GENES AND PROTEINS, AND THEIR USES

Field of the Invention

This invention relates to bacterial genes and proteins, and their uses. More particularly, it relates to their use in therapy, for immunisation and in screening for drugs.

Background of the Invention

Neisseria meningitidis is a Gram-negative bacterial pathogen that is implicated in septic shock and bacterial meningitis. This bacterium is a leading cause of bacterial meningitis in developed countries, and causes large-scale epidemics in Africa and China. In the UK, *Neisseria meningitidis* is the leading cause of death in childhood apart from road traffic accidents. The bacterium naturally inhabits the human naso-pharynx and then gains access to the blood stream from where it causes severe septicaemia or meningitis. Although current anti-microbials are effective in eliminating the bacterium from the body, the mortality from menigococcal septicaemia remains substantial. It would be desirable to provide means for treating or preventing conditions caused by *Neisseria meningitidis,* e.g. by immunisation.

Summary of the Invention

The present invention is based on the discovery of genes in *Neisseria meningitidis*, the products of which may be located on the outer surface of the organism, and therefore may be used as targets for immuno-therapy.

According to one aspect of the invention, a peptide is encoded by a gene having any of the nucleotide sequences identified in claim 1, or a homologue or a functional fragment thereof. Such a peptide is suitable for therapeutic or diagnostic use, e.g. when isolated.

According to a second aspect of the invention, a polynucleotide encoding a peptide defined above, may also be useful in therapy or diagnosis.

According to a further aspect of the invention, the peptide or the polynucleotide may be used for screening potential antimicrobial drugs.

A further aspect of the invention is the use of any of the products identified herein, for the treatment or prevention of a condition associated with infection by *Neisseria* or Gram-negative bacteria.

Description of the Invention

The present invention is based on the discovery of genes encoding peptides which are located on the cell surface of *Neisseria*, and which are therefore useful for the preparation of therapeutic agents to treat infection. It should be understood that

references to therapy also include preventative treatments, e.g. vaccination. Furthermore, while the products of the invention are intended primarily for the treatment of infections in human patients, veterinary applications are also considered to be within the scope of the invention.

The present invention is described with reference to *Neisseria meningitidis*. However, all the *Neisseria* strains, and many other Gram-negative bacterial strains are likely to include related peptides or proteins having amino acid sequence identity or similarity to those identified herein. Organisms likely to contain the peptides include, but are not limited to the genera *Salmonella*, *Enterobacter*, *Klebsiella*, *Shigella* and *Yersinia*.

Preferably, the peptides that may be useful in the various aspects of the invention have greater than a 40% similarity with the peptides identified herein. More preferably, the peptides have greater than 60% sequence similarity. Most preferably, the peptides have greater than 80% sequence similarity, e.g. 95% similarity. With regard to the polynucleotide sequences identified herein, related polynucleotides that may be useful in the various aspects of the invention may have greater than 40% identity with the sequences identified herein. More preferably, the polynucleotide sequences have greater than 60% sequence identity. Most preferably, the polynucleotide sequences have greater than 80% sequence identity, e.g. 95% identity.

The terms "similarity" and "identity" are known in the art. The use of the term "identity" refers to a sequence comparison based on identical matches between correspondingly identical positions in the sequences being compared. The term "similarity" refers to a comparison between amino acid sequences, and takes into account not only identical amino acids in corresponding positions, but also functionally similar amino acids in corresponding positions. Thus similarity between polypeptide sequences indicates functional similarity, in addition to sequence similarity.

Levels of identity between gene sequences and levels of identity or similarity between amino acid sequences can be calculated using known methods. In relation to the present invention, publicly available computer based methods for determining identity and similarity include the BLASTP, BLASTN and FASTA (Atschul *et al.*, J. Molec. Biol., 1990; 215:403-410), the BLASTX program available from NCBI, and the Gap program from Genetics Computer Group, Madison WI. The levels of similarity and identity provided herein, were obtained using the Gap program, with a Gap penalty of 12 and a Gap length penalty of 4 for determining the amino acid sequence

comparisons, and a Gap penalty of 50 and a Gap length penalty of 3 for the polynucleotide sequence comparisons.

Having characterised a gene according to the invention, it is possible to use the gene sequence to search for related genes or peptides in other microorganisms. This may be carried out by searching in existing databases, e.g. EMBL or GenBank.

The techniques mentioned herein are well known in the art. However, reference is made in particular to Sambrook *et al*, Molecular Cloning, A Laboratory Manual (1989) and Ausubel *et al*, current Protocols in Molecular Biology (1995), John Wiley & Sons, Inc.

Peptides or proteins according to the invention may be purified and isolated by methods known in the art. In particular, having identified the gene sequence, it will be possible to use recombinant techniques to express the genes in a suitable host. Active fragments and related molecules can be identified and may be useful in therapy. For example, the peptides or their active fragments may be used as antigenic determinants in a vaccine, to elicit an immune response. They may also be used in the preparation of antibodies, for passive immunisation, or diagnostic applications. Suitable antibodies include monoclonal antibodies, or fragments thereof, including single chain Fv fragments. Humanised antibodies are also within the scope of the invention. Methods for the preparation of antibodies will be apparent to those skilled in the art.

Active fragments of the peptides are those that retain the biological function of the peptide. For example, when used to elicit an immune response, the fragment will be of sufficient size, such that antibodies generated from the fragment will discriminate between that peptide and other peptides on the bacterial microorganism. Typically, the fragment will be at least 30 nucleotides (10 amino acids) in size, preferably 60 nucleotides (20 amino acids) and most preferably greater than 90 nucleotides (30 amino acids) in size.

It should also be understood, that in addition to related molecules from other microorganisms, the invention encompasses modifications made to the peptides and polynucleotides identified herein which do not significantly alter the biological function. It will be apparent to the skilled person that the degeneracy of the genetic code can result in polynucleotides with minor base changes from those specified herein, but which nevertheless encode the same peptides. Complementary polynucleotides are also within the invention. Conservative replacements at the amino acid level are also envisaged, i.e. different acidic or basic amino acids may be substituted without substantial loss of function.

The preparation of vaccines based on the identified peptides will be known to those skilled in the art. Vaccine compositions can be formulated with suitable carriers or adjuvants, e.g. alum, as necessary or desired, to provide effective immunisation against infection. The preparation of vaccine formulations will be apparent to the skilled person.

More generally, and as is well known to those skilled in the art, a suitable amount of an active component of the invention can be selected, for therapeutic use, as can suitable carriers or excipients, and routes of administration. These factors would be chosen or determined according to known criteria such as the nature/severity of the condition to be treated, the type and/or health of the subject etc.

In a separate embodiment, the products of the invention may be used in screening assays for the identification of potential antimicrobial drugs or for the detection for virulence. Routine screening assays are known to those skilled in the art, and can be adapted using the products of the invention in the appropriate way. For example, the products of the invention may be used as the target for a potential drug, with the ability of the drug to inactivate or bind to the target indicating its potential antimicrobial activity.

The genes of the invention may also be implicated in the virulence of the microorganism, and therefore deleting or inactivating the gene may be sufficient to produce an attenuated (avirulent) microorganism.

The attenuated microorganisms may be prepared with a mutation that disrupts the expression of any of the genes identified herein. The skilled person will be aware of methods for disrupting expression of particular genes. Techniques that may be used include insertional inactivation or gene deletion techniques. Attenuated microorganisms according to the invention may also comprise additional mutations in other genes, for example in a second gene identified herein or in a separate gene required for growth of the microorganism, e.g. an *aro* mutation or, with regard to *Salmonella*, in a gene located in the SPI2 region identified in WO-A-96/17951.

Attenuated microorganisms may also be used as carrier systems for the delivery of heterologous antigens, therapeutic proteins or nucleic acids (DNA or RNA). In this embodiment, the attenuated microorganisms are used to deliver a heterologous antigen, protein or nucleic acid to a particular site *in vivo*. Introduction of a heterologous antigen, peptide or nucleic acid into an attenuated microorganism can be carried out by conventional techniques, including the use of recombinant constructs, e.g. vectors, which comprise polynucleotides that express the heterologous antigen or

therapeutic protein, and also include suitable promoter sequences. Alternatively, the gene that encodes the heterologous antigen or protein may be incorporated into the genome of the organism and the endogenous promoters used to control expression.

The various products of the invention may also be used in veterinary applications.

The peptides of the present invention were identified as follows:

Identification of Peptides

A partial gene library of *Neisseria meningitidis* (strain C311+) chromosomal DNA was prepared using the plasmid vectors pFW-*phoA*1, pFW-*phoA*2 and pFW-*phoA*3 (Podbielski, A. *et al*, Gene 1996; 177:137-147). These plasmids possess a constitutive spectinomycin adenyltransferase antibiotic resistance marker, which confers a high level of spectinomycin resistance and is therefore easily selected. Furthermore, these vectors contain a truncated (leaderless) *Escherichia coli phoA* gene for alkaline phosphatase. The three vectors differ only with respect to the reading frame in which the leaderless *phoA* gene exists, as compared to an upstream in-frame *Bam*HI restriction enzyme site. Because this truncated *E. coli phoA* gene lacks the appropriate leader sequence for export of this enzyme across the bacterial membrane, extracellular alkaline phosphatase activity is absent when these plasmids are propagated in an *E. coli phoA* mutant (e.g. strain DH5α). The chromogenic alkaline phosphatase substrate, XP (5-Bromo-4-chloro-3-Indolyl-phosphate), does not enter intact bacterial cells and therefore only exported or surface-associated alkaline phosphatase activity can be detected. When exported or surface-associated alkaline phosphatase activity is present, the chromogenic XP substrate is cleaved to yield a blue pigment and the corresponding bacterial colonies can be identified by their blue colour.

Plasmid DNA was digested to completion with *Bam*HI and dephosphorylated using shrimp alkaline phosphatase. Neisseria genomic DNA was partially digested with *Sau*3AI, such that a majority of fragments appeared to be 0.5 – 1.0 kb in size when observed as bands on a 1% agarose gel stained with ethidium bromide. These *Sau*3AI fragments were ligated into the prepared pFW-*phoA* vectors. *E. coli* strain DH5α was chosen as the cloning host since it lacks a functional *phoA* gene. Recombinant plasmids were selected on Luria agar containing 100 µg/ml of spectinomycin and 40 µg/ml of the chromogenic XP substrate. *E. coli* transformants harbouring plasmids containing *Neisseria meningitidis* insert DNA that complements the export signal

sequence of the leaderless *phoA* gene were identified by the blue colour of the colonies.

Neisseria meningitidis insert DNA that complemented the export signal sequence of the leaderless *phoA* gene was sequenced and the resulting sequence was searched for known proteins in the GenBank database. The results are shown in Table 1.

Table 1

SEQ ID NO.		Ref. Name	Putative Protein	Accession No.
Gene	Protein			
1	2	pho1-94	L-lactate permease	NMB0543
3	4	pho1-61	Membrane fusion protein	NMB1716
5	6	pho1-96	Protein-export membrane protein SECF	NMB0608
7	8	pho2-7	Organic solvent tolerance protein	NMB0280
9	10	pho2-10	Penicillin-binding protein 4	NMB0749
11	12	pho2-6	Thiol:disulphide interchange protein DSBD	NMB1519
13	14	pho2-35	Protein-export membrane protein SECD	NMB0607
15	16	pho2-66	Spermidine/Putrescine-binding protein	NMB0623
17	18	pho2-76	Hypothetical 17.6 kD protein	NMB0350
19	20	pho2-80	Hypothetical 11.9 kD protein	NMB0844
21	22	pho2-81	-	NMB0159
23	24	pho2-86	-	NMB1277
25	26	pho2-90	Sulphate ABC transporter	NMB0880
27	28	pho2-91	-	NMB0580
29	30	pho2-5	FRPC operon protein	NMB1412 NMB0584 NMB0364 NMB1414
31	32	pho2-25	Hypothetical 10.2 kD protein	NMB1546 NMB1631
33	34	pho2-41	-	NMB1830

Protective properties of candidate protein vaccines

Genes identified in the screen were assessed as potential protein vaccine candidates based on the ability of the cloned, expressed, proteins to raise an immune response in rabbits, with the resulting antibodies having the ability to stimulate complement-mediated bacteriolysis of *Neisseria meningitidis*. Protective responses were determined by live bacterial challenge of mice immunised with recombinant proteins.

In summary, the candidate genes were PCR amplified, cloned and the encoded protein expressed and purified. The purified protein was used to generate antibodies for use in Enzyme Linked Immuno-Sorbent Assays (ELISA). The PorA gene was also PCR amplified, cloned, expressed and purified. Monoclonal antibodies against PorA have been shown to passively protect animals in an infant rat model of infection (Saukkonen *et al*, Microb. Pathog., 1987; 3(4): 261-267). Therefore, this protein was used as a positive control in some experiments. PorA has been shown to be unable to protect an animal against challenge from different strains of *N. meningitidis* (Poolman, Infect. Dis., 1995; 4: 13), therefore any candidate that is able to generate a protective immune response against a diverse range of *N. meningitidis* strains, offers advantages over PorA.

PCR amplification of DNA.

Candidate genes were amplified by PCR using genomic DNA from strain MC58 as the DNA template (McGuinness *et al*, Lancet, 1991; 337:514). The primers are listed in Table 2. F denotes the forward primer and R the reverse primer. The primer pair PRAF and PRAR was used to amplify the PorA gene DNA.

Table 2

Candidate	Primer Sequence	SEQ ID NO.
PRAF	5'ATGCGAAAAAAACTTACCGCCCTC	35
PRAR	5'GAATTTGTGGCGCAAACC	36
phoA 1-94R	5'GAGGAAGAAAATCATTGCCGCGAC	37
phoA 1-94F	5'ATGGTGTCCGTATTCGCCGC	38
phoA 1-61F	5'ATGGCTTTTTATGCTTTTAAGGCG	39
phoA 1-61R	5'TTTCGCTTCAGAAGCAGGTTTGGC	40
phoA 2-66R	5'TTTGCCCGCTTTGAGCCCTTG	41
phoA 2-66F	5'ATGCTCAACATCTACAACTGGTCG	42
phoA 2-10R	5'GGAGTCGGCAAAAAGGTGGGC	43
phoA 2-10F	5'ATGCTCTCCTCACAGTCTGCCC	44
phoA 1-97F	5'ATGGAACTCTTTAAAATCAAACGCG	45
phoA 1-97R	5'AACCACGATTTCTTCTTTCTTCTTC	46
phoA 2-5F	5'ATGAGACCATATGCTACTAC	47
phoA 2-5R	5'TTTTTTACTTGGATTGTTTAC	48

Cloning of vaccine candidates.

PCR amplified DNA from candidates was cloned directly into the InVitrogen pCRT7/CT-TOPO vector. This vector provides a T7 promoter, ribosome binding site and C-terminal 6xHis tag fusion to facilitate expression and purification of recombinant proteins using metal affinity chromatography.

For cloning, the ligation reaction was transformed in TOP10F' cells (Invitrogen). DNA preparations from transformant DNA clones were screened to check the orientation of the insert DNA. Clones from candidates that appeared to have the insert DNA in the correct orientation were sequenced to confirm the integrity of the 5' region of the construct.

Expression and purification.

Cloned candidates were tested for expression of the candidate genes following transformation into HMS174(DE3)pLysS competent cells (Invitrogen). Expression of candidate clones was induced with IPTG and expression analysed by SDS PAGE and western blotting using anti-His antibody after four hours induction. Candidate protein was purified via Talon resin (metal affinity column utilising the 6xHis-tag cloned at the

carboxy terminus of the protein (Clontech)) utilizing an imidozole buffer gradient for elution of protein from the resin (10-100mM).

Antibody production.

Prior to antibody production, animal serum was pre-screened for low reactogenicity to whole cell *Neisseria meningitidis* in ELISA assays. Antibodies were raised against each of the cloned and purified candidates in rabbits using 100µg of proteins for initial vaccination with Freund's adjuvant and three subsequent boosts at 28-day intervals with Freund's incomplete adjuvant. Serum was collected after each boost to generate sera samples.

ELISA against whole heat killed N. meningitidis

ELISA assays against heat killed *N. meningitidis* were carried out to confirm that antibodies raised to purified proteins recognise *N. meningitidis* cells. These assays were carried out on strain MC58 as well as:

Neisseria meningitidis (B) Type 1000
Neisseria meningitidis (B) Type SW2 107
Neisseria meningitidis (B) Type NGH38
Neisseria meningitidis (B) Type NGE28
Neisseria meningitidis (B) Type 2996

These are all prevalent disease-causing strains and span the genetic diversity of this species based on dendrograms generated by MLST (multi-locus sequence typing).

Preparation of heat killed N. meningitidis

N. meningitidis was grown on Columbia agar with chocolated horse blood (Oxoid) for 14 hours at 37°C in 5% CO_2. The cells were scraped from agar plate and resuspended the cells in 20ml PBS in a 50ml tube. The cell suspension was heated for 30 minutes at 56°C to kill the bacteria.

A 50 µl sample of the heat killed *N. meningitidis* was spread to Columbia agar with chocolated horse blood (Oxoid) and incubated for 18 hours at 37°C, 5% CO_2. This allows confirmation that all *N. meningitidis* cells have been killed. The heat-killed cells were then washed in PBS. The OD_{620} of the suspension was adjusted to 0.1 OD units versus PBS.

ELISA with heat killed N. meningitidis

ELISA assays were carried out using the heat killed whole cell *N. meningitidis*. ELISA plates were coated overnight with heat-killed cells (50µl of killed bacteria in PBS to each well of 96 well plate and incubated 4°C). Standard ELISA protocols

were followed, with all incubations at 37°C for 1 hour. PBS/3% BSA blocking solution, PBS/Tween 0.1% wash solution, anti-rabbit AP conjugate secondary antibody (Sigma) and Sigma Fast P Nitrophenyl phosphate detection reagent (Sigma) were utilised. The data was read at 405nm using an appropriate micro-titre plate reader. The data was generated using sera available seven days after the first booster vaccination (day 35 after first vaccination).

ELISA data.

The results showed that the anti-sera raised against each candidate protein elicited a strong response against the different strains of *N. meningitidis.*

In vivo screening.

To evaluate the protective efficacy of vaccine candidates, adult mice were immunised with recombinant proteins and the protective response determined by live bacterial challenge.

For each vaccine candidate, 15 six week old balb/C mice were vaccinated (subcutaneously) with 25µg of antigen on two separate occasions at three week intervals. One week after the end of the immunisation schedule, the group was challenged with the homologous bacterial strain MC58. The bacteria were inoculated intraperitoneally in a volume of 500µl in Brain Heart Infusion/ 0.5% iron dextran media at a dose of $1x10^6$cfu. Previous results have shown that iron is required for initiation of bacteraemic disease in these animals. This model has previously been used to demonstrate the protective efficacy of vaccination (Lissolo *et al*, Infect. Immun., 1995; 63: 884-890).

