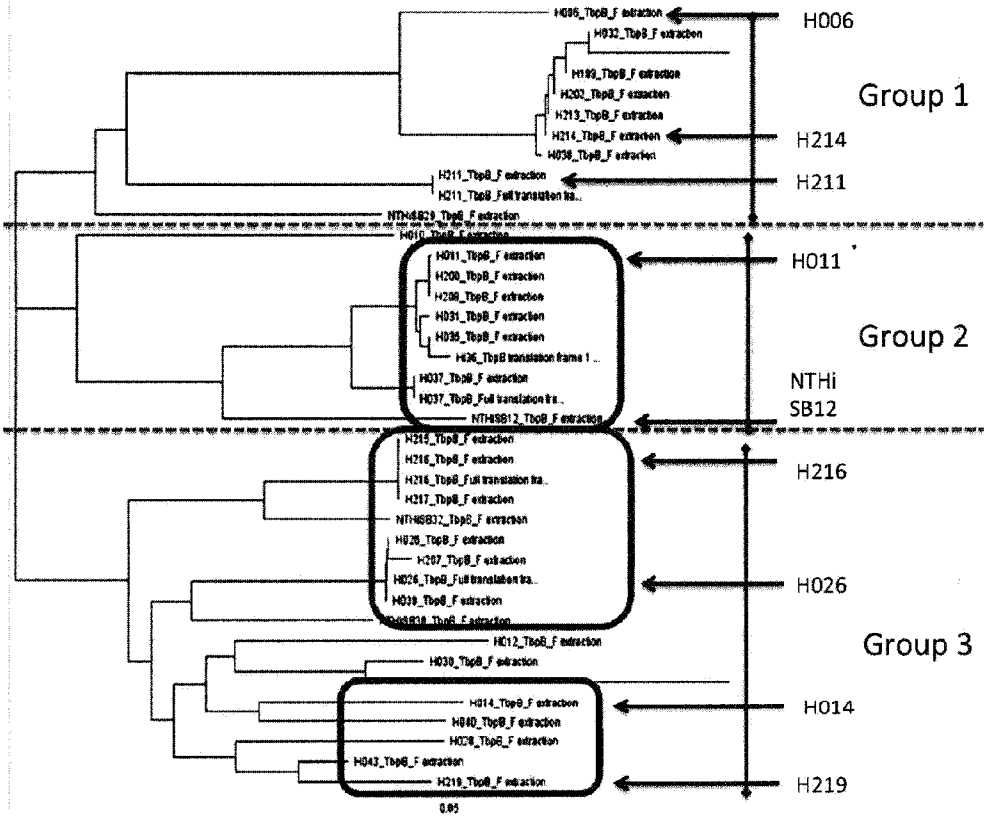


FIGURE 27B

Sequence Diversity of TbpBs from Ruminant pathogens

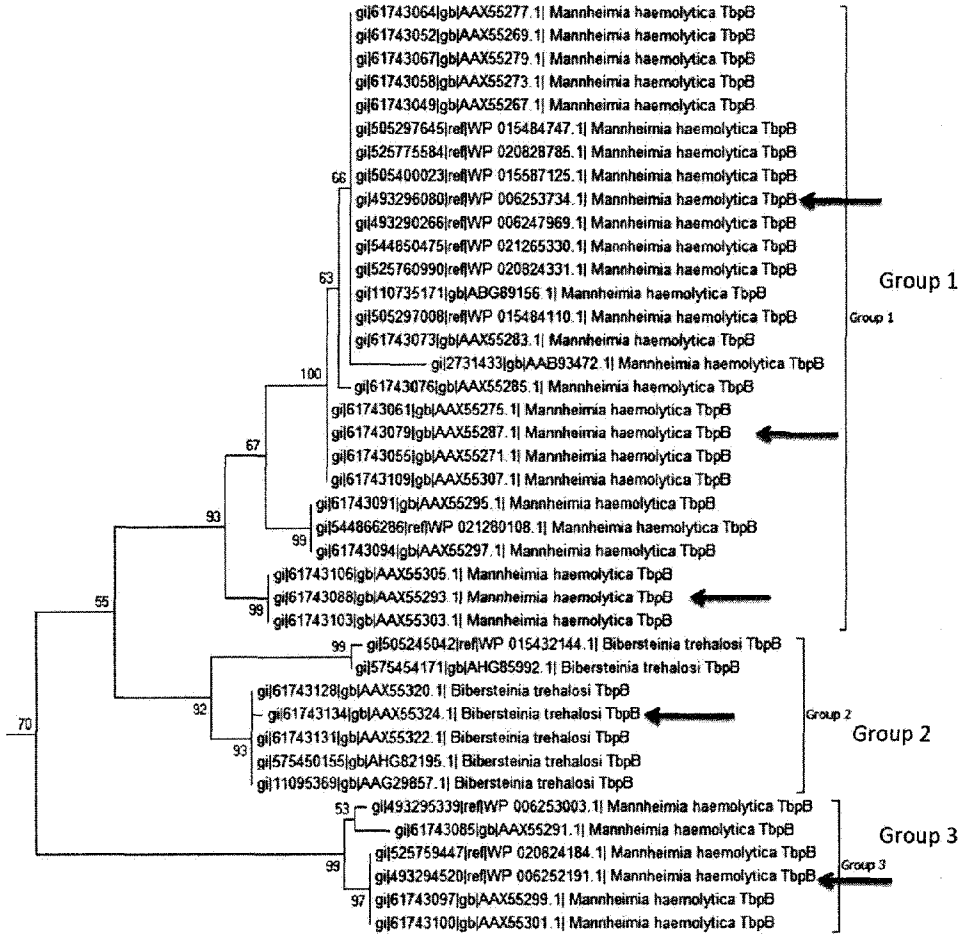


FIGURE 28

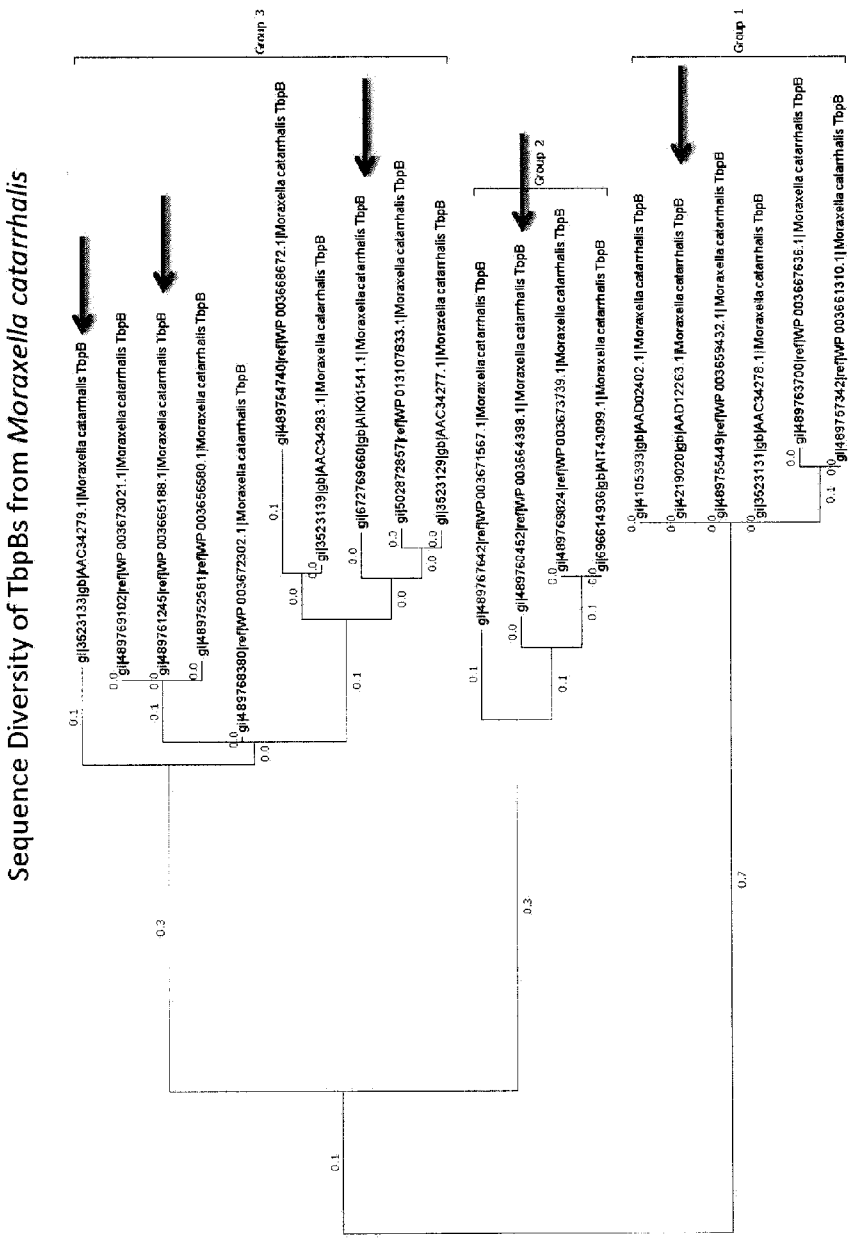

Sequence Diversity of TbpBs from Moraxella catarrhalis
Group 3
Group 2
Group 1
gi|3523133|gb|AAC34279.1|Moraxella catarrhalis TbpB
gi|489769102|ref|WP 003673021.1|Moraxella catarrhalis TbpB
gi|489761245|ref|WP 003665188.1|Moraxella catarrhalis TbpB