Control groups included animals vaccinated with adjuvant alone (negative control), with adjuvant combined with purified PorA (positive control) or an attenuated homologous strain. Survival was monitored following challenge.

Animals vaccinated with the candidate pho2-5 showed 80% (12/15) survival compared to non-vaccinated controls where 13% (2/15) survived. The pho2-5 candidate showed levels of protection equivalent to porA protein (13/15).

Animals vaccinated with candidates pho2-10, pho1-94 or pho2-66 had 40% (6/15), 47% (7/15) or 27% (4/15) survival respectively, compared to the non-vaccinated controls, where 13% (2/15) survived.

CLAIMS

1. A peptide comprising any of the amino acid sequences identified herein as SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32 and 34 or a homologue thereof having at least 60% sequence similarly or identity at the peptide level or a functional fragment thereof, for therapeutic or diagnostic use.

2. A peptide according to any preceding claim, wherein the homologue has at least 90% sequence similarity or identity at the peptide level.

3. A peptide according to claim 1, comprising any of the amino acid sequences defined herein as SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32 and 34.

4. A polynucleotide encoding a peptide according to any preceding claim, for therapeutic or diagnostic use.

5. A host transformed to express a peptide according to any of claims 1 to 3.

6. A microorganism comprising a mutation that disrupts the expression of any of the nucleotide sequences defined in claim 1.

7. A microorganism according to claim 6, wherein the mutation is insertional inactivation or a gene deletion.

8. A microorganism according to claim 6 or claim 7, wherein the microorganism is *Neisseria meningitidis*.

9. A microorganism according to any of claims 6 to 8, comprising a mutation in a second nucleotide sequence.

10. A microorganism according to any of claims 6 to 9, for therapeutic or diagnostic use.

11. A vaccine comprising a peptide according to any of claims 1 to 3, or the means for its expression.

12. An antibody raised against a peptide according to any of claims 1 to 3.

13. Use of a product according to any of claims 1 to 5, in a screening assay.

14. Use of a product according to any of claims 1 to 10, for the manufacture of a medicament for use in the treatment or prevention of a condition associated with infection by *Neisseria* or Gram-negative bacteria.

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gga cag ccg ctg tat cag atc gac agt tcc act tat gaa gca ggt ctg   336
Gly Gln Pro Leu Tyr Gln Ile Asp Ser Ser Thr Tyr Glu Ala Gly Leu
            100                 105                 110

gaa agc gcg cgc gcg caa ctg gca acg gct cag gca acg ctt gcc aaa   384
Glu Ser Ala Arg Ala Gln Leu Ala Thr Ala Gln Ala Thr Leu Ala Lys
        115                 120                 125

gcg gat gcg gat ttg gcg cga tac aag cct ttg gtt gcc gcc gaa gcc   432
Ala Asp Ala Asp Leu Ala Arg Tyr Lys Pro Leu Val Ala Ala Glu Ala
    130                 135                 140

gtc agc cgg cag gaa tac gat gct gcg gta acg gcg aaa cgt tct gcc   480
Val Ser Arg Gln Glu Tyr Asp Ala Ala Val Thr Ala Lys Arg Ser Ala
145                 150                 155                 160

gag gca ggc gtt aaa gcg gcg cag gcg gca atc aaa tcc gcc ggc atc   528
Glu Ala Gly Val Lys Ala Ala Gln Ala Ala Ile Lys Ser Ala Gly Ile
                165                 170                 175

agc ctg aac cgt tcg cgc att acc gcg ccg att tcc ggc ttt atc ggt   576
Ser Leu Asn Arg Ser Arg Ile Thr Ala Pro Ile Ser Gly Phe Ile Gly
            180                 185                 190

cag tcc aaa gtt tcc gaa ggt acg ttg ctg aac gct ggc gat gcg acc   624
Gln Ser Lys Val Ser Glu Gly Thr Leu Leu Asn Ala Gly Asp Ala Thr
        195                 200                 205

gta ctg gcg acc atc cgc caa acc aat ccg atg tat gtg aac gtt acc   672
```

```
Val Leu Ala Thr Ile Arg Gln Thr Asn Pro Met Tyr Val Asn Val Thr
    210                 215                 220

cag tct gca tcc gaa gtg atg aaa ttg cgc cgt cag ata gcc gaa ggc   720
Gln Ser Ala Ser Glu Val Met Lys Leu Arg Arg Gln Ile Ala Glu Gly
225                 230                 235                 240

aaa ctg ctg gcg gcg gat ggt gtg att gcg gtc ggc atc aaa ttt gac   768
Lys Leu Leu Ala Ala Asp Gly Val Ile Ala Val Gly Ile Lys Phe Asp
                245                 250                 255

gac ggc aca gtt tac cct gaa aaa ggc cgc ctg ctg ttt gcc gat ccg   816
Asp Gly Thr Val Tyr Pro Glu Lys Gly Arg Leu Leu Phe Ala Asp Pro
            260                 265                 270

gcc gtc aac gaa tcg acc ggt cag att acc ctg cgc gcc gcc gta ccg   864
Ala Val Asn Glu Ser Thr Gly Gln Ile Thr Leu Arg Ala Ala Val Pro
        275                 280                 285

aac gat cag aat atc ttg atg ccc ggt ctg tat gtg cgc gtg ctg atg   912
Asn Asp Gln Asn Ile Leu Met Pro Gly Leu Tyr Val Arg Val Leu Met
    290                 295                 300

gac caa gtg gcg gtg gat aac gca ttt gtt gtg ccg cag cag gcg gta   960
Asp Gln Val Ala Val Asp Asn Ala Phe Val Val Pro Gln Gln Ala Val
305                 310                 315                 320

acg cgc ggt gcg aaa gat acc gtg atg att gtg aat gcc caa ggc ggt  1008
Thr Arg Gly Ala Lys Asp Thr Val Met Ile Val Asn Ala Gln Gly Gly
                325                 330                 335

atg gaa ccc cgc gag gta acg gtt gcg caa cag cag ggt acg aat tgg  1056
Met Glu Pro Arg Glu Val Thr Val Ala Gln Gln Gln Gly Thr Asn Trp
            340                 345                 350

att gtt acg tcg ggt ctg aag gac ggg gac aag gtg gtt gtg gaa ggc  1104
Ile Val Thr Ser Gly Leu Lys Asp Gly Asp Lys Val Val Val Glu Gly
        355                 360                 365

atc agt atc gcc ggt ata acg ggt gcg aaa aag gta acg ccc aaa gaa  1152
Ile Ser Ile Ala Gly Ile Thr Gly Ala Lys Lys Val Thr Pro Lys Glu
    370                 375                 380

tgg gcg tcg tct gaa aac caa gcc gcc gcg cct caa tcc ggc gtt cag  1200
Trp Ala Ser Ser Glu Asn Gln Ala Ala Ala Pro Gln Ser Gly Val Gln
385                 390                 395                 400

acg gca tct gaa gcc aaa cct gct tct gaa gcg aaa taa              1239
```

Thr Ala Ser Glu Ala Lys Pro Ala Ser Glu Ala Lys
405 410

<210> 4
<211> 412
<212> PRT
<213> Neisseria meningitidis

<400> 4
Met Ala Phe Tyr Ala Phe Lys Ala Met Arg Ala Ala Ala Leu Ala Ala
1 5 10 15

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

Gln Gly Gly Gln Pro Ala Gly Arg Glu Ala Pro Ala Pro Val Val Gly
35 40 45

Val Val Thr Val His Pro Gln Thr Val Ala Leu Thr Val Glu Leu Pro
50 55 60

Gly Arg Leu Glu Ser Leu Arg Thr Ala Asp Val Arg Ala Gln Val Gly
65 70 75 80

Gly Ile Ile Gln Lys Arg Leu Phe Gln Glu Gly Ser Tyr Val Arg Ala
85 90 95

Gly Gln Pro Leu Tyr Gln Ile Asp Ser Ser Thr Tyr Glu Ala Gly Leu
100 105 110

Glu Ser Ala Arg Ala Gln Leu Ala Thr Ala Gln Ala Thr Leu Ala Lys
115 120 125

Ala Asp Ala Asp Leu Ala Arg Tyr Lys Pro Leu Val Ala Ala Glu Ala
130 135 140

Val Ser Arg Gln Glu Tyr Asp Ala Ala Val Thr Ala Lys Arg Ser Ala
145 150 155 160

Glu Ala Gly Val Lys Ala Ala Gln Ala Ala Ile Lys Ser Ala Gly Ile
165 170 175

Ser Leu Asn Arg Ser Arg Ile Thr Ala Pro Ile Ser Gly Phe Ile Gly
180 185 190

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

```
Val Leu Ala Thr Ile Arg Gln Thr Asn Pro Met Tyr Val Asn Val Thr
    210                 215                 220

Gln Ser Ala Ser Glu Val Met Lys Leu Arg Arg Gln Ile Ala Glu Gly
225                 230                 235                 240

Lys Leu Leu Ala Ala Asp Gly Val Ile Ala Val Gly Ile Lys Phe Asp
                245                 250                 255

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

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

Asn Asp Gln Asn Ile Leu Met Pro Gly Leu Tyr Val Arg Val Leu Met
    290                 295                 300

Asp Gln Val Ala Val Asp Asn Ala Phe Val Val Pro Gln Gln Ala Val
305                 310                 315                 320

Thr Arg Gly Ala Lys Asp Thr Val Met Ile Val Asn Ala Gln Gly Gly
                325                 330                 335

Met Glu Pro Arg Glu Val Thr Val Ala Gln Gln Gln Gly Thr Asn Trp
            340                 345                 350

Ile Val Thr Ser Gly Leu Lys Asp Gly Asp Lys Val Val Val Glu Gly
        355                 360                 365

Ile Ser Ile Ala Gly Ile Thr Gly Ala Lys Lys Val Thr Pro Lys Glu
    370                 375                 380

Trp Ala Ser Ser Glu Asn Gln Ala Ala Ala Pro Gln Ser Gly Val Gln
385                 390                 395                 400

Thr Ala Ser Glu Ala Lys Pro Ala Ser Glu Ala Lys
                405                 410
```

<210> 5
<211> 936
<212> DNA
<213> Neisseria meningitidis

<220>

<221> CDS
<222> (1)..(936)

<400> 5

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atg gaa ctc ttt aaa atc aaa cgc gat att ccg ttt atg agc tac ggc   48
Met Glu Leu Phe Lys Ile Lys Arg Asp Ile Pro Phe Met Ser Tyr Gly
 1               5                  10                  15

aaa ctg acg acc ttc att tcg ttg gtt acg ttt atc gct gcc gtg ttc   96
Lys Leu Thr Thr Phe Ile Ser Leu Val Thr Phe Ile Ala Ala Val Phe
            20                  25                  30

ttt ttg gtt acc aga ggt ctg aat ttc tct gtc gaa ttt acc ggc ggt  144
Phe Leu Val Thr Arg Gly Leu Asn Phe Ser Val Glu Phe Thr Gly Gly
        35                  40                  45

acg gta atg gaa gtc caa tat cag cag ggt gcg gat gtc aat aag atg  192
Thr Val Met Glu Val Gln Tyr Gln Gln Gly Ala Asp Val Asn Lys Met
    50                  55                  60

cgc gaa cgc ctc gat acg ctg aaa ata ggt gat gta cag gtt cag gca  240
Arg Glu Arg Leu Asp Thr Leu Lys Ile Gly Asp Val Gln Val Gln Ala
65                  70                  75                  80

ttg ggt acg aac aaa cac atc atg atc cgc ctg ccg aac aaa gaa ggt  288
Leu Gly Thr Asn Lys His Ile Met Ile Arg Leu Pro Asn Lys Glu Gly
                85                  90                  95

gtt act tcc gca cag ttg tcc aat cag gtt atg gat ttg ctg aaa aaa  336
Val Thr Ser Ala Gln Leu Ser Asn Gln Val Met Asp Leu Leu Lys Lys
            100                 105                 110

gac agt ccc gac gtt acc ttg cgc caa gtc gaa ttt atc ggc ccg caa  384
Asp Ser Pro Asp Val Thr Leu Arg Gln Val Glu Phe Ile Gly Pro Gln
        115                 120                 125

gtc ggt gag gaa ttg gta agt aat gga ttg atg gct tta ggt ttt gtc  432
Val Gly Glu Glu Leu Val Ser Asn Gly Leu Met Ala Leu Gly Phe Val
    130                 135                 140

gtt atc ggc atc att att tac ctg tcg atg cgt ttt gaa tgg cgt ttt  480
Val Ile Gly Ile Ile Ile Tyr Leu Ser Met Arg Phe Glu Trp Arg Phe
145                 150                 155                 160

gcc gta tct gcc att atc gcc aat atg cac gac atc gtg att att ctc  528
Ala Val Ser Ala Ile Ile Ala Asn Met His Asp Ile Val Ile Ile Leu
                165                 170                 175
```

```
ggc tgc ttt gcc ttc ttc caa tgg gaa ttt tcg ctg acc gtc ttg gcg   576
Gly Cys Phe Ala Phe Phe Gln Trp Glu Phe Ser Leu Thr Val Leu Ala
            180                 185                 190

ggt atc ctt gcc gta ttg ggc tat tct gtg aac gaa tcc gtc gtc gtc   624
Gly Ile Leu Ala Val Leu Gly Tyr Ser Val Asn Glu Ser Val Val Val
        195                 200                 205

ttc gac cgt atc cgt gaa aac ttc cgc aag ccg gcg atg cgc gga cat   672
Phe Asp Arg Ile Arg Glu Asn Phe Arg Lys Pro Ala Met Arg Gly His
    210                 215                 220

gcc gtg ccg gaa gtc atc gac aac gcg att acc gca acg atg agc cgc   720
Ala Val Pro Glu Val Ile Asp Asn Ala Ile Thr Ala Thr Met Ser Arg
225                 230                 235                 240

acc atc att acc cac ggt tcg acc gag gcg atg gtc gta tcc atg ctg   768
Thr Ile Ile Thr His Gly Ser Thr Glu Ala Met Val Val Ser Met Leu
                245                 250                 255

gtg ttc ggc ggt gcg gcc ttg cac ggc ttt tct atg gcg ttg acc att   816
Val Phe Gly Gly Ala Ala Leu His Gly Phe Ser Met Ala Leu Thr Ile
            260                 265                 270

ggc atc gtg ttc ggc att tat tct tcc gta ttg gtt gcc agc ccg ctt   864
Gly Ile Val Phe Gly Ile Tyr Ser Ser Val Leu Val Ala Ser Pro Leu
        275                 280                 285

ctg cta atg ttc ggt ttg agc cgc gac aat atc ggt aaa gaa ccg aag   912
Leu Leu Met Phe Gly Leu Ser Arg Asp Asn Ile Gly Lys Glu Pro Lys
    290                 295                 300

aag aaa gaa gaa atc gtg gtt tga                                  936
Lys Lys Glu Glu Ile Val Val
305                 310
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<210> 6
<211> 311
<212> PRT
<213> Neisseria meningitidis

<400> 6

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Met Glu Leu Phe Lys Ile Lys Arg Asp Ile Pro Phe Met Ser Tyr Gly
  1               5                  10                  15

Lys Leu Thr Thr Phe Ile Ser Leu Val Thr Phe Ile Ala Ala Val Phe
            20                  25                  30
```

```
Phe Leu Val Thr Arg Gly Leu Asn Phe Ser Val Glu Phe Thr Gly Gly
         35                  40                  45

Thr Val Met Glu Val Gln Tyr Gln Gln Gly Ala Asp Val Asn Lys Met
     50                  55                  60

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

Leu Gly Thr Asn Lys His Ile Met Ile Arg Leu Pro Asn Lys Glu Gly
                 85                  90                  95

Val Thr Ser Ala Gln Leu Ser Asn Gln Val Met Asp Leu Leu Lys Lys
            100                 105                 110

Asp Ser Pro Asp Val Thr Leu Arg Gln Val Glu Phe Ile Gly Pro Gln
        115                 120                 125

Val Gly Glu Glu Leu Val Ser Asn Gly Leu Met Ala Leu Gly Phe Val
    130                 135                 140

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

Ala Val Ser Ala Ile Ile Ala Asn Met His Asp Ile Val Ile Ile Leu
                165                 170                 175

Gly Cys Phe Ala Phe Phe Gln Trp Glu Phe Ser Leu Thr Val Leu Ala
            180                 185                 190

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

Phe Asp Arg Ile Arg Glu Asn Phe Arg Lys Pro Ala Met Arg Gly His
    210                 215                 220

Ala Val Pro Glu Val Ile Asp Asn Ala Ile Thr Ala Thr Met Ser Arg
225                 230                 235                 240

Thr Ile Ile Thr His Gly Ser Thr Glu Ala Met Val Val Ser Met Leu
                245                 250                 255

Val Phe Gly Gly Ala Ala Leu His Gly Phe Ser Met Ala Leu Thr Ile
            260                 265                 270

Gly Ile Val Phe Gly Ile Tyr Ser Ser Val Leu Val Ala Ser Pro Leu
        275                 280                 285
```

```
Leu Leu Met Phe Gly Leu Ser Arg Asp Asn Ile Gly Lys Glu Pro Lys
    290                 295                 300

Lys Lys Glu Glu Ile Val Val
305                 310
```

<210> 7
<211> 2277
<212> DNA
<213> Neisseria meningitidis

<220>
<221> CDS
<222> (1)..(2277)

<400> 7

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gtg tcc gaa ccc ata cag cct acc agc ctg agc ctc ggt tcg acc tgc   48
Val Ser Glu Pro Ile Gln Pro Thr Ser Leu Ser Leu Gly Ser Thr Cys
  1               5                  10                  15

ctg ttt tgc agt aac gaa agc ggc agc ccc gag aga acc gaa gcc gcc   96
Leu Phe Cys Ser Asn Glu Ser Gly Ser Pro Glu Arg Thr Glu Ala Ala
             20                  25                  30

gtc caa ggc agc ggc gaa gca tcc atc ccc gaa gac tat acg cgc att   144
Val Gln Gly Ser Gly Glu Ala Ser Ile Pro Glu Asp Tyr Thr Arg Ile
         35                  40                  45

gtt gcc gac agg atg gaa gga cag tcg cag gtg cag gtg cgt gcc gaa   192
Val Ala Asp Arg Met Glu Gly Gln Ser Gln Val Gln Val Arg Ala Glu
     50                  55                  60

ggc aac gtc gtc gtc gaa cgc aac cgg acg acc ctc aat acc gat tgg   240
Gly Asn Val Val Val Glu Arg Asn Arg Thr Thr Leu Asn Thr Asp Trp
 65                  70                  75                  80

gcg gat tac gac cag tcg ggc gac acc gtt acc gca ggc gac cgg ttc   288
Ala Asp Tyr Asp Gln Ser Gly Asp Thr Val Thr Ala Gly Asp Arg Phe
                 85                  90                  95

gcc ctc caa cag gac ggt acg ctg att cgg ggc gaa acc ctg acc tac   336
Ala Leu Gln Gln Asp Gly Thr Leu Ile Arg Gly Glu Thr Leu Thr Tyr
            100                 105                 110

aat ctc gag cag cag acc ggg gaa gcg cac aac gtc cgc atg gaa atc   384
```

```
Asn Leu Glu Gln Gln Thr Gly Glu Ala His Asn Val Arg Met Glu Ile
        115                 120                 125

gaa caa ggc gga cgg cgg ctg caa agc gtc agc cgc acc gcc gaa atg   432
Glu Gln Gly Gly Arg Arg Leu Gln Ser Val Ser Arg Thr Ala Glu Met
    130                 135                 140

ttg ggc gaa ggg cat tac aaa ctg acg gaa acc caa ttc aac acc tgt   480
Leu Gly Glu Gly His Tyr Lys Leu Thr Glu Thr Gln Phe Asn Thr Cys
145                 150                 155                 160

tcc gcc ggc gat gcc ggc tgg tat gtc aag gca gcc tct gtc gaa gcc   528
Ser Ala Gly Asp Ala Gly Trp Tyr Val Lys Ala Ala Ser Val Glu Ala
                165                 170                 175

gat cgg gaa aaa ggc ata ggc gtt gcc aaa cac gcc gcc ttc gtg ttc   576
Asp Arg Glu Lys Gly Ile Gly Val Ala Lys His Ala Ala Phe Val Phe
            180                 185                 190

ggc ggc gtt ccc att ttc tac acc cct tgg gcg gac ttc ccg ctt gac   624
Gly Gly Val Pro Ile Phe Tyr Thr Pro Trp Ala Asp Phe Pro Leu Asp
        195                 200                 205

ggc aac cgc aaa agc ggc ctg ctt gtt ccc tca ctg tcc gcc ggt tcg   672
Gly Asn Arg Lys Ser Gly Leu Leu Val Pro Ser Leu Ser Ala Gly Ser
    210                 215                 220

gac ggc gtt tcc ctt tcc gtt ccc tat tat ttc aac ctt gcc ccc aat   720
Asp Gly Val Ser Leu Ser Val Pro Tyr Tyr Phe Asn Leu Ala Pro Asn
225                 230                 235                 240

ctc gat gcc acg ttc gcg ccc agc gtg atc ggc gaa cgc ggc gcg gtc   768
Leu Asp Ala Thr Phe Ala Pro Ser Val Ile Gly Glu Arg Gly Ala Val
                245                 250                 255

ttt gac ggg cag gta cgc tac ctg cgg ccg gat tat gcc ggc cag tcc   816
Phe Asp Gly Gln Val Arg Tyr Leu Arg Pro Asp Tyr Ala Gly Gln Ser
            260                 265                 270

gac ctg acc tgg ctg ccg cac gac aag aaa agc ggc agg aat aac cgc   864
Asp Leu Thr Trp Leu Pro His Asp Lys Lys Ser Gly Arg Asn Asn Arg
        275                 280                 285

tat cag gcg aaa tgg cag cat cgg cac gac att tcc gac acg ctt cag   912
Tyr Gln Ala Lys Trp Gln His Arg His Asp Ile Ser Asp Thr Leu Gln
    290                 295                 300

gcg ggt gtc gat ttc aac caa gtc tcc gac agc ggc tac tac cgc gac   960
```

```
Ala Gly Val Asp Phe Asn Gln Val Ser Asp Ser Gly Tyr Tyr Arg Asp
305                 310                 315                 320

ttt tac ggc aac aaa gaa atc gcc ggc aac gtc aac ctc aac cgc cgt   1008
Phe Tyr Gly Asn Lys Glu Ile Ala Gly Asn Val Asn Leu Asn Arg Arg
                325                 330                 335

gta tgg ctg gat tat ggc ggc agg gcg gcg ggc ggc agc ctg aat gcc   1056
Val Trp Leu Asp Tyr Gly Gly Arg Ala Ala Gly Gly Ser Leu Asn Ala
            340                 345                 350

ggc ctt tcg gtt ctg aaa tac cag acg ctg gca aac caa agc ggc tac   1104
Gly Leu Ser Val Leu Lys Tyr Gln Thr Leu Ala Asn Gln Ser Gly Tyr
        355                 360                 365

aaa gac aaa ccg tat gcc ctc atg ccg cgc ctt tcg gtc gag tgg cgt   1152
Lys Asp Lys Pro Tyr Ala Leu Met Pro Arg Leu Ser Val Glu Trp Arg
    370                 375                 380

aaa aac acc ggc agg gcg caa atc ggc gtg tcc gca caa ttt acc cga   1200
Lys Asn Thr Gly Arg Ala Gln Ile Gly Val Ser Ala Gln Phe Thr Arg
385                 390                 395                 400

ttc agc cac gac agc cgc caa gac ggc agc cgc ctg gtc gtc tat ccc   1248
Phe Ser His Asp Ser Arg Gln Asp Gly Ser Arg Leu Val Val Tyr Pro
                405                 410                 415

gac atc aaa tgg gat ttc agc aac agc tgg ggc tat gtc cgt ccc aaa   1296
Asp Ile Lys Trp Asp Phe Ser Asn Ser Trp Gly Tyr Val Arg Pro Lys
            420                 425                 430

ctc gga ctg cac gcc acc tat tac agc ctc aac cgc ttc ggc agc caa   1344
Leu Gly Leu His Ala Thr Tyr Tyr Ser Leu Asn Arg Phe Gly Ser Gln
        435                 440                 445

gaa gcc cga cgc gtc agc cgc act ctg ccc att gtc aac atc gac agc   1392
Glu Ala Arg Arg Val Ser Arg Thr Leu Pro Ile Val Asn Ile Asp Ser
    450                 455                 460

ggc gca act ttt gag cgg aat acg cgg atg ttc ggc gga gaa gtc ctg   1440
Gly Ala Thr Phe Glu Arg Asn Thr Arg Met Phe Gly Gly Glu Val Leu
465                 470                 475                 480

caa acc ctc gag ccg cgc ctg ttc tac aac tat att cct gcc aaa tcc   1488
Gln Thr Leu Glu Pro Arg Leu Phe Tyr Asn Tyr Ile Pro Ala Lys Ser
                485                 490                 495

caa aac gac ctg ccc aat ttc gat tcg tcg gaa agc agc ttc ggc tac   1536
```

```
Gln Asn Asp Leu Pro Asn Phe Asp Ser Ser Glu Ser Ser Phe Gly Tyr
            500                 505                 510

ggg cag ctc ttt cgc gaa aac ctc tat tac ggc aac gac agg att aac  1584
Gly Gln Leu Phe Arg Glu Asn Leu Tyr Tyr Gly Asn Asp Arg Ile Asn
        515                 520                 525

acc gca aac agc ctt tcc gcc gcc gtg caa agc cgt att ttg gac ggc  1632
Thr Ala Asn Ser Leu Ser Ala Ala Val Gln Ser Arg Ile Leu Asp Gly
    530                 535                 540

gcg acg ggg gaa gag cgt ttc cgc gcc ggc atc ggt cag aaa ttc tat  1680
Ala Thr Gly Glu Glu Arg Phe Arg Ala Gly Ile Gly Gln Lys Phe Tyr
545                 550                 555                 560

ttc aag gat gat gcg gtg atg ctt gac ggc agc gtc ggc aaa aaa ccg  1728
Phe Lys Asp Asp Ala Val Met Leu Asp Gly Ser Val Gly Lys Lys Pro
                565                 570                 575

cgc aac cgt tcc gac tgg gtg gca ttt gcc tcc ggc agc atc ggc agc  1776
Arg Asn Arg Ser Asp Trp Val Ala Phe Ala Ser Gly Ser Ile Gly Ser
            580                 585                 590

cgc ttc atc ctc gac agc agc atc cac tac aac caa aac gac aaa cgc  1824
Arg Phe Ile Leu Asp Ser Ser Ile His Tyr Asn Gln Asn Asp Lys Arg
        595                 600                 605

gcc gag aac tac gcc gtc ggt gca agc tac cgt ccc gca cag ggc aaa  1872
Ala Glu Asn Tyr Ala Val Gly Ala Ser Tyr Arg Pro Ala Gln Gly Lys
    610                 615                 620

gtg ctg aac gcc cgc tac aaa tac ggg cgc aac gaa aaa atc tac ctg  1920
Val Leu Asn Ala Arg Tyr Lys Tyr Gly Arg Asn Glu Lys Ile Tyr Leu
625                 630                 635                 640

aag tcc gac ggt tcc tat ttt tac gac aaa ctc agc cag ctc gac ctg  1968
Lys Ser Asp Gly Ser Tyr Phe Tyr Asp Lys Leu Ser Gln Leu Asp Leu
                645                 650                 655

tcc gca caa tgg ccg ctg acg cgc aac ctg tcg gcc gtc gtc cgt tac  2016
Ser Ala Gln Trp Pro Leu Thr Arg Asn Leu Ser Ala Val Val Arg Tyr
            660                 665                 670

aac tac ggt ttt gaa gcc aaa aaa ccg ata gag gtg ctg gcg ggt gcg  2064
Asn Tyr Gly Phe Glu Ala Lys Lys Pro Ile Glu Val Leu Ala Gly Ala
        675                 680                 685