gi|489752581|ref|WP 003656580.1|Moraxella catarrhalis TbpB
gi|489768380|ref|WP 003672302.1|Moraxella catarrhalis TbpB
gi|489764740|ref|WP 003668672.1|Moraxella catarrhalis TbpB
gi|3523139|gb|AAC34283.1|Moraxella catarrhalis TbpB
gi|672769660|gb|AIK01541.1|Moraxella catarrhalis TbpB
gi|502872857|ref|WP 013107833.1|Moraxella catarrhalis TbpB
gi|3523129|gb|AAC34277.1|Moraxella catarrhalis TbpB
gi|489767642|ref|WP 003671567.1|Moraxella catarrhalis TbpB
gi|489760452|ref|WP 003664398.1|Moraxella catarrhalis TbpB
gi|489769824|ref|WP 003673739.1|Moraxella catarrhalis TbpB
gi|966149356|gb|AIT43099.1|Moraxella catarrhalis TbpB
gi|4105393|gb|AAD02402.1|Moraxella catarrhalis TbpB
gi|4219020|gb|AAD12263.1|Moraxella catarrhalis TbpB
gi|489755449|ref|WP 003659432.1|Moraxella catarrhalis TbpB
gi|3523131|gb|AAC34278.1|Moraxella catarrhalis TbpB
gi|489763700|ref|WP 003667635.1|Moraxella catarrhalis TbpB
gi|489757342|ref|WP 003661310.1|Moraxella catarrhalis TbpB
0.1

FIGURE 29

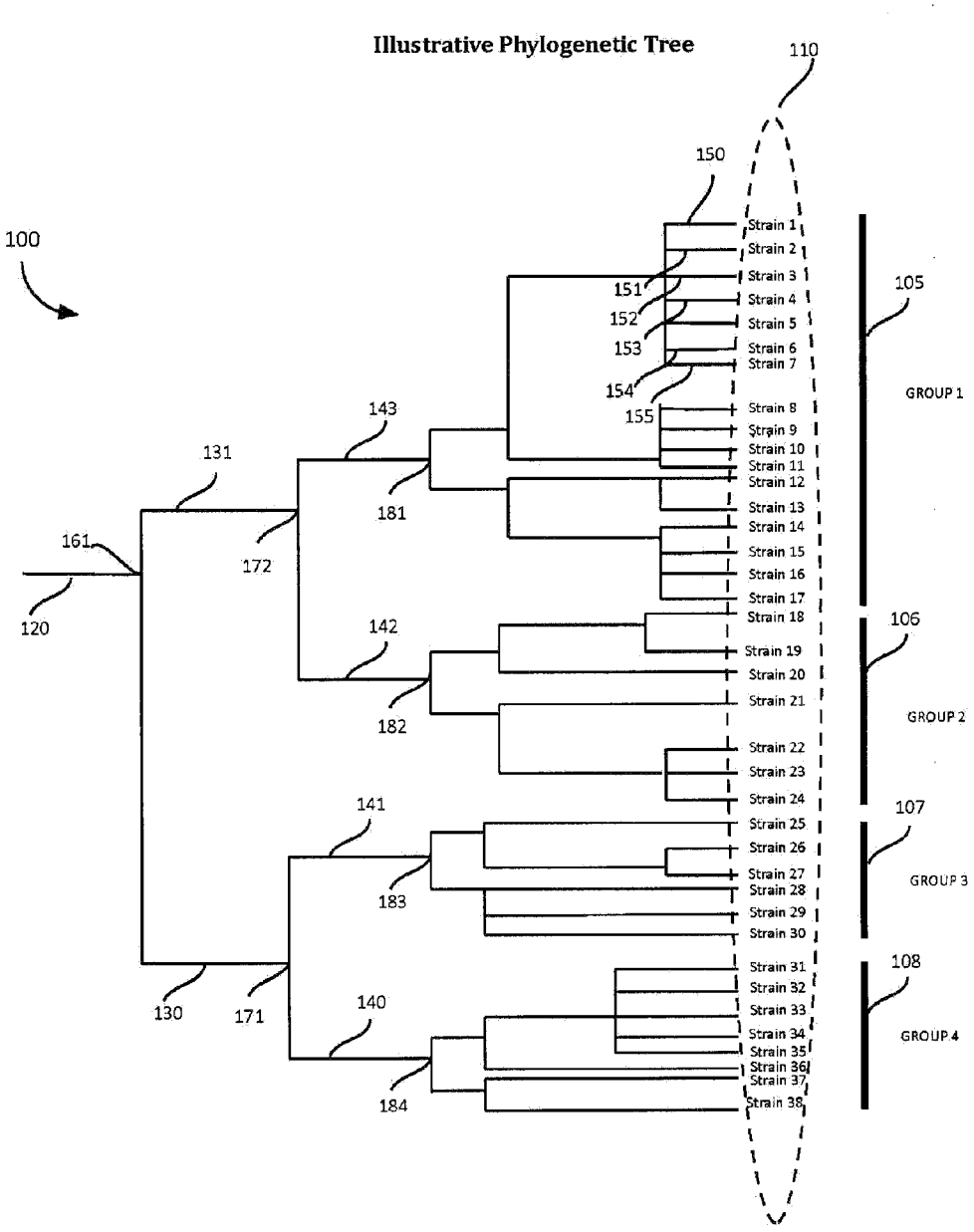

Illustrative Phylogenetic Tree
100
110
150
151
152
153
154
155
143
131
181
161
172
120
142
182
141
183
130
171
140
184
105
GROUP 1
106
GROUP 2
107
GROUP 3
108
GROUP 4
Strain 1
Strain 2
Strain 3
Strain 4
Strain 5
Strain 6
Strain 7
Strain 8
Strain 9
Strain 10
Strain 11
Strain 12
Strain 13
Strain 14
Strain 15
Strain 16
Strain 17
Strain 18
Strain 19
Strain 20
Strain 21
Strain 22
Strain 23
Strain 24
Strain 25
Strain 26
Strain 27
Strain 28
Strain 29
Strain 30
Strain 31
Strain 32
Strain 33
Strain 34
Strain 35
Strain 36
Strain 37
Strain 38

FIGURE 30