gaa tac aaa agc agt tgc ggc tgc tgg ggc gcg ggc gtg tac gcc caa  2112
```

Glu Tyr Lys Ser Ser Cys Gly Cys Trp Gly Ala Gly Val Tyr Ala Gln
690 695 700

cgc tac gtt acc ggc gaa aac acc tac aaa aac gct gtc ttt ttc tca 2160
Arg Tyr Val Thr Gly Glu Asn Thr Tyr Lys Asn Ala Val Phe Phe Ser
705 710 715 720

ctt cag ttg aaa gac ctc agc agt gtc ggc aga aac ccc gca gac agg 2208
Leu Gln Leu Lys Asp Leu Ser Ser Val Gly Arg Asn Pro Ala Asp Arg
725 730 735

atg gat gtc gcc gtt ccc ggc tat atc acc gcc cac tct ctt tcc gcc 2256
Met Asp Val Ala Val Pro Gly Tyr Ile Thr Ala His Ser Leu Ser Ala
740 745 750

gga cgc aac aaa cga ccc tga 2277
Gly Arg Asn Lys Arg Pro
755

<210> 8
<211> 758
<212> PRT
<213> Neisseria meningitidis

<400> 8
Val Ser Glu Pro Ile Gln Pro Thr Ser Leu Ser Leu Gly Ser Thr Cys
1 5 10 15

Leu Phe Cys Ser Asn Glu Ser Gly Ser Pro Glu Arg Thr Glu Ala Ala
20 25 30

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

Val Ala Asp Arg Met Glu Gly Gln Ser Gln Val Gln Val Arg Ala Glu
50 55 60

Gly Asn Val Val Val Glu Arg Asn Arg Thr Thr Leu Asn Thr Asp Trp
65 70 75 80

Ala Asp Tyr Asp Gln Ser Gly Asp Thr Val Thr Ala Gly Asp Arg Phe
85 90 95

Ala Leu Gln Gln Asp Gly Thr Leu Ile Arg Gly Glu Thr Leu Thr Tyr
100 105 110

Asn Leu Glu Gln Gln Thr Gly Glu Ala His Asn Val Arg Met Glu Ile

115 120 125

Glu Gln Gly Gly Arg Arg Leu Gln Ser Val Ser Arg Thr Ala Glu Met
130 135 140

Leu Gly Glu Gly His Tyr Lys Leu Thr Glu Thr Gln Phe Asn Thr Cys
145 150 155 160

Ser Ala Gly Asp Ala Gly Trp Tyr Val Lys Ala Ala Ser Val Glu Ala
165 170 175

Asp Arg Glu Lys Gly Ile Gly Val Ala Lys His Ala Ala Phe Val Phe
180 185 190

Gly Gly Val Pro Ile Phe Tyr Thr Pro Trp Ala Asp Phe Pro Leu Asp
195 200 205

Gly Asn Arg Lys Ser Gly Leu Leu Val Pro Ser Leu Ser Ala Gly Ser
210 215 220

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

Leu Asp Ala Thr Phe Ala Pro Ser Val Ile Gly Glu Arg Gly Ala Val
245 250 255

Phe Asp Gly Gln Val Arg Tyr Leu Arg Pro Asp Tyr Ala Gly Gln Ser
260 265 270

Asp Leu Thr Trp Leu Pro His Asp Lys Lys Ser Gly Arg Asn Asn Arg
275 280 285

Tyr Gln Ala Lys Trp Gln His Arg His Asp Ile Ser Asp Thr Leu Gln
290 295 300

Ala Gly Val Asp Phe Asn Gln Val Ser Asp Ser Gly Tyr Tyr Arg Asp
305 310 315 320

Phe Tyr Gly Asn Lys Glu Ile Ala Gly Asn Val Asn Leu Asn Arg Arg
325 330 335

Val Trp Leu Asp Tyr Gly Gly Arg Ala Ala Gly Gly Ser Leu Asn Ala
340 345 350

Gly Leu Ser Val Leu Lys Tyr Gln Thr Leu Ala Asn Gln Ser Gly Tyr
355 360 365

Lys Asp Lys Pro Tyr Ala Leu Met Pro Arg Leu Ser Val Glu Trp Arg

370 375 380

Lys Asn Thr Gly Arg Ala Gln Ile Gly Val Ser Ala Gln Phe Thr Arg
385 390 395 400

Phe Ser His Asp Ser Arg Gln Asp Gly Ser Arg Leu Val Val Tyr Pro
405 410 415

Asp Ile Lys Trp Asp Phe Ser Asn Ser Trp Gly Tyr Val Arg Pro Lys
420 425 430

Leu Gly Leu His Ala Thr Tyr Tyr Ser Leu Asn Arg Phe Gly Ser Gln
435 440 445

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

Gly Ala Thr Phe Glu Arg Asn Thr Arg Met Phe Gly Gly Glu Val Leu
465 470 475 480

Gln Thr Leu Glu Pro Arg Leu Phe Tyr Asn Tyr Ile Pro Ala Lys Ser
485 490 495

Gln Asn Asp Leu Pro Asn Phe Asp Ser Ser Glu Ser Ser Phe Gly Tyr
500 505 510

Gly Gln Leu Phe Arg Glu Asn Leu Tyr Tyr Gly Asn Asp Arg Ile Asn
515 520 525

Thr Ala Asn Ser Leu Ser Ala Ala Val Gln Ser Arg Ile Leu Asp Gly
530 535 540

Ala Thr Gly Glu Glu Arg Phe Arg Ala Gly Ile Gly Gln Lys Phe Tyr
545 550 555 560

Phe Lys Asp Asp Ala Val Met Leu Asp Gly Ser Val Gly Lys Lys Pro
565 570 575

Arg Asn Arg Ser Asp Trp Val Ala Phe Ala Ser Gly Ser Ile Gly Ser
580 585 590

Arg Phe Ile Leu Asp Ser Ser Ile His Tyr Asn Gln Asn Asp Lys Arg
595 600 605

Ala Glu Asn Tyr Ala Val Gly Ala Ser Tyr Arg Pro Ala Gln Gly Lys
610 615 620

Val Leu Asn Ala Arg Tyr Lys Tyr Gly Arg Asn Glu Lys Ile Tyr Leu

625 630 635 640

Lys Ser Asp Gly Ser Tyr Phe Tyr Asp Lys Leu Ser Gln Leu Asp Leu
645 650 655

Ser Ala Gln Trp Pro Leu Thr Arg Asn Leu Ser Ala Val Val Arg Tyr
660 665 670

Asn Tyr Gly Phe Glu Ala Lys Lys Pro Ile Glu Val Leu Ala Gly Ala
675 680 685

Glu Tyr Lys Ser Ser Cys Gly Cys Trp Gly Ala Gly Val Tyr Ala Gln
690 695 700

Arg Tyr Val Thr Gly Glu Asn Thr Tyr Lys Asn Ala Val Phe Phe Ser
705 710 715 720

Leu Gln Leu Lys Asp Leu Ser Ser Val Gly Arg Asn Pro Ala Asp Arg
725 730 735

Met Asp Val Ala Val Pro Gly Tyr Ile Thr Ala His Ser Leu Ser Ala
740 745 750

Gly Arg Asn Lys Arg Pro
755

<210> 9
<211> 939
<212> DNA
<213> Neisseria meningitidis

<220>
<221> CDS
<222> (1)..(939)

<400> 9
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Met Ser Ile His Thr Leu Lys Arg Leu Pro Ser Ser Leu Leu Leu Gly
1 5 10 15

ctc tgc ctt tcc ctg ccg tca gcc cac ctt ttt gcc gac aac gac att 96
Leu Cys Leu Ser Leu Pro Ser Ala His Leu Phe Ala Asp Asn Asp Ile
20 25 30

tta ggg caa ttt tta gaa cag aac atg ctt acc tcc tcc gat ccg ata 144
Leu Gly Gln Phe Leu Glu Gln Asn Met Leu Thr Ser Ser Asp Pro Ile

35 40 45

gaa ata ttc gcc gaa agc acg ata cac ccc acc aac acc caa gcc att 192
Glu Ile Phe Ala Glu Ser Thr Ile His Pro Thr Asn Thr Gln Ala Ile
50 55 60

aca ggc ggt ctg att ctc tcc tca cag tct gcc ctg gtc gtc aac aac 240
Thr Gly Gly Leu Ile Leu Ser Ser Gln Ser Ala Leu Val Val Asn Asn
65 70 75 80

aaa acc gga cag ata ctg tat cag aaa aac gcc gac agg att atg ccc 288
Lys Thr Gly Gln Ile Leu Tyr Gln Lys Asn Ala Asp Arg Ile Met Pro
85 90 95

atc gcc tcc att tcc aaa ctg atg agc gcg atg gtc gtt ttg gat gca 336
Ile Ala Ser Ile Ser Lys Leu Met Ser Ala Met Val Val Leu Asp Ala
100 105 110

aac ttg gac atg aac gaa acc gtt acc att acg ccc gac gaa atc gac 384
Asn Leu Asp Met Asn Glu Thr Val Thr Ile Thr Pro Asp Glu Ile Asp
115 120 125

cgc atc aaa ggg acc ggc agc cgt ctt gcc ata ggt acg gca ctt aca 432
Arg Ile Lys Gly Thr Gly Ser Arg Leu Ala Ile Gly Thr Ala Leu Thr
130 135 140

cgc aaa aaa ctg ctg cac ctg agc ctg atg agc agc gaa aac cgc gcc 480
Arg Lys Lys Leu Leu His Leu Ser Leu Met Ser Ser Glu Asn Arg Ala
145 150 155 160

acc cat gca ttg ggc aga acc tac ccc ggc ggc atg ggc gca ttt gtc 528
Thr His Ala Leu Gly Arg Thr Tyr Pro Gly Gly Met Gly Ala Phe Val
165 170 175

gcc gcc atg aac cgc aaa gcc caa agc ctc ggt atg tac ggc agc cgc 576
Ala Ala Met Asn Arg Lys Ala Gln Ser Leu Gly Met Tyr Gly Ser Arg
180 185 190

ttt tac gaa ccg acc gga ctc aac ttc caa aac gtt tct acc gcc aaa 624
Phe Tyr Glu Pro Thr Gly Leu Asn Phe Gln Asn Val Ser Thr Ala Lys
195 200 205

gac ctg agc ctt atg gtc aac gcc gcc gcc caa tat ccg caa atc cgc 672
Asp Leu Ser Leu Met Val Asn Ala Ala Ala Gln Tyr Pro Gln Ile Arg
210 215 220

acc aac tcg act tcc aac tac gcc tcg gta cag acc aaa aac ggg cag 720
Thr Asn Ser Thr Ser Asn Tyr Ala Ser Val Gln Thr Lys Asn Gly Gln

225 230 235 240

cag aac tac aaa aac tcc aat gcc ctg gtc aga gaa ggc atg tgg aac 768
Gln Asn Tyr Lys Asn Ser Asn Ala Leu Val Arg Glu Gly Met Trp Asn
245 250 255

atc gaa ttg cag aaa acc ggc tac ata cgc gaa gca ggc agg tct atg 816
Ile Glu Leu Gln Lys Thr Gly Tyr Ile Arg Glu Ala Gly Arg Ser Met
260 265 270

gtt gtc aaa gcc aac att caa aac caa ccc gtt acc atc gta ttg ctg 864
Val Val Lys Ala Asn Ile Gln Asn Gln Pro Val Thr Ile Val Leu Leu
275 280 285

aac tcg ccc aca tcc gcc aca cgc gtc aac gac gcc cgc aaa atc gaa 912
Asn Ser Pro Thr Ser Ala Thr Arg Val Asn Asp Ala Arg Lys Ile Glu
290 295 300

tcg tgg atg ctg cag caa cgc tcc tga 939
Ser Trp Met Leu Gln Gln Arg Ser
305 310

<210> 10
<211> 312
<212> PRT
<213> Neisseria meningitidis

<400> 10
Met Ser Ile His Thr Leu Lys Arg Leu Pro Ser Ser Leu Leu Leu Gly
1 5 10 15

Leu Cys Leu Ser Leu Pro Ser Ala His Leu Phe Ala Asp Asn Asp Ile
20 25 30

Leu Gly Gln Phe Leu Glu Gln Asn Met Leu Thr Ser Ser Asp Pro Ile
35 40 45

Glu Ile Phe Ala Glu Ser Thr Ile His Pro Thr Asn Thr Gln Ala Ile
50 55 60

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

Lys Thr Gly Gln Ile Leu Tyr Gln Lys Asn Ala Asp Arg Ile Met Pro
85 90 95

Ile Ala Ser Ile Ser Lys Leu Met Ser Ala Met Val Val Leu Asp Ala

100 105 110

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

Arg Ile Lys Gly Thr Gly Ser Arg Leu Ala Ile Gly Thr Ala Leu Thr
130 135 140

Arg Lys Lys Leu Leu His Leu Ser Leu Met Ser Ser Glu Asn Arg Ala
145 150 155 160

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

Ala Ala Met Asn Arg Lys Ala Gln Ser Leu Gly Met Tyr Gly Ser Arg
180 185 190

Phe Tyr Glu Pro Thr Gly Leu Asn Phe Gln Asn Val Ser Thr Ala Lys
195 200 205

Asp Leu Ser Leu Met Val Asn Ala Ala Ala Gln Tyr Pro Gln Ile Arg
210 215 220

Thr Asn Ser Thr Ser Asn Tyr Ala Ser Val Gln Thr Lys Asn Gly Gln
225 230 235 240

Gln Asn Tyr Lys Asn Ser Asn Ala Leu Val Arg Glu Gly Met Trp Asn
245 250 255

Ile Glu Leu Gln Lys Thr Gly Tyr Ile Arg Glu Ala Gly Arg Ser Met
260 265 270

Val Val Lys Ala Asn Ile Gln Asn Gln Pro Val Thr Ile Val Leu Leu
275 280 285

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

Ser Trp Met Leu Gln Gln Arg Ser
305 310

<210> 11
<211> 1806
<212> DNA
<213> Neisseria meningitidis

<220>
<221> CDS
<222> (1)..(1806)

<400> 11

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Met Lys Lys Leu Ile Cys Leu Phe Ala Val Phe Leu Met Leu Cys Gly
 1               5                  10                  15

cga gct ttc gcg ctg gat gcg aac gat ctg ctg ccg ccg gaa aag gca   96
Arg Ala Phe Ala Leu Asp Ala Asn Asp Leu Leu Pro Pro Glu Lys Ala
            20                  25                  30

ttc gtg ccg gag ctt gcc gtt gcc gac gac ggt gtg aac gtc cgt ttc  144
Phe Val Pro Glu Leu Ala Val Ala Asp Asp Gly Val Asn Val Arg Phe
        35                  40                  45

agg att gcc gac gga tac tat atg tat cag gcg aaa atc gtc ggc aag  192
Arg Ile Ala Asp Gly Tyr Tyr Met Tyr Gln Ala Lys Ile Val Gly Lys
    50                  55                  60

acc gat ccg gcg gat ttg ttg gga cag cct tct ttc agc aag ggc gaa  240
Thr Asp Pro Ala Asp Leu Leu Gly Gln Pro Ser Phe Ser Lys Gly Glu
65                  70                  75                  80

gag aag gaa gac gag ttt ttc ggc agg cag acg gtt tac cat cac gag  288
Glu Lys Glu Asp Glu Phe Phe Gly Arg Gln Thr Val Tyr His His Glu
                85                  90                  95

gcg cag gtt gcc ttt cct tat gca aag gct gtc ggc gaa ccg tat aaa  336
Ala Gln Val Ala Phe Pro Tyr Ala Lys Ala Val Gly Glu Pro Tyr Lys
            100                 105                 110

ttg gtt ttg acc tat cag ggc tgt gcc gaa gcc ggc gtg tgc tat ccg  384
Leu Val Leu Thr Tyr Gln Gly Cys Ala Glu Ala Gly Val Cys Tyr Pro
        115                 120                 125

ccc gtg gat acc gag ttt gat att ttc ggc aac ggc act tac cat ccg  432
Pro Val Asp Thr Glu Phe Asp Ile Phe Gly Asn Gly Thr Tyr His Pro
    130                 135                 140

caa acc gac gaa ccg gca tcc gcc aaa gac cgc ttt ttg cag cct tcc  480
Gln Thr Asp Glu Pro Ala Ser Ala Lys Asp Arg Phe Leu Gln Pro Ser
145                 150                 155                 160

tct caa aac ggc agc ggg gcg ctg ccg ccc ccg aag ggg gat gag ggc  528
Ser Gln Asn Gly Ser Gly Ala Leu Pro Pro Pro Lys Gly Asp Glu Gly
                165                 170                 175
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ggc gac agc cgt ttc aag ctg tct tgg gat acg ctc aac gcc aat ctt   576
Gly Asp Ser Arg Phe Lys Leu Ser Trp Asp Thr Leu Asn Ala Asn Leu
            180                 185                 190

ttg gcg ttt ttt ctc gct ggt ttg ggc ctg agt ttt acc gcc tgt atg   624
Leu Ala Phe Phe Leu Ala Gly Leu Gly Leu Ser Phe Thr Ala Cys Met
        195                 200                 205

tat ccc ctg ttg ccg att gtt tcc agt att gtg gtc ggc gac aaa aag   672
Tyr Pro Leu Leu Pro Ile Val Ser Ser Ile Val Val Gly Asp Lys Lys
    210                 215                 220

gcg ggc aag gcg cgg gcg ttt gtg ctg tcc gtc gtt tat gtt cag ggt   720
Ala Gly Lys Ala Arg Ala Phe Val Leu Ser Val Val Tyr Val Gln Gly
225                 230                 235                 240

ttg gct ctg act tat acg ctg gtc ggc att gtt gcc gga ctg acg ggc   768
Leu Ala Leu Thr Tyr Thr Leu Val Gly Ile Val Ala Gly Leu Thr Gly
                245                 250                 255

gca ctg ctg acc gta tgg ttg cag cag gct tgg gtg gta ttg gcg gca   816
Ala Leu Leu Thr Val Trp Leu Gln Gln Ala Trp Val Val Leu Ala Ala
            260                 265                 270

tcg gct tta atg gtc gtc ttg gca ctg tct atg ttc ggg ctg ttc aac   864
Ser Ala Leu Met Val Val Leu Ala Leu Ser Met Phe Gly Leu Phe Asn
        275                 280                 285

atc cag ctt ccc aac gcc gtg cag tcg tat ttt cag aat caa agc agc   912
Ile Gln Leu Pro Asn Ala Val Gln Ser Tyr Phe Gln Asn Gln Ser Ser
    290                 295                 300

agg ctt tca ggc ggt aaa atc gtt tcc gtc ttt att atg ggc ata ttg   960
Arg Leu Ser Gly Gly Lys Ile Val Ser Val Phe Ile Met Gly Ile Leu
305                 310                 315                 320

tcc gcg ctg att gtc ggg ccg tgc gtc gcc ccg ccg ctg gca ttt gct  1008
Ser Ala Leu Ile Val Gly Pro Cys Val Ala Pro Pro Leu Ala Phe Ala
                325                 330                 335

ttg ggc tac atc ggt cag acg ggc gat gcg gtt tta ggc ggt ttg gca  1056
Leu Gly Tyr Ile Gly Gln Thr Gly Asp Ala Val Leu Gly Gly Leu Ala
            340                 345                 350

ctt tac act ttg gcg ttg ggc acc ggc gtt ccg ctg att gcc atc ggc  1104
Leu Tyr Thr Leu Ala Leu Gly Thr Gly Val Pro Leu Ile Ala Ile Gly
        355                 360                 365
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acg ttc ggc ggg cat atc ctg cct aag gca ggc gat tgg atg aat gcc   1152
Thr Phe Gly Gly His Ile Leu Pro Lys Ala Gly Asp Trp Met Asn Ala
    370                 375                 380

gtc aaa tac gca ttc ggc ttc atc ctg cta gcc gtc gcc gtt tac ctc   1200
Val Lys Tyr Ala Phe Gly Phe Ile Leu Leu Ala Val Ala Val Tyr Leu
385                 390                 395                 400

gcc acg ccg cac ttg ccc tat tat ctc gtc gtc gcg ctg tac acg ctg   1248
Ala Thr Pro His Leu Pro Tyr Tyr Leu Val Val Ala Leu Tyr Thr Leu
                405                 410                 415

ctg atg ctg gtt cct gcc ttt atg ctg ctg gtc aac gga cgc agg cag   1296
Leu Met Leu Val Pro Ala Phe Met Leu Leu Val Asn Gly Arg Arg Gln
            420                 425                 430

aaa cgc cgt ccg aaa gct gtg gca ttc gca ttg ggc ggt ata ttg ctg   1344
Lys Arg Arg Pro Lys Ala Val Ala Phe Ala Leu Gly Gly Ile Leu Leu
        435                 440                 445

ata ggc ggc gcg tgg ttc ggc tgg cag ggc gca aac ggc aaa acg acc   1392
Ile Gly Gly Ala Trp Phe Gly Trp Gln Gly Ala Asn Gly Lys Thr Thr
    450                 455                 460

gcg ctg cac cat ttc ctg acc ctc aat cca cca gcc gaa gca ggc aaa   1440
Ala Leu His His Phe Leu Thr Leu Asn Pro Pro Ala Glu Ala Gly Lys
465                 470                 475                 480

tct tcg gaa cac ggc aaa atg ttt gcc gat act gcc gcg ctg aag gca   1488
Ser Ser Glu His Gly Lys Met Phe Ala Asp Thr Ala Ala Leu Lys Ala
                485                 490                 495

gcg atg gat acg gcg ttg aaa gaa cat ccc gac aaa ccc gtc gtt ttg   1536
Ala Met Asp Thr Ala Leu Lys Glu His Pro Asp Lys Pro Val Val Leu
            500                 505                 510

gat ttt tat gcc gac tgg tgc att tcc tgc aaa gaa atg gcg gct tac   1584
Asp Phe Tyr Ala Asp Trp Cys Ile Ser Cys Lys Glu Met Ala Ala Tyr
        515                 520                 525

acg ctc aat cag ccg gaa gtg cat cag gca gtc gat atg gaa cgc ttt   1632
Thr Leu Asn Gln Pro Glu Val His Gln Ala Val Asp Met Glu Arg Phe
    530                 535                 540

ttc caa atc gac gta acc gcc aac acg ccc gaa cat cag gcg ttg ttg   1680
Phe Gln Ile Asp Val Thr Ala Asn Thr Pro Glu His Gln Ala Leu Leu
545                 550                 555                 560
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aaa gaa tac ggt ctg ttc ggg ccg ccg ggc gtg ttt gtc gtc cgc tcc 1728
Lys Glu Tyr Gly Leu Phe Gly Pro Pro Gly Val Phe Val Val Arg Ser
565 570 575

gac ggc agc cgc agc gag ccg ctg ctg ggt ttt gtc aaa gca gac aag 1776
Asp Gly Ser Arg Ser Glu Pro Leu Leu Gly Phe Val Lys Ala Asp Lys
580 585 590

ttt atc gag tgg tat gaa caa aac cgc tga 1806
Phe Ile Glu Trp Tyr Glu Gln Asn Arg
595 600

<210> 12
<211> 601
<212> PRT
<213> Neisseria meningitidis

<400> 12
Met Lys Lys Leu Ile Cys Leu Phe Ala Val Phe Leu Met Leu Cys Gly
1 5 10 15

Arg Ala Phe Ala Leu Asp Ala Asn Asp Leu Leu Pro Pro Glu Lys Ala
20 25 30

Phe Val Pro Glu Leu Ala Val Ala Asp Asp Gly Val Asn Val Arg Phe
35 40 45

Arg Ile Ala Asp Gly Tyr Tyr Met Tyr Gln Ala Lys Ile Val Gly Lys
50 55 60

Thr Asp Pro Ala Asp Leu Leu Gly Gln Pro Ser Phe Ser Lys Gly Glu
65 70 75 80

Glu Lys Glu Asp Glu Phe Phe Gly Arg Gln Thr Val Tyr His His Glu
85 90 95

Ala Gln Val Ala Phe Pro Tyr Ala Lys Ala Val Gly Glu Pro Tyr Lys
100 105 110

Leu Val Leu Thr Tyr Gln Gly Cys Ala Glu Ala Gly Val Cys Tyr Pro
115 120 125

Pro Val Asp Thr Glu Phe Asp Ile Phe Gly Asn Gly Thr Tyr His Pro
130 135 140

Gln Thr Asp Glu Pro Ala Ser Ala Lys Asp Arg Phe Leu Gln Pro Ser

145 150 155 160

Ser Gln Asn Gly Ser Gly Ala Leu Pro Pro Pro Lys Gly Asp Glu Gly
165 170 175

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

Leu Ala Phe Phe Leu Ala Gly Leu Gly Leu Ser Phe Thr Ala Cys Met
195 200 205

Tyr Pro Leu Leu Pro Ile Val Ser Ser Ile Val Val Gly Asp Lys Lys
210 215 220

Ala Gly Lys Ala Arg Ala Phe Val Leu Ser Val Val Tyr Val Gln Gly
225 230 235 240

Leu Ala Leu Thr Tyr Thr Leu Val Gly Ile Val Ala Gly Leu Thr Gly
245 250 255

Ala Leu Leu Thr Val Trp Leu Gln Gln Ala Trp Val Val Leu Ala Ala
260 265 270

Ser Ala Leu Met Val Val Leu Ala Leu Ser Met Phe Gly Leu Phe Asn
275 280 285

Ile Gln Leu Pro Asn Ala Val Gln Ser Tyr Phe Gln Asn Gln Ser Ser
290 295 300

Arg Leu Ser Gly Gly Lys Ile Val Ser Val Phe Ile Met Gly Ile Leu
305 310 315 320

Ser Ala Leu Ile Val Gly Pro Cys Val Ala Pro Pro Leu Ala Phe Ala
325 330 335

Leu Gly Tyr Ile Gly Gln Thr Gly Asp Ala Val Leu Gly Gly Leu Ala
340 345 350

Leu Tyr Thr Leu Ala Leu Gly Thr Gly Val Pro Leu Ile Ala Ile Gly
355 360 365

Thr Phe Gly Gly His Ile Leu Pro Lys Ala Gly Asp Trp Met Asn Ala
370 375 380

Val Lys Tyr Ala Phe Gly Phe Ile Leu Leu Ala Val Ala Val Tyr Leu
385 390 395 400

Ala Thr Pro His Leu Pro Tyr Tyr Leu Val Val Ala Leu Tyr Thr Leu

405 410 415

Leu Met Leu Val Pro Ala Phe Met Leu Leu Val Asn Gly Arg Arg Gln
420 425 430

Lys Arg Arg Pro Lys Ala Val Ala Phe Ala Leu Gly Gly Ile Leu Leu
435 440 445

Ile Gly Gly Ala Trp Phe Gly Trp Gln Gly Ala Asn Gly Lys Thr Thr
450 455 460

Ala Leu His His Phe Leu Thr Leu Asn Pro Pro Ala Glu Ala Gly Lys
465 470 475 480

Ser Ser Glu His Gly Lys Met Phe Ala Asp Thr Ala Ala Leu Lys Ala
485 490 495

Ala Met Asp Thr Ala Leu Lys Glu His Pro Asp Lys Pro Val Val Leu
500 505 510

Asp Phe Tyr Ala Asp Trp Cys Ile Ser Cys Lys Glu Met Ala Ala Tyr
515 520 525

Thr Leu Asn Gln Pro Glu Val His Gln Ala Val Asp Met Glu Arg Phe
530 535 540

Phe Gln Ile Asp Val Thr Ala Asn Thr Pro Glu His Gln Ala Leu Leu
545 550 555 560

Lys Glu Tyr Gly Leu Phe Gly Pro Pro Gly Val Phe Val Val Arg Ser
565 570 575

Asp Gly Ser Arg Ser Glu Pro Leu Leu Gly Phe Val Lys Ala Asp Lys
580 585 590

Phe Ile Glu Trp Tyr Glu Gln Asn Arg
595 600

<210> 13
<211> 1857
<212> DNA
<213> Neisseria meningitidis

<220>
<221> CDS
<222> (1)..(1857)

<400> 13

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Met Met Asn Arg Tyr Pro Leu Trp Lys Tyr Leu Leu Ile Val Phe Thr
1 5 10 15

att gcg gtt gcc gca gtg tat tcg ctg ccc aac cta ttc ggc gaa aca 96
Ile Ala Val Ala Ala Val Tyr Ser Leu Pro Asn Leu Phe Gly Glu Thr
20 25 30

ccc gcc gtg cag gta tcg acc aac cga caa gcc atc atc atc aac gaa 144
Pro Ala Val Gln Val Ser Thr Asn Arg Gln Ala Ile Ile Ile Asn Glu
35 40 45

cag act caa ttc aaa gtg gat gcc gcg ctg aaa aac gca ggt att cag 192
Gln Thr Gln Phe Lys Val Asp Ala Ala Leu Lys Asn Ala Gly Ile Gln
50 55 60

acc gac ggg atg ttt gtt gtg gac aat tca ctg aaa gtg cgt ttc aaa 240
Thr Asp Gly Met Phe Val Val Asp Asn Ser Leu Lys Val Arg Phe Lys
65 70 75 80

gac aca gaa acg cag ctt aaa gcg cgc gac gtc atc gaa aac act ttg 288
Asp Thr Glu Thr Gln Leu Lys Ala Arg Asp Val Ile Glu Asn Thr Leu
85 90 95

ggc gaa ggg tat att acc gcg ctc aac ctg ttg gcg gac agc ccc gaa 336
Gly Glu Gly Tyr Ile Thr Ala Leu Asn Leu Leu Ala Asp Ser Pro Glu
100 105 110

tgg atg gcg aaa atc aaa gcc aat ccg atg ttt ttg ggt ttg gac ctg 384
Trp Met Ala Lys Ile Lys Ala Asn Pro Met Phe Leu Gly Leu Asp Leu
115 120 125

cgc ggc ggc gtg cat ttc acc atg cag gtc gat atg aaa gcg gcg atg 432
Arg Gly Gly Val His Phe Thr Met Gln Val Asp Met Lys Ala Ala Met
130 135 140

cag aaa acg ttt gaa cgt tat tcg ggc gac atc cgc cgc gaa ctg cgc 480
Gln Lys Thr Phe Glu Arg Tyr Ser Gly Asp Ile Arg Arg Glu Leu Arg
145 150 155 160

cgc gaa aaa atc cgc agc ggc acg gtg cgt cag gct gga aac agc ctg 528
Arg Glu Lys Ile Arg Ser Gly Thr Val Arg Gln Ala Gly Asn Ser Leu
165 170 175

acc gtc cct ttg cag gat gca ggt gat gtg caa aag gct ctg ccg cag 576
Thr Val Pro Leu Gln Asp Ala Gly Asp Val Gln Lys Ala Leu Pro Gln

180 185 190

ttg cgc aag ctg ttt cct gaa gca acg ctg aat tca gac ggc agc aat 624
Leu Arg Lys Leu Phe Pro Glu Ala Thr Leu Asn Ser Asp Gly Ser Asn
195 200 205

atc gtc ttg acg ctt tcg gaa gag gcg gtc aat aaa gtg tgt tcc gat 672
Ile Val Leu Thr Leu Ser Glu Glu Ala Val Asn Lys Val Cys Ser Asp
210 215 220

gcg gtc aaa cag aac atc act acc ctg cac aac cgt gtg aac gag ttg 720
Ala Val Lys Gln Asn Ile Thr Thr Leu His Asn Arg Val Asn Glu Leu
225 230 235 240

ggc gtg gcc gag ccc gtc atc cag cag tcc ggt gca gac cgt atc gtc 768
Gly Val Ala Glu Pro Val Ile Gln Gln Ser Gly Ala Asp Arg Ile Val
245 250 255

gtg cag ctt ccg ggc gtt cag gat act gcc aag gca aaa gac atc atc 816
Val Gln Leu Pro Gly Val Gln Asp Thr Ala Lys Ala Lys Asp Ile Ile
260 265 270

ggc cgt acc gcg act ttg gaa ttg cgt atg gtg gag gac gat cct gcc 864
Gly Arg Thr Ala Thr Leu Glu Leu Arg Met Val Glu Asp Asp Pro Ala
275 280 285

aag ttg cgc gag gca ttg gaa ggc aac gtg ccg agc ggt tat gag ctg 912
Lys Leu Arg Glu Ala Leu Glu Gly Asn Val Pro Ser Gly Tyr Glu Leu
290 295 300

ctt tca agc ggc gga gat cgt ccc gaa att ctg ctg atc agc aaa cag 960
Leu Ser Ser Gly Gly Asp Arg Pro Glu Ile Leu Leu Ile Ser Lys Gln
305 310 315 320

gtc gag ctg acg ggc gac aac atc aac gat gcg caa ccg agt ttc gac 1008
Val Glu Leu Thr Gly Asp Asn Ile Asn Asp Ala Gln Pro Ser Phe Asp
325 330 335

caa atg ggc gca cct gcc gtc agt ctg agc ttg gac agc gcg ggc ggc 1056
Gln Met Gly Ala Pro Ala Val Ser Leu Ser Leu Asp Ser Ala Gly Gly
340 345 350

agc att ttc ggc gaa ctg act gcc gca aat gtc ggc aaa cgc atg gcg 1104
Ser Ile Phe Gly Glu Leu Thr Ala Ala Asn Val Gly Lys Arg Met Ala
355 360 365

atg gtt ttg atc gac caa gga aaa tcc gag gtt gta acc gcg ccg gtt 1152
Met Val Leu Ile Asp Gln Gly Lys Ser Glu Val Val Thr Ala Pro Val

370 375 380

atc cgt act gcc att acc ggc gga cgc gtg gaa att tcc gga agc atg 1200
Ile Arg Thr Ala Ile Thr Gly Gly Arg Val Glu Ile Ser Gly Ser Met
385 390 395 400

acg aca gcc gaa gcc aat gat acg tct ttg ctg ttg cgt gcc ggt tct 1248
Thr Thr Ala Glu Ala Asn Asp Thr Ser Leu Leu Leu Arg Ala Gly Ser
405 410 415

ctt gcc gca ccg atg cag att gtc gaa gaa cgt acc atc ggt ccg tct 1296
Leu Ala Ala Pro Met Gln Ile Val Glu Glu Arg Thr Ile Gly Pro Ser
420 425 430

ttg ggt aag gag aac atc gaa aaa ggc ttc cat tcg act tta tgg ggt 1344
Leu Gly Lys Glu Asn Ile Glu Lys Gly Phe His Ser Thr Leu Trp Gly
435 440 445

ttt gcc atc gtt gct gca ttc atg gtg gtt tac tat cgt ctg atg ggt 1392
Phe Ala Ile Val Ala Ala Phe Met Val Val Tyr Tyr Arg Leu Met Gly
450 455 460

ttc ttt tct acc att gca ttg agt gcc aac ata ctg ttc cta atc ggt 1440
Phe Phe Ser Thr Ile Ala Leu Ser Ala Asn Ile Leu Phe Leu Ile Gly
465 470 475 480

att ttg tct gcc atg cag gca acg ttg acg tta ccg ggt atg gcc gcg 1488
Ile Leu Ser Ala Met Gln Ala Thr Leu Thr Leu Pro Gly Met Ala Ala
485 490 495

ctg gcg ttg act ttg ggt atg gca atc gac tcc aac gtc ttg att aac 1536
Leu Ala Leu Thr Leu Gly Met Ala Ile Asp Ser Asn Val Leu Ile Asn
500 505 510

gaa cgt atc cgc gaa gaa ttg cgt gcc ggc gtg ccg ccg cag cag gca 1584
Glu Arg Ile Arg Glu Glu Leu Arg Ala Gly Val Pro Pro Gln Gln Ala
515 520 525

atc aat ctc ggt ttc caa cac gca tgg gcg acc att gtc gat tcg aac 1632
Ile Asn Leu Gly Phe Gln His Ala Trp Ala Thr Ile Val Asp Ser Asn
530 535 540

ctg act tcg ctg att gcc ggt atc gcg ctt ttg gta ttc ggt tcc ggc 1680
Leu Thr Ser Leu Ile Ala Gly Ile Ala Leu Leu Val Phe Gly Ser Gly
545 550 555 560

ccg gta cgc ggt ttt gcg gtc gta cac tgt ttg ggt att ctg act tcg 1728
Pro Val Arg Gly Phe Ala Val Val His Cys Leu Gly Ile Leu Thr Ser

565 570 575

atg tat tca tcc gtc gtc gta ttc cgt gcg ttg gtc aat ctg tgg tac 1776
Met Tyr Ser Ser Val Val Val Phe Arg Ala Leu Val Asn Leu Trp Tyr
580 585 590

gga cgc aga cgc aaa ttg cag aat att tcc att ggt tcg gtg tgg aag 1824
Gly Arg Arg Arg Lys Leu Gln Asn Ile Ser Ile Gly Ser Val Trp Lys
595 600 605

ccg aaa gcc gaa atg gca gga ggc aag gag taa 1857
Pro Lys Ala Glu Met Ala Gly Gly Lys Glu
610 615

<210> 14
<211> 618
<212> PRT
<213> Neisseria meningitidis

<400> 14
Met Met Asn Arg Tyr Pro Leu Trp Lys Tyr Leu Leu Ile Val Phe Thr
1 5 10 15

Ile Ala Val Ala Ala Val Tyr Ser Leu Pro Asn Leu Phe Gly Glu Thr
20 25 30

Pro Ala Val Gln Val Ser Thr Asn Arg Gln Ala Ile Ile Ile Asn Glu
35 40 45

Gln Thr Gln Phe Lys Val Asp Ala Ala Leu Lys Asn Ala Gly Ile Gln
50 55 60

Thr Asp Gly Met Phe Val Val Asp Asn Ser Leu Lys Val Arg Phe Lys
65 70 75 80

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

Gly Glu Gly Tyr Ile Thr Ala Leu Asn Leu Leu Ala Asp Ser Pro Glu
100 105 110

Trp Met Ala Lys Ile Lys Ala Asn Pro Met Phe Leu Gly Leu Asp Leu
115 120 125

Arg Gly Gly Val His Phe Thr Met Gln Val Asp Met Lys Ala Ala Met
130 135 140

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

Arg Glu Lys Ile Arg Ser Gly Thr Val Arg Gln Ala Gly Asn Ser Leu
                165                 170                 175

Thr Val Pro Leu Gln Asp Ala Gly Asp Val Gln Lys Ala Leu Pro Gln
            180                 185                 190

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

Ile Val Leu Thr Leu Ser Glu Glu Ala Val Asn Lys Val Cys Ser Asp
    210                 215                 220

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

Gly Val Ala Glu Pro Val Ile Gln Gln Ser Gly Ala Asp Arg Ile Val
                245                 250                 255

Val Gln Leu Pro Gly Val Gln Asp Thr Ala Lys Ala Lys Asp Ile Ile
            260                 265                 270

Gly Arg Thr Ala Thr Leu Glu Leu Arg Met Val Glu Asp Asp Pro Ala
        275                 280                 285

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

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

Val Glu Leu Thr Gly Asp Asn Ile Asn Asp Ala Gln Pro Ser Phe Asp
                325                 330                 335

Gln Met Gly Ala Pro Ala Val Ser Leu Ser Leu Asp Ser Ala Gly Gly
            340                 345                 350

Ser Ile Phe Gly Glu Leu Thr Ala Ala Asn Val Gly Lys Arg Met Ala
        355                 360                 365

Met Val Leu Ile Asp Gln Gly Lys Ser Glu Val Val Thr Ala Pro Val
    370                 375                 380

Ile Arg Thr Ala Ile Thr Gly Gly Arg Val Glu Ile Ser Gly Ser Met
385                 390                 395                 400
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Thr Thr Ala Glu Ala Asn Asp Thr Ser Leu Leu Leu Arg Ala Gly Ser
405 410 415

Leu Ala Ala Pro Met Gln Ile Val Glu Glu Arg Thr Ile Gly Pro Ser
420 425 430

Leu Gly Lys Glu Asn Ile Glu Lys Gly Phe His Ser Thr Leu Trp Gly
435 440 445

Phe Ala Ile Val Ala Ala Phe Met Val Val Tyr Tyr Arg Leu Met Gly
450 455 460

Phe Phe Ser Thr Ile Ala Leu Ser Ala Asn Ile Leu Phe Leu Ile Gly
465 470 475 480

Ile Leu Ser Ala Met Gln Ala Thr Leu Thr Leu Pro Gly Met Ala Ala
485 490 495

Leu Ala Leu Thr Leu Gly Met Ala Ile Asp Ser Asn Val Leu Ile Asn
500 505 510

Glu Arg Ile Arg Glu Glu Leu Arg Ala Gly Val Pro Pro Gln Gln Ala
515 520 525

Ile Asn Leu Gly Phe Gln His Ala Trp Ala Thr Ile Val Asp Ser Asn
530 535 540

Leu Thr Ser Leu Ile Ala Gly Ile Ala Leu Leu Val Phe Gly Ser Gly
545 550 555 560

Pro Val Arg Gly Phe Ala Val Val His Cys Leu Gly Ile Leu Thr Ser
565 570 575

Met Tyr Ser Ser Val Val Val Phe Arg Ala Leu Val Asn Leu Trp Tyr
580 585 590

Gly Arg Arg Arg Lys Leu Gln Asn Ile Ser Ile Gly Ser Val Trp Lys
595 600 605

Pro Lys Ala Glu Met Ala Gly Gly Lys Glu
610 615

<210> 15
<211> 1140
<212> DNA
<213> Neisseria meningitidis

<220>
<221> CDS
<222> (1)..(1140)

<400> 15

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atg aaa aaa aca ctg gtg gcg gcg gca atc ctg agc ctc gcc ttg act   48
Met Lys Lys Thr Leu Val Ala Ala Ala Ile Leu Ser Leu Ala Leu Thr
 1               5                  10                  15

gcg tgc ggc ggc gga agc gat acc gcc gcc caa acc ccc tcc gcc aag   96
Ala Cys Gly Gly Gly Ser Asp Thr Ala Ala Gln Thr Pro Ser Ala Lys
            20                  25                  30

ccc gaa gcc gaa caa tcg ggc aaa ctc aac atc tac aac tgg tcg gat   144
Pro Glu Ala Glu Gln Ser Gly Lys Leu Asn Ile Tyr Asn Trp Ser Asp
        35                  40                  45

tat gtc gat ccc gaa acc gtt gcc gcc ttt gaa aaa gaa acc ggc atc   192
Tyr Val Asp Pro Glu Thr Val Ala Ala Phe Glu Lys Glu Thr Gly Ile
    50                  55                  60

aag acg cgt tcc gat tat tac gac agc aac gaa aca ctg gag gca aaa   240
Lys Thr Arg Ser Asp Tyr Tyr Asp Ser Asn Glu Thr Leu Glu Ala Lys
65                  70                  75                  80

gtc ctg acc ggc aaa tcc ggc tac gac ctg acc gcg ccg tcc atc gcc   288
Val Leu Thr Gly Lys Ser Gly Tyr Asp Leu Thr Ala Pro Ser Ile Ala
                85                  90                  95

aac gtc ggc cgg caa atc aaa gcg ggc gcg tat cag aaa atc gac aag   336
Asn Val Gly Arg Gln Ile Lys Ala Gly Ala Tyr Gln Lys Ile Asp Lys
            100                 105                 110

gcg caa atc ccc cat tac ggc aac atc gat aaa gat ttg ctg aaa atg   384
Ala Gln Ile Pro His Tyr Gly Asn Ile Asp Lys Asp Leu Leu Lys Met
        115                 120                 125

atg gaa gcc gtc gat ccg ggc aac gaa tac gcc gtc ccc tat ttc tgg   432
Met Glu Ala Val Asp Pro Gly Asn Glu Tyr Ala Val Pro Tyr Phe Trp
    130                 135                 140

ggc atc aat acc ttg gca atc aat acc cag cag gtg aaa aaa gca ttg   480
Gly Ile Asn Thr Leu Ala Ile Asn Thr Gln Gln Val Lys Lys Ala Leu
145                 150                 155                 160

ggt acg gac aag ctg ccc gaa aac gaa tgg gat ttg gtg ttc aaa ccc   528
Gly Thr Asp Lys Leu Pro Glu Asn Glu Trp Asp Leu Val Phe Lys Pro
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165 170 175

gaa tac acc gcc aaa ctc aaa tcc tgc ggc atc agc tat ttc gac agc 576
Glu Tyr Thr Ala Lys Leu Lys Ser Cys Gly Ile Ser Tyr Phe Asp Ser
180 185 190

gca atc gaa cag att ccc ttg gcg ttg cac tat ttg ggc aaa gac ccc 624
Ala Ile Glu Gln Ile Pro Leu Ala Leu His Tyr Leu Gly Lys Asp Pro
195 200 205

aac agt gag aat ccc gaa gac atc aaa gcc gcc gtc gat atg atg aaa 672
Asn Ser Glu Asn Pro Glu Asp Ile Lys Ala Ala Val Asp Met Met Lys
210 215 220

gcc gtc cgg ggc gac gtg aaa cgc ttc agc tct tcc ggc tat atc gac 720
Ala Val Arg Gly Asp Val Lys Arg Phe Ser Ser Ser Gly Tyr Ile Asp
225 230 235 240

gat atg gcg gcg ggc aac ctg tgt gcc gcc atc ggt tac ggc ggc gat 768
Asp Met Ala Ala Gly Asn Leu Cys Ala Ala Ile Gly Tyr Gly Gly Asp
245 250 255

ttg aac att gcc aaa acc cgt gcc gaa gaa gcc gca aac ggc gtg gaa 816
Leu Asn Ile Ala Lys Thr Arg Ala Glu Glu Ala Ala Asn Gly Val Glu
260 265 270

atc aaa gta ttg acc ccg aaa acc ggc gtg ggc gtg tgg gtg gat tcc 864
Ile Lys Val Leu Thr Pro Lys Thr Gly Val Gly Val Trp Val Asp Ser
275 280 285

ttt atg att ccg cgc gac gcg caa aac gtt gcc aat gcc cac cgc tat 912
Phe Met Ile Pro Arg Asp Ala Gln Asn Val Ala Asn Ala His Arg Tyr
290 295 300

atc gac tac acg ctc cgg ccc gag gtg gcg gcg aaa aac ggc agc ttc 960
Ile Asp Tyr Thr Leu Arg Pro Glu Val Ala Ala Lys Asn Gly Ser Phe
305 310 315 320

gtt acc tac gcg ccc gcc agc cgt ccc gcg cgc gag ctg atg gat gaa 1008
Val Thr Tyr Ala Pro Ala Ser Arg Pro Ala Arg Glu Leu Met Asp Glu
325 330 335

aaa tac acc tcc gac gca tcg att ttc ccg aac aaa gaa ctg atg gaa 1056
Lys Tyr Thr Ser Asp Ala Ser Ile Phe Pro Asn Lys Glu Leu Met Glu
340 345 350

aaa agt ttc atc gta tcg ccc aaa tcc gca gaa tcc gtc aaa ctg ggc 1104
Lys Ser Phe Ile Val Ser Pro Lys Ser Ala Glu Ser Val Lys Leu Gly

355 360 365

gtg aag ctg tgg caa ggg ctc aaa gcg ggc aaa taa 1140
Val Lys Leu Trp Gln Gly Leu Lys Ala Gly Lys
370 375 380

<210> 16
<211> 379
<212> PRT
<213> Neisseria meningitidis

<400> 16
Met Lys Lys Thr Leu Val Ala Ala Ala Ile Leu Ser Leu Ala Leu Thr
1 5 10 15

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

Pro Glu Ala Glu Gln Ser Gly Lys Leu Asn Ile Tyr Asn Trp Ser Asp
35 40 45

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

Lys Thr Arg Ser Asp Tyr Tyr Asp Ser Asn Glu Thr Leu Glu Ala Lys
65 70 75 80

Val Leu Thr Gly Lys Ser Gly Tyr Asp Leu Thr Ala Pro Ser Ile Ala
85 90 95

Asn Val Gly Arg Gln Ile Lys Ala Gly Ala Tyr Gln Lys Ile Asp Lys
100 105 110

Ala Gln Ile Pro His Tyr Gly Asn Ile Asp Lys Asp Leu Leu Lys Met
115 120 125

Met Glu Ala Val Asp Pro Gly Asn Glu Tyr Ala Val Pro Tyr Phe Trp
130 135 140

Gly Ile Asn Thr Leu Ala Ile Asn Thr Gln Gln Val Lys Lys Ala Leu
145 150 155 160

Gly Thr Asp Lys Leu Pro Glu Asn Glu Trp Asp Leu Val Phe Lys Pro
165 170 175

Glu Tyr Thr Ala Lys Leu Lys Ser Cys Gly Ile Ser Tyr Phe Asp Ser
180 185 190

Ala Ile Glu Gln Ile Pro Leu Ala Leu His Tyr Leu Gly Lys Asp Pro
195 200 205

Asn Ser Glu Asn Pro Glu Asp Ile Lys Ala Ala Val Asp Met Met Lys
210 215 220

Ala Val Arg Gly Asp Val Lys Arg Phe Ser Ser Ser Gly Tyr Ile Asp
225 230 235 240

Asp Met Ala Ala Gly Asn Leu Cys Ala Ala Ile Gly Tyr Gly Gly Asp
245 250 255

Leu Asn Ile Ala Lys Thr Arg Ala Glu Glu Ala Ala Asn Gly Val Glu
260 265 270

Ile Lys Val Leu Thr Pro Lys Thr Gly Val Gly Val Trp Val Asp Ser
275 280 285

Phe Met Ile Pro Arg Asp Ala Gln Asn Val Ala Asn Ala His Arg Tyr
290 295 300

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

Val Thr Tyr Ala Pro Ala Ser Arg Pro Ala Arg Glu Leu Met Asp Glu
325 330 335

Lys Tyr Thr Ser Asp Ala Ser Ile Phe Pro Asn Lys Glu Leu Met Glu
340 345 350

Lys Ser Phe Ile Val Ser Pro Lys Ser Ala Glu Ser Val Lys Leu Gly
355 360 365

Val Lys Leu Trp Gln Gly Leu Lys Ala Gly Lys
370 375

<210> 17
<211> 453
<212> DNA
<213> Neisseria meningitidis

<220>
<221> CDS
<222> (1)..(453)

<400> 17
atg gca aaa gca atc gaa atc att tca ccc aat gaa att tat tca gat 48
Met Ala Lys Ala Ile Glu Ile Ile Ser Pro Asn Glu Ile Tyr Ser Asp
1 5 10 15

ctg att ttt aag gat ccg gta cct ccc cat act att gaa tat aaa atg 96
Leu Ile Phe Lys Asp Pro Val Pro Pro His Thr Ile Glu Tyr Lys Met
20 25 30

att aac cta gaa ttg aaa gcc atc aat ctt tac gat tgt gcc ttt gaa 144
Ile Asn Leu Glu Leu Lys Ala Ile Asn Leu Tyr Asp Cys Ala Phe Glu
35 40 45

gat ttc gtt ccc gaa atc aaa gac aat ttt tgt gtg gga att gat tta 192
Asp Phe Val Pro Glu Ile Lys Asp Asn Phe Cys Val Gly Ile Asp Leu
50 55 60

gac ata gga act gat gat agt gat gct gca gat ata ttt tct gtt cgc 240
Asp Ile Gly Thr Asp Asp Ser Asp Ala Ala Asp Ile Phe Ser Val Arg
65 70 75 80

ata tgc tct cct aaa tgg att ttg cat aat tgt ttc caa aat caa agg 288
Ile Cys Ser Pro Lys Trp Ile Leu His Asn Cys Phe Gln Asn Gln Arg
85 90 95

gtt aaa tgg ggg gcg ggt atg atg att atg aat gaa ttt aat cat tct 336
Val Lys Trp Gly Ala Gly Met Met Ile Met Asn Glu Phe Asn His Ser
100 105 110

gtt att aaa tcg gaa att gag aaa att ctt aaa gaa tgt tca aaa gaa 384
Val Ile Lys Ser Glu Ile Glu Lys Ile Leu Lys Glu Cys Ser Lys Glu
115 120 125

act tgg gaa aag tca ttg act tat tta ctt cgt ttt ttt tcg tgg gaa 432
Thr Trp Glu Lys Ser Leu Thr Tyr Leu Leu Arg Phe Phe Ser Trp Glu
130 135 140

ttt gaa gat tat cag tgc taa 453
Phe Glu Asp Tyr Gln Cys
145 150

<210> 18
<211> 150
<212> PRT
<213> Neisseria meningitidis

<400> 18

Met Ala Lys Ala Ile Glu Ile Ile Ser Pro Asn Glu Ile Tyr Ser Asp
1 5 10 15

Leu Ile Phe Lys Asp Pro Val Pro Pro His Thr Ile Glu Tyr Lys Met
20 25 30

Ile Asn Leu Glu Leu Lys Ala Ile Asn Leu Tyr Asp Cys Ala Phe Glu
35 40 45

Asp Phe Val Pro Glu Ile Lys Asp Asn Phe Cys Val Gly Ile Asp Leu
50 55 60

Asp Ile Gly Thr Asp Asp Ser Asp Ala Ala Asp Ile Phe Ser Val Arg
65 70 75 80

Ile Cys Ser Pro Lys Trp Ile Leu His Asn Cys Phe Gln Asn Gln Arg
85 90 95

Val Lys Trp Gly Ala Gly Met Met Ile Met Asn Glu Phe Asn His Ser
100 105 110

Val Ile Lys Ser Glu Ile Glu Lys Ile Leu Lys Glu Cys Ser Lys Glu
115 120 125

Thr Trp Glu Lys Ser Leu Thr Tyr Leu Leu Arg Phe Phe Ser Trp Glu
130 135 140

Phe Glu Asp Tyr Gln Cys
145 150

<210> 19
<211> 324
<212> DNA
<213> Neisseria meningitidis

<220>
<221> CDS
<222> (1)..(324)

<400> 19
atg aaa aaa tgt att ttg ggc att ttg acc gcg tgt gcc gcc atg cct 48
Met Lys Lys Cys Ile Leu Gly Ile Leu Thr Ala Cys Ala Ala Met Pro
1 5 10 15

gca ttt gcc gac aga atc ggc gat ttg gaa gca cgt ctg gcg cag ttg 96
Ala Phe Ala Asp Arg Ile Gly Asp Leu Glu Ala Arg Leu Ala Gln Leu

20 25 30

gaa cac cgt gtc gcc gta ttg gaa agc ggc ggc aat acc gtc aaa atc 144
Glu His Arg Val Ala Val Leu Glu Ser Gly Gly Asn Thr Val Lys Ile
35 40 45

gac ctt ttc ggt tca aat tcc acc atg tat gta tgc agc gtt acg cct 192
Asp Leu Phe Gly Ser Asn Ser Thr Met Tyr Val Cys Ser Val Thr Pro
50 55 60

ttt cag aag acg ttt gag gca agc gat cgg aat gaa ggc gtg gcg cgg 240
Phe Gln Lys Thr Phe Glu Ala Ser Asp Arg Asn Glu Gly Val Ala Arg
65 70 75 80

cag aaa gtg cgt cag gcg tgc aac cgc gaa act tcg gca atg ttt tgc 288
Gln Lys Val Arg Gln Ala Cys Asn Arg Glu Thr Ser Ala Met Phe Cys
85 90 95

gaa gat gag gca atc cga tgc aga aaa ttc gat tga 324
Glu Asp Glu Ala Ile Arg Cys Arg Lys Phe Asp
100 105

<210> 20
<211> 107
<212> PRT
<213> Neisseria meningitidis

<400> 20
Met Lys Lys Cys Ile Leu Gly Ile Leu Thr Ala Cys Ala Ala Met Pro
1 5 10 15

Ala Phe Ala Asp Arg Ile Gly Asp Leu Glu Ala Arg Leu Ala Gln Leu
20 25 30

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

Asp Leu Phe Gly Ser Asn Ser Thr Met Tyr Val Cys Ser Val Thr Pro
50 55 60

Phe Gln Lys Thr Phe Glu Ala Ser Asp Arg Asn Glu Gly Val Ala Arg
65 70 75 80

Gln Lys Val Arg Gln Ala Cys Asn Arg Glu Thr Ser Ala Met Phe Cys
85 90 95

Glu Asp Glu Ala Ile Arg Cys Arg Lys Phe Asp

100 105

<210> 21
<211> 519
<212> DNA
<213> Neisseria meningitidis

<220>
<221> CDS
<222> (1)..(519)

<400> 21
atg gca aaa cat gaa att gaa gaa cgc ggt gac ggt ctg att gaa aag 48
Met Ala Lys His Glu Ile Glu Glu Arg Gly Asp Gly Leu Ile Glu Lys
1 5 10 15

atg gtc gct gtt aat cgc gta act aaa gta gtt aaa ggt ggc cgt atc 96
Met Val Ala Val Asn Arg Val Thr Lys Val Val Lys Gly Gly Arg Ile
20 25 30

atg gct ttc tca gca ctg act gtt gtt ggt gat ggt gat ggt cgc att 144
Met Ala Phe Ser Ala Leu Thr Val Val Gly Asp Gly Asp Gly Arg Ile
35 40 45

ggt atg ggc aaa ggt aaa tca aaa gaa gta cca gtt gct gtt caa aaa 192
Gly Met Gly Lys Gly Lys Ser Lys Glu Val Pro Val Ala Val Gln Lys
50 55 60

gca atg gat caa gct cga cgc tct atg att aaa gta cct ttg aaa aac 240
Ala Met Asp Gln Ala Arg Arg Ser Met Ile Lys Val Pro Leu Lys Asn
65 70 75 80

ggt act att cat cat gag gtt att ggc cgt cat ggt gct act aaa gta 288
Gly Thr Ile His His Glu Val Ile Gly Arg His Gly Ala Thr Lys Val
85 90 95

ttt atg cag cct gct aaa gag ggt agt ggc gta aaa gcc ggt gga cct 336
Phe Met Gln Pro Ala Lys Glu Gly Ser Gly Val Lys Ala Gly Gly Pro
100 105 110

atg cgt ttg gtt ttt gat gct atg ggc att cat aat atc tcc gcc aaa 384
Met Arg Leu Val Phe Asp Ala Met Gly Ile His Asn Ile Ser Ala Lys
115 120 125

gtg cac gga tct act aac cca tat aat atc gta cgt gca aca tta gat 432
Val His Gly Ser Thr Asn Pro Tyr Asn Ile Val Arg Ala Thr Leu Asp

130 135 140

ggt ttg tct aag ttg cat act cct gct gat atc gca gcc aaa cgt ggc 480
Gly Leu Ser Lys Leu His Thr Pro Ala Asp Ile Ala Ala Lys Arg Gly
145 150 155 160

ttg aca gtg gaa gac att ttg gga gtt aac cat ggc tga 519
Leu Thr Val Glu Asp Ile Leu Gly Val Asn His Gly
165 170

<210> 22
<211> 172
<212> PRT
<213> Neisseria meningitidis

<400> 22
Met Ala Lys His Glu Ile Glu Glu Arg Gly Asp Gly Leu Ile Glu Lys
1 5 10 15

Met Val Ala Val Asn Arg Val Thr Lys Val Val Lys Gly Gly Arg Ile
20 25 30

Met Ala Phe Ser Ala Leu Thr Val Val Gly Asp Gly Asp Gly Arg Ile
35 40 45

Gly Met Gly Lys Gly Lys Ser Lys Glu Val Pro Val Ala Val Gln Lys
50 55 60

Ala Met Asp Gln Ala Arg Arg Ser Met Ile Lys Val Pro Leu Lys Asn
65 70 75 80

Gly Thr Ile His His Glu Val Ile Gly Arg His Gly Ala Thr Lys Val
85 90 95

Phe Met Gln Pro Ala Lys Glu Gly Ser Gly Val Lys Ala Gly Gly Pro
100 105 110

Met Arg Leu Val Phe Asp Ala Met Gly Ile His Asn Ile Ser Ala Lys
115 120 125

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

Gly Leu Ser Lys Leu His Thr Pro Ala Asp Ile Ala Ala Lys Arg Gly
145 150 155 160

Leu Thr Val Glu Asp Ile Leu Gly Val Asn His Gly

165 170

<210> 23
<211> 2028
<212> DNA
<213> Neisseria meningitidis

<220>
<221> CDS
<222> (1)..(2028)

<400> 23
ttg tcc ctg tct gaa ttt ata gaa cgc cga acg tca ttt aat ccg atg 48
Leu Ser Leu Ser Glu Phe Ile Glu Arg Arg Thr Ser Phe Asn Pro Met
1 5 10 15

gtt att ttg acg act ttg ttt ttt gtg tgt gtt ttg gtg gta ttg gtt 96
Val Ile Leu Thr Thr Leu Phe Phe Val Cys Val Leu Val Val Leu Val
20 25 30

tta acc gtg ccg gat cag gtg cag atg tgg ctc gat cgg gca aaa gaa 144
Leu Thr Val Pro Asp Gln Val Gln Met Trp Leu Asp Arg Ala Lys Glu
35 40 45

gtc att ttt acc gag ttc agc tgg ttt tat gtt tta acg ttt tcc att 192
Val Ile Phe Thr Glu Phe Ser Trp Phe Tyr Val Leu Thr Phe Ser Ile
50 55 60

ttt ctg ggt ttc ctg ctg ata ctc tcg gtc agc agt ttg gga aac atc 240
Phe Leu Gly Phe Leu Leu Ile Leu Ser Val Ser Ser Leu Gly Asn Ile
65 70 75 80

agg ctc gga cgg gat gaa gat gtg ccg gaa ttc ggc ttc ctg tcg tgg 288
Arg Leu Gly Arg Asp Glu Asp Val Pro Glu Phe Gly Phe Leu Ser Trp
85 90 95

ctg gcg atg ctg ttt gcg gcc ggg atg ggc gtg ggt ctg atg ttt ttc 336
Leu Ala Met Leu Phe Ala Ala Gly Met Gly Val Gly Leu Met Phe Phe
100 105 110

ggc gtg gca gag ccg ttg atg cat tat ttt tcg gac att acg gcc ggc 384
Gly Val Ala Glu Pro Leu Met His Tyr Phe Ser Asp Ile Thr Ala Gly
115 120 125

acg ccg gaa cac agg cag cag cag gca ttg ctg cac acg gtg ttc cat 432
Thr Pro Glu His Arg Gln Gln Gln Ala Leu Leu His Thr Val Phe His

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      130                 135                 140

tgg ggc gtt cac gct tgg tcg gtg tac ggt acg att gca ttg gct ttg   480
Trp Gly Val His Ala Trp Ser Val Tyr Gly Thr Ile Ala Leu Ala Leu
145                 150                 155                 160

gct tat ttc ggt ttc cgc tac aag ctg ccg ctt gcc ctg cgt tct tgt   528
Ala Tyr Phe Gly Phe Arg Tyr Lys Leu Pro Leu Ala Leu Arg Ser Cys
                165                 170                 175

ttt tac ccc ctg ttg aaa gaa aaa att tcc gga agg ttc ggc gat gcc   576
Phe Tyr Pro Leu Leu Lys Glu Lys Ile Ser Gly Arg Phe Gly Asp Ala
            180                 185                 190

att gat att atg gcg ttg ctt gct act ttt ttc ggc atc atc acc aca   624
Ile Asp Ile Met Ala Leu Leu Ala Thr Phe Phe Gly Ile Ile Thr Thr
        195                 200                 205

ttg ggg ttc ggg gct tcg caa ctg ggc gcc gga ttg cag gaa atg ggc   672
Leu Gly Phe Gly Ala Ser Gln Leu Gly Ala Gly Leu Gln Glu Met Gly
    210                 215                 220

tgg att gcc gaa aac agc ttc agc gtg cag gtt ttg att atc gcc gcc   720
Trp Ile Ala Glu Asn Ser Phe Ser Val Gln Val Leu Ile Ile Ala Ala
225                 230                 235                 240

gtc atg tcc ctc gcc gtc gtt tcg gca ata tcc ggc gtg ggg aag ggc   768
Val Met Ser Leu Ala Val Val Ser Ala Ile Ser Gly Val Gly Lys Gly
                245                 250                 255

gtg aag gtg ttg agc gag ttg aac ctg ggc ctt gcg ttt ttg ctg ctg   816
Val Lys Val Leu Ser Glu Leu Asn Leu Gly Leu Ala Phe Leu Leu Leu
            260                 265                 270

ttt ttt gtt ttg gcg gcg gga ccc act gtt tac ctg ttg tcg gca ttc   864
Phe Phe Val Leu Ala Ala Gly Pro Thr Val Tyr Leu Leu Ser Ala Phe
        275                 280                 285

ggc gac aac ata ggg aac tac ctc gga aat ctg gtg cgc ctc agt ttt   912
Gly Asp Asn Ile Gly Asn Tyr Leu Gly Asn Leu Val Arg Leu Ser Phe
    290                 295                 300

aaa act tat gcg tac gaa cgg gaa cac aag ccg tgg ttt gaa tct tgg   960
Lys Thr Tyr Ala Tyr Glu Arg Glu His Lys Pro Trp Phe Glu Ser Trp
305                 310                 315                 320

acg gtg ctt tat tgg gcg tgg tgg tgt tct tgg gcg ccg ttt gtg ggt  1008
Thr Val Leu Tyr Trp Ala Trp Trp Cys Ser Trp Ala Pro Phe Val Gly
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                    325                 330                 335

ttg ttt atc gcg cgc att tca aag ggg cgc acc atc cgc gag ttt gtc   1056
Leu Phe Ile Ala Arg Ile Ser Lys Gly Arg Thr Ile Arg Glu Phe Val
            340                 345                 350

ttc ggg gtt ttg ctc atc ccc ggc ctg ttc ggc gtt ttg tgg ttt acc   1104
Phe Gly Val Leu Leu Ile Pro Gly Leu Phe Gly Val Leu Trp Phe Thr
        355                 360                 365

gtc ttc ggc aat acg gcg att tgg ctg aat gac ggg gtt gcg ggg gga   1152
Val Phe Gly Asn Thr Ala Ile Trp Leu Asn Asp Gly Val Ala Gly Gly
    370                 375                 380

atg ctc gaa aag atg acc tcc tct ccg gaa acg ctg ctt ttt aaa ttc   1200
Met Leu Glu Lys Met Thr Ser Ser Pro Glu Thr Leu Leu Phe Lys Phe
385                 390                 395                 400

ttt aat tac ctc ccc ctg ccc gaa ttg acg agc atc gtc agc ctg ctg   1248
Phe Asn Tyr Leu Pro Leu Pro Glu Leu Thr Ser Ile Val Ser Leu Leu
                405                 410                 415

gtc att tct ctg ttt ttt gta act tct gcc gat tcc ggg att tat gtc   1296
Val Ile Ser Leu Phe Phe Val Thr Ser Ala Asp Ser Gly Ile Tyr Val
            420                 425                 430

ctg aac aat att acc tct cgg gac aaa ggc ttg agc gcg cca cgg tgg   1344
Leu Asn Asn Ile Thr Ser Arg Asp Lys Gly Leu Ser Ala Pro Arg Trp
        435                 440                 445

cag gcg gtt atg tgg ggc gtg ctg atg tct gcc gtt gcc gtt ttg ctg   1392
Gln Ala Val Met Trp Gly Val Leu Met Ser Ala Val Ala Val Leu Leu
    450                 455                 460

atg cgc tcg ggc gga ctc ggc aac ctg cag tct atg acc ctg att gtt   1440
Met Arg Ser Gly Gly Leu Gly Asn Leu Gln Ser Met Thr Leu Ile Val
465                 470                 475                 480

tcc ctg ccg ttt gcc ctg ctg atg ctg ata atg tgt ttc agc ctg tgg   1488
Ser Leu Pro Phe Ala Leu Leu Met Leu Ile Met Cys Phe Ser Leu Trp
                485                 490                 495

aaa ggc ttg agt gcg gat aag aaa tat ttt gag acc cgg gtt aac cct   1536
Lys Gly Leu Ser Ala Asp Lys Lys Tyr Phe Glu Thr Arg Val Asn Pro
            500                 505                 510

acc agt gta ttt tgg acg ggc ggc aag tgg aaa gaa cgg ctg gtg cag   1584
Thr Ser Val Phe Trp Thr Gly Gly Lys Trp Lys Glu Arg Leu Val Gln
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        515                 520                 525

ata atg agc cag acg cag gag cag gat att tta aaa ttc ctc aaa cag   1632
Ile Met Ser Gln Thr Gln Glu Gln Asp Ile Leu Lys Phe Leu Lys Gln
    530                 535                 540

act gca tcg ccc gct atg cac gag ttg caa cgg gag ctt tcg gaa gaa   1680
Thr Ala Ser Pro Ala Met His Glu Leu Gln Arg Glu Leu Ser Glu Glu
545                 550                 555                 560

tac ggc ttg agc gtc cgg gtc gat aaa atg ttt cat cgg gac gag ccc   1728
Tyr Gly Leu Ser Val Arg Val Asp Lys Met Phe His Arg Asp Glu Pro
                565                 570                 575

gca atc gag ttc gtc att cgg aaa gag acg atg cgc gat ttt atg tac   1776
Ala Ile Glu Phe Val Ile Arg Lys Glu Thr Met Arg Asp Phe Met Tyr
            580                 585                 590

ggg att aag tct gtc ggg cag gat gta tcc gac cag ttg att aac gac   1824
Gly Ile Lys Ser Val Gly Gln Asp Val Ser Asp Gln Leu Ile Asn Asp
        595                 600                 605

ggc aag ctg ccg cat atc cgg cat cag aca act tac aaa ccc tac gct   1872
Gly Lys Leu Pro His Ile Arg His Gln Thr Thr Tyr Lys Pro Tyr Ala
    610                 615                 620

tat ttt ttc gac ggg cgc gtc ggg tac gat gtg cag tat atg aac aag   1920
Tyr Phe Phe Asp Gly Arg Val Gly Tyr Asp Val Gln Tyr Met Asn Lys
625                 630                 635                 640

gac gag ctg att gcc gac att ttg aaa aac tac gaa cgt tat ttg atg   1968
Asp Glu Leu Ile Ala Asp Ile Leu Lys Asn Tyr Glu Arg Tyr Leu Met
                645                 650                 655

ttg ttg gat gat gtc ggt cag gaa ctg atg gcg cac gag cag gtg gaa   2016
Leu Leu Asp Asp Val Gly Gln Glu Leu Met Ala His Glu Gln Val Glu
            660                 665                 670

ttg gca gag taa                                                  2028
Leu Ala Glu
        675
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<210> 24
<211> 675
<212> PRT
<213> Neisseria meningitidis

<400> 24

Leu Ser Leu Ser Glu Phe Ile Glu Arg Arg Thr Ser Phe Asn Pro Met
1 5 10 15

Val Ile Leu Thr Thr Leu Phe Phe Val Cys Val Leu Val Val Leu Val
20 25 30

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

Val Ile Phe Thr Glu Phe Ser Trp Phe Tyr Val Leu Thr Phe Ser Ile
50 55 60

Phe Leu Gly Phe Leu Leu Ile Leu Ser Val Ser Ser Leu Gly Asn Ile
65 70 75 80

Arg Leu Gly Arg Asp Glu Asp Val Pro Glu Phe Gly Phe Leu Ser Trp
85 90 95

Leu Ala Met Leu Phe Ala Ala Gly Met Gly Val Gly Leu Met Phe Phe
100 105 110

Gly Val Ala Glu Pro Leu Met His Tyr Phe Ser Asp Ile Thr Ala Gly
115 120 125

Thr Pro Glu His Arg Gln Gln Gln Ala Leu Leu His Thr Val Phe His
130 135 140

Trp Gly Val His Ala Trp Ser Val Tyr Gly Thr Ile Ala Leu Ala Leu
145 150 155 160

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

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

Ile Asp Ile Met Ala Leu Leu Ala Thr Phe Phe Gly Ile Ile Thr Thr
195 200 205

Leu Gly Phe Gly Ala Ser Gln Leu Gly Ala Gly Leu Gln Glu Met Gly
210 215 220

Trp Ile Ala Glu Asn Ser Phe Ser Val Gln Val Leu Ile Ile Ala Ala
225 230 235 240

Val Met Ser Leu Ala Val Val Ser Ala Ile Ser Gly Val Gly Lys Gly
245 250 255

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

Phe Phe Val Leu Ala Ala Gly Pro Thr Val Tyr Leu Leu Ser Ala Phe
275 280 285

Gly Asp Asn Ile Gly Asn Tyr Leu Gly Asn Leu Val Arg Leu Ser Phe
290 295 300

Lys Thr Tyr Ala Tyr Glu Arg Glu His Lys Pro Trp Phe Glu Ser Trp
305 310 315 320

Thr Val Leu Tyr Trp Ala Trp Trp Cys Ser Trp Ala Pro Phe Val Gly
325 330 335

Leu Phe Ile Ala Arg Ile Ser Lys Gly Arg Thr Ile Arg Glu Phe Val
340 345 350

Phe Gly Val Leu Leu Ile Pro Gly Leu Phe Gly Val Leu Trp Phe Thr
355 360 365

Val Phe Gly Asn Thr Ala Ile Trp Leu Asn Asp Gly Val Ala Gly Gly
370 375 380

Met Leu Glu Lys Met Thr Ser Ser Pro Glu Thr Leu Leu Phe Lys Phe
385 390 395 400

Phe Asn Tyr Leu Pro Leu Pro Glu Leu Thr Ser Ile Val Ser Leu Leu
405 410 415

Val Ile Ser Leu Phe Phe Val Thr Ser Ala Asp Ser Gly Ile Tyr Val
420 425 430

Leu Asn Asn Ile Thr Ser Arg Asp Lys Gly Leu Ser Ala Pro Arg Trp
435 440 445

Gln Ala Val Met Trp Gly Val Leu Met Ser Ala Val Ala Val Leu Leu
450 455 460

Met Arg Ser Gly Gly Leu Gly Asn Leu Gln Ser Met Thr Leu Ile Val
465 470 475 480

Ser Leu Pro Phe Ala Leu Leu Met Leu Ile Met Cys Phe Ser Leu Trp
485 490 495

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

Thr Ser Val Phe Trp Thr Gly Gly Lys Trp Lys Glu Arg Leu Val Gln
515 520 525

Ile Met Ser Gln Thr Gln Glu Gln Asp Ile Leu Lys Phe Leu Lys Gln
530 535 540

Thr Ala Ser Pro Ala Met His Glu Leu Gln Arg Glu Leu Ser Glu Glu
545 550 555 560

Tyr Gly Leu Ser Val Arg Val Asp Lys Met Phe His Arg Asp Glu Pro
565 570 575

Ala Ile Glu Phe Val Ile Arg Lys Glu Thr Met Arg Asp Phe Met Tyr
580 585 590

Gly Ile Lys Ser Val Gly Gln Asp Val Ser Asp Gln Leu Ile Asn Asp
595 600 605

Gly Lys Leu Pro His Ile Arg His Gln Thr Thr Tyr Lys Pro Tyr Ala
610 615 620

Tyr Phe Phe Asp Gly Arg Val Gly Tyr Asp Val Gln Tyr Met Asn Lys
625 630 635 640

Asp Glu Leu Ile Ala Asp Ile Leu Lys Asn Tyr Glu Arg Tyr Leu Met
645 650 655

Leu Leu Asp Asp Val Gly Gln Glu Leu Met Ala His Glu Gln Val Glu
660 665 670

Leu Ala Glu
675

<210> 25
<211> 861
<212> DNA
<213> Neisseria meningitidis

<220>
<221> CDS
<222> (1)..(861)

<400> 25
atg aaa ccc tat tcc gcc aat ccc aac ctg acc gaa ccg cgc cgg ctg 48
Met Lys Pro Tyr Ser Ala Asn Pro Asn Leu Thr Glu Pro Arg Arg Leu

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1               5                  10                  15

cgc gtg ttg ctg att gcc gcc gcg ctg ggc ttt ctg ctg ctg atg ctg   96
Arg Val Leu Leu Ile Ala Ala Ala Leu Gly Phe Leu Leu Leu Met Leu
            20                  25                  30

gtc gtg ccg ctc gtc gcc gtg ttt tac gaa gcc tta aaa ggc ggt tgg   144
Val Val Pro Leu Val Ala Val Phe Tyr Glu Ala Leu Lys Gly Gly Trp
        35                  40                  45

gat ttg tac ctg aaa tcc tta aac gat ccc gaa gcg tgg tct gcc atc   192
Asp Leu Tyr Leu Lys Ser Leu Asn Asp Pro Glu Ala Trp Ser Ala Ile
    50                  55                  60

aaa ttg acg ctg att acc gcg ctg att gtc gtt ccc gtc aat gcc gta   240
Lys Leu Thr Leu Ile Thr Ala Leu Ile Val Val Pro Val Asn Ala Val
65                  70                  75                  80

ttg ggt gtg gcg atg gcg tgg ctg ctg acc cgt ttt gat ttt cgc ggc   288
Leu Gly Val Ala Met Ala Trp Leu Leu Thr Arg Phe Asp Phe Arg Gly
                85                  90                  95

aag cag ttg ctg acc acc ctg ctc gat ttg ccg ttt tcc gta tcg ccc   336
Lys Gln Leu Leu Thr Thr Leu Leu Asp Leu Pro Phe Ser Val Ser Pro
            100                 105                 110

gtg gtg gcc ggt ttg atg ttc gtc tta ttg ttc ggc gcg cat acg gca   384
Val Val Ala Gly Leu Met Phe Val Leu Leu Phe Gly Ala His Thr Ala
        115                 120                 125

ttg ggt ggc tgg ctc gaa gcg caa ggc ata cag att atc ttc gcc atc   432
Leu Gly Gly Trp Leu Glu Ala Gln Gly Ile Gln Ile Ile Phe Ala Ile
    130                 135                 140

ccc ggt att gtt ttg gcg acg ctg ttc gtt acc ttc ccc ttt gtc gca   480
Pro Gly Ile Val Leu Ala Thr Leu Phe Val Thr Phe Pro Phe Val Ala
145                 150                 155                 160

cgc gaa atc atc ccg ctg atg cag gca cag ggc gac agc gaa gaa cag   528
Arg Glu Ile Ile Pro Leu Met Gln Ala Gln Gly Asp Ser Glu Glu Gln
                165                 170                 175

gcg gca ttg ata ctc ggc gca agc ggc tgg cag atg ttt tgg cgc gtt   576
Ala Ala Leu Ile Leu Gly Ala Ser Gly Trp Gln Met Phe Trp Arg Val
            180                 185                 190

acc ctg ccc aac atc aaa tgg gcg tta ctc tac ggc atc atc ctc acc   624
Thr Leu Pro Asn Ile Lys Trp Ala Leu Leu Tyr Gly Ile Ile Leu Thr
```

195 200 205

aac gcc cgc gcg atg ggc gag ttc ggc gcg gtc agc gtg gta tcg gga 672
Asn Ala Arg Ala Met Gly Glu Phe Gly Ala Val Ser Val Val Ser Gly
210 215 220

cac ata cgc ggc gaa acc aac acc gtc ccg ctt ttg gtc gaa atc ttc 720
His Ile Arg Gly Glu Thr Asn Thr Val Pro Leu Leu Val Glu Ile Phe
225 230 235 240

tac aac gaa tac aac ttc acc ggc gca ttc gcc ctc tcc ggc gta ttg 768
Tyr Asn Glu Tyr Asn Phe Thr Gly Ala Phe Ala Leu Ser Gly Val Leu
245 250 255

gca ctt ttg gca ctg gcg acg ctg gcg gtg cag aac atc att acc aaa 816
Ala Leu Leu Ala Leu Ala Thr Leu Ala Val Gln Asn Ile Ile Thr Lys
260 265 270

tta caa gac aaa aaa ctc gcc gcc gcc gaa agg aat gca ata tga 861
Leu Gln Asp Lys Lys Leu Ala Ala Ala Glu Arg Asn Ala Ile
275 280 285

<210> 26
<211> 286
<212> PRT
<213> Neisseria meningitidis

<400> 26
Met Lys Pro Tyr Ser Ala Asn Pro Asn Leu Thr Glu Pro Arg Arg Leu
1 5 10 15

Arg Val Leu Leu Ile Ala Ala Ala Leu Gly Phe Leu Leu Leu Met Leu
20 25 30

Val Val Pro Leu Val Ala Val Phe Tyr Glu Ala Leu Lys Gly Gly Trp
35 40 45

Asp Leu Tyr Leu Lys Ser Leu Asn Asp Pro Glu Ala Trp Ser Ala Ile
50 55 60

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

Leu Gly Val Ala Met Ala Trp Leu Leu Thr Arg Phe Asp Phe Arg Gly
85 90 95

Lys Gln Leu Leu Thr Thr Leu Leu Asp Leu Pro Phe Ser Val Ser Pro

100 105 110

Val Val Ala Gly Leu Met Phe Val Leu Leu Phe Gly Ala His Thr Ala
115 120 125

Leu Gly Gly Trp Leu Glu Ala Gln Gly Ile Gln Ile Ile Phe Ala Ile
130 135 140

Pro Gly Ile Val Leu Ala Thr Leu Phe Val Thr Phe Pro Phe Val Ala
145 150 155 160

Arg Glu Ile Ile Pro Leu Met Gln Ala Gln Gly Asp Ser Glu Glu Gln
165 170 175

Ala Ala Leu Ile Leu Gly Ala Ser Gly Trp Gln Met Phe Trp Arg Val
180 185 190

Thr Leu Pro Asn Ile Lys Trp Ala Leu Leu Tyr Gly Ile Ile Leu Thr
195 200 205

Asn Ala Arg Ala Met Gly Glu Phe Gly Ala Val Ser Val Val Ser Gly
210 215 220

His Ile Arg Gly Glu Thr Asn Thr Val Pro Leu Leu Val Glu Ile Phe
225 230 235 240

Tyr Asn Glu Tyr Asn Phe Thr Gly Ala Phe Ala Leu Ser Gly Val Leu
245 250 255

Ala Leu Leu Ala Leu Ala Thr Leu Ala Val Gln Asn Ile Ile Thr Lys
260 265 270

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

<210> 27
<211> 495
<212> DNA
<213> Neisseria meningitidis

<220>
<221> CDS
<222> (1)..(495)

<400> 27
atg aaa aaa acc ctg ttg gca att gtt gcc gtt tcc gcc tta agt gcc 48

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

tgc cgg cag gcg gaa gag gga ccg ccg cct tta ccc cgg cag att agc   96
Cys Arg Gln Ala Glu Glu Gly Pro Pro Pro Leu Pro Arg Gln Ile Ser
            20                  25                  30

gac cgt tcg gtc gga cac tat tgc agt atg aac ctg acc gaa cac aac  144
Asp Arg Ser Val Gly His Tyr Cys Ser Met Asn Leu Thr Glu His Asn
        35                  40                  45

ggc ccc aaa gcc cag att ttc ttg aac ggc aaa ccc gat cag ccc gtt  192
Gly Pro Lys Ala Gln Ile Phe Leu Asn Gly Lys Pro Asp Gln Pro Val
    50                  55                  60

tgg ttc tcc acc atc aag cag atg ttc ggc tat acc aag ctg ccc gaa  240
Trp Phe Ser Thr Ile Lys Gln Met Phe Gly Tyr Thr Lys Leu Pro Glu
65                  70                  75                  80

gag cct aaa ggc atc cgc gtg att tac gtt acc gat atg ggc aat gtt  288
Glu Pro Lys Gly Ile Arg Val Ile Tyr Val Thr Asp Met Gly Asn Val
                85                  90                  95

acc gat tgg acg aat ccc aat gcc gac acg gag tgg atg gat gcg aaa  336
Thr Asp Trp Thr Asn Pro Asn Ala Asp Thr Glu Trp Met Asp Ala Lys
            100                 105                 110

aaa gcc ttt tac gtc atc gac agc ggc ttt atc ggc ggt atg ggt gcg  384
Lys Ala Phe Tyr Val Ile Asp Ser Gly Phe Ile Gly Gly Met Gly Ala
        115                 120                 125

gaa gac gcg ctg ccg ttc ggc aac aaa gag cag gct gag aaa ttt gca  432
Glu Asp Ala Leu Pro Phe Gly Asn Lys Glu Gln Ala Glu Lys Phe Ala
    130                 135                 140

aag gat aaa ggc ggt aag gtt gtc ggt ttc gac gat atg cct gat acc  480
Lys Asp Lys Gly Gly Lys Val Val Gly Phe Asp Asp Met Pro Asp Thr
145                 150                 155                 160

tat att ttc aaa taa                                            495
Tyr Ile Phe Lys
                165
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<210> 28
<211> 164
<212> PRT
<213> Neisseria meningitidis

<400> 28

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

Cys Arg Gln Ala Glu Glu Gly Pro Pro Pro Leu Pro Arg Gln Ile Ser
20 25 30

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

Gly Pro Lys Ala Gln Ile Phe Leu Asn Gly Lys Pro Asp Gln Pro Val
50 55 60

Trp Phe Ser Thr Ile Lys Gln Met Phe Gly Tyr Thr Lys Leu Pro Glu
65 70 75 80

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

Thr Asp Trp Thr Asn Pro Asn Ala Asp Thr Glu Trp Met Asp Ala Lys
100 105 110

Lys Ala Phe Tyr Val Ile Asp Ser Gly Phe Ile Gly Gly Met Gly Ala
115 120 125

Glu Asp Ala Leu Pro Phe Gly Asn Lys Glu Gln Ala Glu Lys Phe Ala
130 135 140

Lys Asp Lys Gly Gly Lys Val Val Gly Phe Asp Asp Met Pro Asp Thr
145 150 155 160

Tyr Ile Phe Lys

<210> 29
<211> 810
<212> DNA
<213> Neisseria meningitidis

<220>
<221> CDS
<222> (1)..(810)

<400> 29
atg aga cca tat gct act act att tat caa ctt ttt att ttg ttt att 48
Met Arg Pro Tyr Ala Thr Thr Ile Tyr Gln Leu Phe Ile Leu Phe Ile

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1               5                  10                  15

ggg agt gtt ttt act atg acc tca tgt gaa cct gtg aat gaa aag aca   96
Gly Ser Val Phe Thr Met Thr Ser Cys Glu Pro Val Asn Glu Lys Thr
            20                  25                  30

gat caa aaa gca gta agt gcg caa cag gct aaa gaa caa acc agt ttc  144
Asp Gln Lys Ala Val Ser Ala Gln Gln Ala Lys Glu Gln Thr Ser Phe
        35                  40                  45

aac aat ccc gag cca atg aca gga ttt gaa cat acg gtt aca ttt gat  192
Asn Asn Pro Glu Pro Met Thr Gly Phe Glu His Thr Val Thr Phe Asp
    50                  55                  60

ttt cag ggc acc aaa atg gtt atc ccc tat ggc tat ctt gca cgg tat  240
Phe Gln Gly Thr Lys Met Val Ile Pro Tyr Gly Tyr Leu Ala Arg Tyr
65                  70                  75                  80

acg caa gac aat gcc aca aaa tgg ctt tcc gac acg cca ggg cag gat  288
Thr Gln Asp Asn Ala Thr Lys Trp Leu Ser Asp Thr Pro Gly Gln Asp
                85                  90                  95

gct tac tcc att aat ttg ata gag att agc gtc tat tac aaa aaa acc  336
Ala Tyr Ser Ile Asn Leu Ile Glu Ile Ser Val Tyr Tyr Lys Lys Thr
            100                 105                 110

gac caa ggc tgg gtg ctc gaa cca tac aac cag caa aac aaa gcg cac  384
Asp Gln Gly Trp Val Leu Glu Pro Tyr Asn Gln Gln Asn Lys Ala His
        115                 120                 125

ttt atc caa ttt cta cgc gac ggt ttg gat agc gtg gac gat att gtt  432
Phe Ile Gln Phe Leu Arg Asp Gly Leu Asp Ser Val Asp Asp Ile Val
    130                 135                 140

atc cga aaa gat gcg tgt agt tta agc acg act atg gga gaa aga ttg  480
Ile Arg Lys Asp Ala Cys Ser Leu Ser Thr Thr Met Gly Glu Arg Leu
145                 150                 155                 160

ctt act tac ggg gtt aaa aaa atg cca tct gcc tat cct gaa tac gag  528
Leu Thr Tyr Gly Val Lys Lys Met Pro Ser Ala Tyr Pro Glu Tyr Glu
                165                 170                 175

gct tat gaa gat aaa aga cat att cct gaa aat cca tat ttt cat gaa  576
Ala Tyr Glu Asp Lys Arg His Ile Pro Glu Asn Pro Tyr Phe His Glu
            180                 185                 190

ttt tac tat att aaa aaa gga gaa aat ccg gcg att att act cat cgg  624
Phe Tyr Tyr Ile Lys Lys Gly Glu Asn Pro Ala Ile Ile Thr His Arg
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195 200 205

aac tat cat agg tat gga gag aac gat tac agc act agc gta ggt tcc 672
Asn Tyr His Arg Tyr Gly Glu Asn Asp Tyr Ser Thr Ser Val Gly Ser
210 215 220

tgt att aac ggt ttc acg gta cgg tat tac ccg ttt att cgg gaa aag 720
Cys Ile Asn Gly Phe Thr Val Arg Tyr Tyr Pro Phe Ile Arg Glu Lys
225 230 235 240

cag cag ctc aca cag cag gag ttg gta ggt tat cac caa caa gta gag 768
Gln Gln Leu Thr Gln Gln Glu Leu Val Gly Tyr His Gln Gln Val Glu
245 250 255

caa ttg gta cag agt ttt gta aac aat cca agt aaa aaa taa 810
Gln Leu Val Gln Ser Phe Val Asn Asn Pro Ser Lys Lys
260 265 270

<210> 30
<211> 269
<212> PRT
<213> Neisseria meningitidis

<400> 30
Met Arg Pro Tyr Ala Thr Thr Ile Tyr Gln Leu Phe Ile Leu Phe Ile
1 5 10 15

Gly Ser Val Phe Thr Met Thr Ser Cys Glu Pro Val Asn Glu Lys Thr
20 25 30

Asp Gln Lys Ala Val Ser Ala Gln Gln Ala Lys Glu Gln Thr Ser Phe
35 40 45

Asn Asn Pro Glu Pro Met Thr Gly Phe Glu His Thr Val Thr Phe Asp
50 55 60

Phe Gln Gly Thr Lys Met Val Ile Pro Tyr Gly Tyr Leu Ala Arg Tyr
65 70 75 80

Thr Gln Asp Asn Ala Thr Lys Trp Leu Ser Asp Thr Pro Gly Gln Asp
85 90 95

Ala Tyr Ser Ile Asn Leu Ile Glu Ile Ser Val Tyr Tyr Lys Lys Thr
100 105 110

Asp Gln Gly Trp Val Leu Glu Pro Tyr Asn Gln Gln Asn Lys Ala His
115 120 125

Phe Ile Gln Phe Leu Arg Asp Gly Leu Asp Ser Val Asp Asp Ile Val
130 135 140

Ile Arg Lys Asp Ala Cys Ser Leu Ser Thr Thr Met Gly Glu Arg Leu
145 150 155 160

Leu Thr Tyr Gly Val Lys Lys Met Pro Ser Ala Tyr Pro Glu Tyr Glu
165 170 175

Ala Tyr Glu Asp Lys Arg His Ile Pro Glu Asn Pro Tyr Phe His Glu
180 185 190

Phe Tyr Tyr Ile Lys Lys Gly Glu Asn Pro Ala Ile Ile Thr His Arg
195 200 205

Asn Tyr His Arg Tyr Gly Glu Asn Asp Tyr Ser Thr Ser Val Gly Ser
210 215 220

Cys Ile Asn Gly Phe Thr Val Arg Tyr Tyr Pro Phe Ile Arg Glu Lys
225 230 235 240

Gln Gln Leu Thr Gln Gln Glu Leu Val Gly Tyr His Gln Gln Val Glu
245 250 255

Gln Leu Val Gln Ser Phe Val Asn Asn Pro Ser Lys Lys
260 265

<210> 31
<211> 285
<212> DNA
<213> Neisseria meningitidis

<220>
<221> CDS
<222> (1)..(285)

<400> 31
atg aag caa gtc aag aag tcg tct tat ttt aaa tat caa aaa agg aaa 48
Met Lys Gln Val Lys Lys Ser Ser Tyr Phe Lys Tyr Gln Lys Arg Lys
1 5 10 15

aaa acg atg aac atc gtt aaa aaa tac gct gta aaa gca gcc ttg gca 96
Lys Thr Met Asn Ile Val Lys Lys Tyr Ala Val Lys Ala Ala Leu Ala
20 25 30

gcc ggt atc ttc aca ccg gcc att gtt atg gca gat acc ttt gat cca 144
Ala Gly Ile Phe Thr Pro Ala Ile Val Met Ala Asp Thr Phe Asp Pro
35 40 45

tcc gcg att ggt acg caa gta gcg aat gta atc atg ggt ttc gtg tca 192
Ser Ala Ile Gly Thr Gln Val Ala Asn Val Ile Met Gly Phe Val Ser
50 55 60

atg gtt tcc gcc gtg ggt atg gcg gcc att acc gtg att ctt gca atc 240
Met Val Ser Ala Val Gly Met Ala Ala Ile Thr Val Ile Leu Ala Ile
65 70 75 80

caa ggc ttc aaa atg gct tgg agc atg att aaa tct gtc aaa taa 285
Gln Gly Phe Lys Met Ala Trp Ser Met Ile Lys Ser Val Lys
85 90 95

<210> 32
<211> 94
<212> PRT
<213> Neisseria meningitidis

<400> 32
Met Lys Gln Val Lys Lys Ser Ser Tyr Phe Lys Tyr Gln Lys Arg Lys
1 5 10 15

Lys Thr Met Asn Ile Val Lys Lys Tyr Ala Val Lys Ala Ala Leu Ala
20 25 30

Ala Gly Ile Phe Thr Pro Ala Ile Val Met Ala Asp Thr Phe Asp Pro
35 40 45

Ser Ala Ile Gly Thr Gln Val Ala Asn Val Ile Met Gly Phe Val Ser
50 55 60

Met Val Ser Ala Val Gly Met Ala Ala Ile Thr Val Ile Leu Ala Ile
65 70 75 80

Gln Gly Phe Lys Met Ala Trp Ser Met Ile Lys Ser Val Lys
85 90

<210> 33
<211> 966
<212> DNA
<213> Neisseria meningitidis

<220>
<221> CDS
<222> (1)..(966)

<400> 33
gtg aaa ccg cgt ttt tat tgg gca gcc tgc gcc gtc ctg ctg acc gcc 48
Val Lys Pro Arg Phe Tyr Trp Ala Ala Cys Ala Val Leu Leu Thr Ala
1 5 10 15

tgt tcg ccc gaa cct gcc gcc gaa aaa act gta tcc gcc gca tcc gca 96
Cys Ser Pro Glu Pro Ala Ala Glu Lys Thr Val Ser Ala Ala Ser Ala
20 25 30

tct gcc gcc acg ctg acc gtg ccg acc gcg cgg ggc gat gcc gtt gtg 144
Ser Ala Ala Thr Leu Thr Val Pro Thr Ala Arg Gly Asp Ala Val Val
35 40 45

ccg aag aat ccc gaa cgc gtc gcc gtg tac gac tgg gcg gcg ttg gat 192
Pro Lys Asn Pro Glu Arg Val Ala Val Tyr Asp Trp Ala Ala Leu Asp
50 55 60

acg ctg acc gaa ttg ggc gtg aat gtg ggc gca acc acc gcg ccg gtg 240
Thr Leu Thr Glu Leu Gly Val Asn Val Gly Ala Thr Thr Ala Pro Val
65 70 75 80

cgc gtg gat tat ttg cag cct gca ttt gac aag gcg gca acg gtg ggg 288
Arg Val Asp Tyr Leu Gln Pro Ala Phe Asp Lys Ala Ala Thr Val Gly
85 90 95

acg ctg ttc gag ccc gat tac gaa gcc ctg cac cgc tac aat cct cag 336
Thr Leu Phe Glu Pro Asp Tyr Glu Ala Leu His Arg Tyr Asn Pro Gln
100 105 110

ctt gtc att acc ggc ggg ccg ggc gcg gaa gcg tat gaa cag tta gcg 384
Leu Val Ile Thr Gly Gly Pro Gly Ala Glu Ala Tyr Glu Gln Leu Ala
115 120 125

aaa aac gcg acc acc ata gat ctg acg gtg gac aac ggc aat atc cgc 432
Lys Asn Ala Thr Thr Ile Asp Leu Thr Val Asp Asn Gly Asn Ile Arg
130 135 140

acc agc ggc gaa aag cag atg gag acc ttg gcg cgg att ttc ggc aag 480
Thr Ser Gly Glu Lys Gln Met Glu Thr Leu Ala Arg Ile Phe Gly Lys
145 150 155 160

gaa gcg cgc gcg gcg gaa ttg aag gcg cag att gac gcg ctg ttc gcc 528
Glu Ala Arg Ala Ala Glu Leu Lys Ala Gln Ile Asp Ala Leu Phe Ala
165 170 175

caa acg cgc gaa gcc gcc aaa ggc aaa gga cgc ggg ctg gtg ctg tcg 576
Gln Thr Arg Glu Ala Ala Lys Gly Lys Gly Arg Gly Leu Val Leu Ser
180 185 190

gtt acg ggc aac aag gtg tcc gcc ttc ggc acg cag tcg cgg ttg gca 624
Val Thr Gly Asn Lys Val Ser Ala Phe Gly Thr Gln Ser Arg Leu Ala
195 200 205

agt tgg ata cac ggc gac atc ggc cta ccg cct gta gac gaa tct tta 672
Ser Trp Ile His Gly Asp Ile Gly Leu Pro Pro Val Asp Glu Ser Leu
210 215 220

cgc aac gag ggg cac ggg cag cct gtt tcc ttc gaa tac atc aaa gag 720
Arg Asn Glu Gly His Gly Gln Pro Val Ser Phe Glu Tyr Ile Lys Glu
225 230 235 240

aaa aac ccc gat tgg att ttc atc atc gac cgt acc gcc gcc atc ggg 768
Lys Asn Pro Asp Trp Ile Phe Ile Ile Asp Arg Thr Ala Ala Ile Gly
245 250 255

cag gaa ggg ccg gcg gct gtc gaa gta ttg gat aac gcg ctg gta cgc 816
Gln Glu Gly Pro Ala Ala Val Glu Val Leu Asp Asn Ala Leu Val Arg
260 265 270

ggc acg aac gct tgg aag cgc aag caa atc atc gtc atg cct gcc gcg 864
Gly Thr Asn Ala Trp Lys Arg Lys Gln Ile Ile Val Met Pro Ala Ala
275 280 285

aac tac att gtc gcg ggc ggc gcg cgg cag ttg att cag gcg gcg gag 912
Asn Tyr Ile Val Ala Gly Gly Ala Arg Gln Leu Ile Gln Ala Ala Glu
290 295 300

cag ttg aag gcg gcg ttt aaa aag gca gaa ccc gtt gcg gcg ggg aaa 960
Gln Leu Lys Ala Ala Phe Lys Lys Ala Glu Pro Val Ala Ala Gly Lys
305 310 315 320

aag tag 966
Lys

<210> 34
<211> 321
<212> PRT
<213> Neisseria meningitidis

<400> 34
Val Lys Pro Arg Phe Tyr Trp Ala Ala Cys Ala Val Leu Leu Thr Ala

1 5 10 15

Cys Ser Pro Glu Pro Ala Ala Glu Lys Thr Val Ser Ala Ala Ser Ala
20 25 30

Ser Ala Ala Thr Leu Thr Val Pro Thr Ala Arg Gly Asp Ala Val Val
35 40 45

Pro Lys Asn Pro Glu Arg Val Ala Val Tyr Asp Trp Ala Ala Leu Asp
50 55 60

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

Arg Val Asp Tyr Leu Gln Pro Ala Phe Asp Lys Ala Ala Thr Val Gly
85 90 95

Thr Leu Phe Glu Pro Asp Tyr Glu Ala Leu His Arg Tyr Asn Pro Gln
100 105 110

Leu Val Ile Thr Gly Gly Pro Gly Ala Glu Ala Tyr Glu Gln Leu Ala
115 120 125

Lys Asn Ala Thr Thr Ile Asp Leu Thr Val Asp Asn Gly Asn Ile Arg
130 135 140

Thr Ser Gly Glu Lys Gln Met Glu Thr Leu Ala Arg Ile Phe Gly Lys
145 150 155 160

Glu Ala Arg Ala Ala Glu Leu Lys Ala Gln Ile Asp Ala Leu Phe Ala
165 170 175

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

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

Ser Trp Ile His Gly Asp Ile Gly Leu Pro Pro Val Asp Glu Ser Leu
210 215 220

Arg Asn Glu Gly His Gly Gln Pro Val Ser Phe Glu Tyr Ile Lys Glu
225 230 235 240

Lys Asn Pro Asp Trp Ile Phe Ile Ile Asp Arg Thr Ala Ala Ile Gly
245 250 255

Gln Glu Gly Pro Ala Ala Val Glu Val Leu Asp Asn Ala Leu Val Arg

260 265 270

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

Asn Tyr Ile Val Ala Gly Gly Ala Arg Gln Leu Ile Gln Ala Ala Glu
290 295 300

Gln Leu Lys Ala Ala Phe Lys Lys Ala Glu Pro Val Ala Ala Gly Lys
305 310 315 320

Lys

<210> 35
<211> 24
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<220>
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<400> 35
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<210> 36
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<213> Artificial Sequence

<220>
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<400> 36
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<210> 37
<211> 24
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Oligonucleotide

<400> 37
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<210> 38
<211> 20
<212> DNA
<213> Artificial Sequence

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<400> 38
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<210> 39
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<213> Artificial Sequence

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<400> 39
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<210> 40
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<212> DNA
<213> Artificial Sequence

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<210> 41
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<212> DNA

<213> Artificial Sequence

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<400> 41
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<210> 42
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<210> 43
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<400> 43
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<210> 44
<211> 22
<212> DNA
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<210> 45
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<212> DNA
<213> Artificial Sequence

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<400> 45
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<210> 46
<211> 25
<212> DNA
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<400> 46
aaccacgatt tcttctttct tcttc 25

<210> 47
<211> 20
<212> DNA
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<400> 47
atgagaccat atgctactac 20

<210> 48
<211> 21
<212> DNA
<213> Artificial Sequence

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<400> 48
tttttttactt ggattgttta c 21